

CURRICULUM VITAE
George M. Weinstock, Ph.D.

DATE September 26, 2014

BIRTHDATE February 6, 1949

CITIZENSHIP USA

ADDRESS The Jackson Laboratory for Genomic Medicine
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PRESENT POSITION Associate Director for Microbial Genomics
Professor
Jackson Laboratory for Genomic Medicine

UNDERGRADUATE EDUCATION

1966-1967	Washington University
1967-1970	University of Michigan
1970	B.S. (with distinction) Biophysics, Univ. Mich.

GRADUATE EDUCATION

1970-1977	PHS Predoctoral Trainee, Dept. Biology, Mass. Institute of Technology, Cambridge, MA
1977	Ph.D., Advisor: David Botstein Thesis title: Genetic and physical studies of bacteriophage P22 genomes containing translocatable drug resistance elements.

POSTDOCTORAL TRAINING

1977-1980	Postdoctoral Fellow, Department of Biochemistry Stanford University Medical School, Stanford, CA. Advisor: Dr. I. Robert Lehman.
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ACADEMIC POSITIONS/EMPLOYMENT/EXPERIENCE

1980-1981	Staff Scientist, Molec. Gen. Section, NCI-Frederick Cancer Research Facility, Frederick, MD
1981-1983	Staff Scientist, Laboratory of Genetics and Recombinant DNA, NCI-Frederick Cancer Research Facility, Frederick, MD
1981-1984	Adjunct Associate Professor, Department of Biological Sciences, University of Maryland, Baltimore County, Catonsville, MD
1983-1984	Senior Scientist and Head, DNA Metabolism Section, Lab. Genetics and Recombinant DNA, NCI-Frederick Cancer Research Facility, Frederick, MD
1984-1990	Associate Professor with tenure (1985) Department of Biochemistry and Molecular Biology, Medical School, The University of Texas-Houston Health Science Center
1985-2008	Member, Graduate School of Biomedical Sciences, UTHHSC
1986-1990	Instructor, Advanced Bacterial Genetics Course, Cold Spring Harbor Laboratory, New York
1990-1993	Instructor, Bacterial Genetics and Pathogenesis International Centre for Gen. Engineering and Biotechnology, Trieste, Italy
1990-2001	Professor, Department of Biochemistry and Molecular Biology, Medical School, The University of Texas-Houston Health Science Center
1990-2008	Professor (Adjunct Professor, 2001) Department of Microbiology and Molecular Genetics, Medical School, The University of Texas-Houston Health Science Center
1993-1994	Fellow and Visiting Professor, Stanford DNA Sequencing and Technology Center, Stanford University School of Medicine, Stanford, CA
1995-2001	Co-Director, Center for the Study of Emerging and Re-emerging Pathogens, The University of Texas-Houston Medical School
1999-2008	Co-Director, Human Genome Sequencing Center, Baylor College of Medicine
1999-2008	Adjunct Professor, Professor (2001), Dept. of Human & Molec. Gen., Baylor College of Medicine

1999-2008 Adjunct Professor, Department of Health Informatics
The University of Texas-Houston School of Allied Health Sciences
2001-2008 Member, Genetics Graduate Program, Baylor College of Medicine
2001-2010 Member (adjunct 2009), Structural and Computational Biochemistry and Molecular Biology
Graduate Program, Baylor College of Medicine
2001-2008 Professor, Department of Molecular Virology and Microbiology, Baylor College of Medicine
2006-2010 Member (adjunct 2009), Translational Biology and Molecular Medicine Graduate Program
Baylor College of Medicine
2008-2014 Associate Director, The Genome Institute, Washington University School of Medicine
2008-2014 Professor, Dept. Genetics, Washington University School of Medicine
2008-2014 Professor, Dept. Molecular Microbiology, Washington University School of Medicine
2008-2009 Member, Center for Genome Sciences, Wash. U. Sch. Med.
2008-2014 Member, Center for Women's Infectious Disease Research, Wash. U. Sch. Med.
2008-2014 Member, Digestive Diseases Research Core Center, Wash. U. Sch. Med.
2009-2014 Member, Molecular Genetics & Genomics Graduate Program, Wash. Univ.
2009-2014 Member, Molecular Microbiology Graduate Program, Wash. Univ.
2009-2014 Member, Computational and Systems Biology Graduate Program, Wash. Univ.
2009-2014 Member, Human and Statistical Genetics Graduate Program, Wash. Univ.
2013-2014 Visiting Distinguished Adjunct Professor, King Abdulaziz University, Jeddah, Saudi Arabia
2013-Present Professor and Associate Director for Microbial Genomics, Jackson Lab. for Genomic Medicine
2013-Present Faculty Member, Universidad El Bosque, Colombia
2014-Present Visiting Professor, Univ. Connecticut Health Center

HONORS AND AWARDS

1977-1979 Fellow of the Jane Coffin Childs Memorial Fund for Medical Research
1979-1980 Fellow of the Bank of America - Giannini Foundation
1985-1997 Deans' Teaching Excellence List, Univ. Texas Houston Health Sciences Center
1987 John P. McGovern Outstanding Teacher Award, Univ. Texas Grad. Sch. Biomed. Sci.
1993 Human Genome Program Senior Fellow
1994 Fellow of the American Academy of Microbiology
1994-1995 Vice-President/President Elect, Graduate Faculty, UTHHSC Grad. Sch. Biomed. Sci.
1995-1996 President, Graduate Faculty, UTHHSC Grad. Sch. Biomed. Sci.
1999 Special Commendation, UTHHSC Graduate School of Biomedical Sciences
2002-2005 Waksman Foundation for Microbiology Lecturer
2007 Univ. Texas Chancellor's Entrepreneurship and Innovation Award
2008 Fellow, American Association for the Advancement of Science

OTHER EXPERIENCE, CONSULTING RELATIONSHIPS, AND BOARD MEMBERSHIPS:

1985 NIH Microbial Genetics and Physiology Study Section
1985 Search Committee for Chairman of Genetics Dept., M.D. Anderson Cancer Ctr.
1985-1990 Consultant - Cactus Feeders, Inc. (Dumas, TX)
1989-1991 Scientific Advisory Board, Center for Comparative Animal Genetics, Institute for Biosciences,
Texas A & M University
1989-1993 Consultant - Pfizer, Inc.(Groton, CT)
1990 NIH Microbial Genetics and Physiology Study Section
1990 National Center for Human Genome Research, Site Visit Team
1991 National Center for Human Genome Research, Site Visit Team
1991 American Society for Microbiology, Microbial Genomics Committee
1991-1995 Consultant - NASA/Johnson Space Center (Houston)
1992 Oklahoma Center for Advancement Sci. & Tech. Sci. Review Panel, Chairman
1992 USDA Program on Mechanisms of Animal Disease, Grant Review Panel
1992 Oklahoma Center for Advancement Sci. & Tech. Performance Evaluation Panel

1992-1994 Consultant - Dalkon Shield Trust (Denver, CO)

1993 USDA Program on Mech. Animal Disease, Grant Review Panel, Manager

1993 Oklahoma Center for Advancement Sci. & Tech. Performance Evaluation Panel

1993-1995 Councilor, Division H, American Society for Microbiology

1993-1996 Vice-Chairman, Conferences Committee, ASM

1996 Natl. Center for Human Genome Res., NIH, study section

1996-2002 Chairman, Conferences Committee, ASM

1996-1998 Panel of Scientific Advisors, Pilot Projects for Human Gen. Proj., NHGRI, NIH

1996-1997 Faculty Search Committee, Center for Comparative Medicine, Institute for Bioscience and Technology, Texas A & M Univ.

1996-1997 Search Comm for Chairman, Dept. of Biochem., M.D. Anderson Cancer Center

1996-1997 Panel member, Genomics of Sexually Transmitted Dis. Pathogens, NIAID, NIH

1997 Panel member, Workshop on Exploiting *M. tuberculosis* Genome, NIAID, NIH

1997 Panel member, Planning Workshop on Infectious Diseases, NIDR, NIH

1998 Advisory Board, *Neisseria gonorrhoeae* Genome project, Univ. Oklahoma

1998 Genome Study Section, NIHGR, NIH

1998-1999 Consultant - Lederle-Praxis Biologicals (Rochester, NY)

1999 Advisory Board, Microbial Genome Projects, Univ. Wisconsin

1999 Panel Member, Univ. Cal. Sci. & Tech. Panel, Pres. Council on Natl. Labs.

1999-2003 Consultant - Phytera, Inc. (Worcester, MA)

1999-2005 Consultant - SeqWright (Houston)

2000 Peer Review Panel, Ontario Genomics Institute, Toronto CANADA

2000 Peer Review Panel, Atlantic Genome Center, Halifax CANADA

2000-2001 Consultant - Sequel, Inc., (Pittsburgh, PA), Scientific Advisory Board

2000-2004 Consultant - Prokaryon (Houston), Founder

2000-2005 Oral Pathogens Sequencing Database Advisory Group, NIDCR, NIH

2000-2006 Consultant - Xenogen, Inc. (Oakland, CA), Scientific Advisory Board

2000-2006 Divn. Rev. Comm., Biosciences Divn, Los Alamos National Lab., (Chair, 2004)

2000-2007 Scientific Advisory Comm., DOE - Joint Genome Institute (Chair, 2000-2001)

2001 Review Panel, Genome Canada

2001 NIH Study Section, Bacteriology and Microbiology I

2001 NIH-CSR Infectious Diseases and Mycology Working Group

2001 Letters of Intent Panel, Genome Canada

2001 NIH Special Emphasis Panel, Chairman

2002 Due Diligence Review, Genome Canada

2002 Review Panel, Beckman Institute, California Institute of Technology

2002 NIH Special Emphasis Panel, Chairman

2002 Interagency Working Group on Domestic Animal Genomics

2002 NHGRI workshop on The Future of Genomics

2002-2006 Pathogen Sequencing Advisory Group, Wellcome Trust Sanger Institute

2003-2007 National Advisory Council for Human Genome Research

2003-2009 Member, Genome Canada Interim Science Review Committee

2003-2006 LANL Threat Reduction Program Review Committee

2003-2007 NHGRI / NIH ENCODE Scientific Advisory Panel (Chair)

2003 Review Panel, Genome Atlantic Genome Center

2004 BioHouston Genomics Task Force

2004 Rev. Panel, Functional Genomics of Mucosal Immunity (Chair), Genome Canada

2004-2006 Consultant - Codon Biosciences (Houston), Founder

2005-2008 Scientific Advisory Panel, Center for Rodent Genetics, NIEHS

2005 Genome Canada Platform Review Committee (Chair)

2005-2008 Maize Genome Project External Advisory Committee (Chair)

2006-2007 Consultant - Vantage Point Venture Partners (San Bruno, CA)

2006-2008	GCC Research Consortia Advisory Committee
2007	Co-Chair, Human Microbiome Project Workshop
2007	Comparative Medicine Review Committee, National Center Research Resources
2007	Review Comm. for Technol. Development Competition, Genome Canada (Chair)
2007-2009	Scientific Advisory Board - Cobalt Biofuels (Mountain View, CA)
2007-2010	Sci. Adv. Board, Center for Cancer Systems Biology, Dana-Farber Cancer Inst.
2007-2008	Intl Coordination Board, European Union Human Metagenomics Project
2008	Genomics, Computational Biology and Technology Study Section
2008	Applied Genomics Innovation Program Panel, Genome BC
2008-2011	Scientific Adv. Board, Metagenomics of the Human Intestinal Tract Consortium
2008-2010	ORALGEN Database Advisory Board
2008-Present	Steering Comm, Midwest Reg. Cen. Excell. Biodefense & Emerging Inf. Dis.
2008	NIH Genetic Variation and Evolution, Special Emphasis Panel (Chair)
2008	Due Diligence Team, Min. Dével. Écon., de l'Innov. et de l'Export. du Québec
2008-Present	International Human Microbiome Consortium, Steering Comm. (co-Chair, 2010)
2008-2013	Intl Human Microbiome Consortium, Data Release Working Group (co-Chair)
2008	American Academy of Microbiology Workshop on Bioinformatics
2009	Due Diligence Panel, Appl. Genomics Res. Bioprod or Crops, Genome Canada
2009-Present	Scientific Advisory Board, Wellcome Trust Sanger Institute
2009-2011	Board of Trustees, Molecular Sciences Institute, Berkeley, CA (Secretary)
2009	Review Committee, Wellcome Trust Centre for Human Genetics (Oxford)
2009-2013	Advisory Board, Center for Molecular Epidemiology (Copenhagen)
2009	Scientific Review Committee, Intl Collaboration to Sequence the Atlantic Salmon Genome (ICSASG)
2010	Blue Ribbon Panel on Genomics Research (NIAID, DMID)
2010-Present	NHLBI Lung Human Microbiome Project Steering Committee (co-chair 2010)
2010-Present	Scientific Advisory Board, Michael Smith Genome Sciences Centre (Vancouver)
2010-Present	Board of Directors, Genome Canada; Program Committee chairman
2010-2011	NHLBI Lung Human Microbiome Project Publications Committee, chair
2010-2011	NHLBI Lung Human Microbiome Project Sequencing Committee, chair
2011	NIH Workshop on Future of Human Microbiome Research
2011	White House briefing on Microbial Forensics
2011-2012	Genome Canada SIAC Bioinformatics Working Group
2011	WHO Grand Challenges in Genomics for Public Health in Developing Countries, Expert Panel
2011-Present	Committee on Elections, American Academy of Microbiology (Chair, 2014)
2011-Present	Scientific Advisory Board, Program for Health, Philippine Genome Center, University of the Philippines
2012	Next-generation sequencing workshop, Genentech
2012-Present	Sci. Adv. Board EU METACARDIS project
2012-2013	Genome Canada Disruptive Technology Task Force
2013-Present	Global Microbial Identifier Task Force
2013-2014	Scientific Advisory Board, Real Time Genomics
2013-Present	Scientific Advisory Board, OpGen
2013-Present	Advisory Panel, Vervet Research Colony, Wake Forest Univ. Primate Cen.
2013-Present	Inspiration Mars Personalized Medicine Team
2014	NSERC Discovery Frontiers: Advancing Big Data Science in Genomics Research Panel
2014-Present	Science & Technol. Innov. Centres Oversight Comm, Genome Canada

MAJOR INVITED PROFESSORSHIPS AND LECTURESHIPS

1979-1984:	C.N.R.S. (Gif-sur-Yvette, France)
	Cold Spring Harbor Laboratory (Cold Spring Harbor, NY)
	Conference on DNA Replication (Corsica, France 1980)

Conference on Mutagenesis (Toulouse, France 1981)
Cornell University (Biochemistry) (Ithaca, NY)
Duke University Medical School (Biochemistry) (Durham, NC)
Gordon Conference on Nucleic Acids (1979)
Johns Hopkins University (Biology) (Washington, DC)
Massachusetts Institute of Technology (Biology) (Cambridge, MA)
National Institute for Medical Research (Mill Hill, UK)
Penn State Univ. Summer Symposium (Philadelphia, PA 1982)
Roswell Park Memorial Institute (Molecular Biology) (Buffalo, NY)
Stanford University Medical School (Biochemistry) (Stanford, CA)
University of Arizona (Molecular Biology) (Tempe, AZ)
University of California at Berkeley (Molecular Biology) (Berkeley, CA)
University of California at Irvine Medical School (Biochemistry) (Irvine, CA)
U.C.L.A. Medical School (Biochemistry) (Los Angeles, CA)
University of Illinois (Biochemistry) (Urbana, IL)
University of Maryland, Baltimore County (Biology) (College Park, MD)
University of Massachusetts Medical School (Microbiology) (Worcester, MA)
University of Pennsylvania (Biology) (Philadelphia, PA)
University of Utah (Biology) (Salt Lake City, UT)
Washington State University (Genetics) (Pullman, WA)

1985-1989: Abbott Laboratories, Inc. (Drug Discovery) (Abbott Park, IL)
Baylor College of Medicine (Biochemistry) (Houston, TX)
Baylor College of Medicine (Cell Biology) (Houston, TX)
Burroughs-Wellcome, Inc. (1985, Microbiology) (Durham, NC)
Burroughs-Wellcome, Inc. (1988, Microbiology) (Durham, NC)
California Institute of Technology (Biology) (Pasadena, CA)
Carnegie Mellon University (Biological Sciences) (Pittsburgh, PA)
Columbia Univ., Col. of Physicians & Surgeons (Microbiology) (New York, NY)
DNAX, Inc. (Palo Alto, CA)
DuPont, Inc. (1986, Molecular Biology) (Wilmington, DE)
DuPont, Inc. (1987, Molecular Biology) (Wilmington, DE)
Fort Dodge Laboratories (Fort Dodge, IA)
ICN-UCLA Symposium on Gene Expression (Los Angeles, CA)
Lost Pines Molecular Biology Conference (Smithville, TX)
M.D. Anderson (Genetics) (Houston, TX)
Pfizer, Inc. (Animal Health)
Rice University (Biochemistry) (Houston, TX)
Squibb Institute for Medical Research (New Brunswick, NJ)
Univ. Tennessee Health Science Center (Microbiology) (Memphis, TN)
Univ. Texas Health Science Center - Dallas (1986, Microbiol.) (Dallas, TX)
Univ. Texas Health Science Center - Dallas (1987, Microbiol.) (Dallas, TX)
Univ. Texas Medical Branch - Galveston (Microbiology) (Galveston, TX)
University of Colorado (Molecular Biology) (Boulder, CO)
Western Veterinary Association Meeting

1990-1994: ASM Ann. Mtg, Seminar "Analysis of Prokaryotic Genomes"
ASM Ann. Mtg, Seminar "Molec. Biol. of Bact. Respiratory Dis."
ASM Ann. Mtg, Seminar "Virul. Mech. of Vet. Bact. Pathogens"
Baylor College of Medicine (Biochemistry)
Baylor College of Medicine (Molecular Genetics)
CNRS, Gif-sur-Yvette (Enzymologie)

CNRS, Toulouse (Toxicologie)
Cold Spring Harbor Lab (Adv. Bacterial Genetics Course)
Conference "Breakthroughs in Genetics" (Cold Spring Harbor)
Conference on "Complex Processes in Prokaryotes"
E. coli Genome Conference (Woods Hole)
Eli Lilly
Institut Curie (Orsay, France)
International Marine Biotech. Conference (Tromso, Norway)
Max Planck Institut (Marburg Germany)
Michigan State University (Center for Microbial Ecology)
Microcide, Inc. (Mountain View)
NASA/Johnson Space Center (Microbiology)
Pfizer, Inc. (Animal Health)
Robert Lehman Symposium (Sonoma)
Rockefeller University
Spirochete Gordon Conference
Symposium on Mapping and Sequencing Small Genomes (Paris)
Symposium on Biochemical and Metabolic Diversity (Houston)
Texas Branch, ASM Meeting
Texas branch, ASM Annual Meeting (Austin)
Univ. Texas Medical School (Pathology)
University of Arizona (Molecular Biology)
University of Arizona (Veterinary Science)
University of Illinois (Microbiology)
University of Maryland (Microbiology)
University of Utah (Cell, Molecular, and Developmental)
University of Utrecht
University of Washington (Depts. of Microbiol. & Biotechnol.)
Wind River Conference on Prokaryotic Biology (Keynote)

1995-1999: 5th Annual E. coli and Small Genome Conference, Snowbird, UT
5th Intl. Symp. Genet. of Streptococci, Enterococci and Lactococci (Vichy)
6th Annual E. coli and Small Genome Conference, Lake Arrowhead, CA
7th Conference on Small Genomes (Washington DC)
American Society of Human Genetics Annual Meeting
Analytical Genetics Conference (Snowbird)
ASM Annual Meeting (Chicago)
ASM Annual Meeting (Miami)
Baylor College of Medicine (Biochemistry)
Baylor College of Medicine (Molecular Genetics)
Baylor College of Medicine, Dept. Microbiology and Immunology
Blaffer Seminar, M.D. Anderson Cancer Center
Center for Disease Control, Atlanta
Cold Spring Harbor Lab (Adv. Bacterial Genetics Course)
Conf. "Genome Sequencing of STD Pathogens", NIAID, NIH
Conference on Analytical Genetics, Snowbird, UT
ESPE Dental-Medizin GmbH & Co.KG (Munich)
Genetics Work Group (NIDCR,NIH)
Genomics and Infectious Disease Conference (Wuerzburg, Germany)
Gordon Conference on Biology of Spirochetes (Ventura, CA)
Gordon Conference on Microbial Population Biology
Hanford Conference on Microbial Genomes

INSERM Workshop: Pulsed Field Gel Electrophoresis (Paris)
Institute of Bioscience and Technology (Texas A&M University)
Institute of Bioscience and Technology, Texas A&M University
Keck Center for Computational Biology Annual Retreat (Galveston)
Los Alamos National Laboratory (Theoretical Biology)
Microbial Biodiversity Conference (Chicago)
Microbial Pathogenesis and Host Response (Cold Spring Harbor)
NASA Symposium on Research for the NASA-Mir Program
New England Biolabs (Boston)
Phytera (Worcester, MA)
Prairie View A&M (Biology)
Praxis Biologicals, Rochester, NY
Rice University (Biochemistry)
Rice University (RABIES)
Rocky Mountain Laboratories, NIAID, NIH
Sequencing of Bacterial Genomes (England)
SmithKline-Beecham (Anti-infectives Division)
STD Centers Annual P.I. Meeting (NIH)
STD Genomics Workshop (Santa Fe Institute)
SUNY-Albany (Biology)
Texas A&M University (Genetics)
Texas Branch ASM Meeting (College Station)
Univ. Oregon Health Science Center (Microbiology)
Univ. Washington (Molecular Biotechnology)
University of Georgia (Biochemistry and Microbiology)
University of Guelph (Biochemistry)
University of North Texas - Texas Women's University (Denton)
University of Tennessee (Microbiol, Biochem, Cell & Molecular Biology)
University of Texas Dental Branch
Virulence Mechanisms of Bacterial Pathogens (Ames)
Wadsworth Center, NY Dept. Health (Albany, NY)
Workshop on Genomic Alterations in Genetic Disease (NHGRI/NIH, Bethesda)
Workshop on Infectious Diseases (NIDR, NIH – Bethesda, MD)
Workshop on Oral Microbial Genomes Database (Vancouver, BC)
Workshop on Syphilis vaccine development in the "genome era" (Memphis, TN)
Wyeth-Lederle, Inc. (Rochester, NY)

2000-2004: 1st Annual Genome Sciences Symposium (Seattle, WA)
11th International Conference on Microbial Genomes (Durham, NC)
8th International Small Genomes Conf. (Lake Arrowhead, CA)
9th International Conference on Microbial Genomes (Gatlinburg, TN)
40th ICAAC (Toronto, ON)
Advanced Bacterial Genetics Course (Cold Spring Harbor)
Amer. Soc. Microbiol. Annual Meeting (Washington, DC)
Annual Biotech Conf - Stephen F. Austin State Univ. (Nacogdoches, TX)
ASM Waksman Foundation Lecture (Madison, WI)
ASM Waksman Foundation Lecture (Philadelphia, PA)
ASM Waksman Foundation Lectures (Athens, GA)
ASM Waksman Foundation Lectures (Vancouver, BC)
Australian Society for Microbiology Annual Meeting (Sydney, Australia)
Banbury Conference on "New Approaches to Understanding the Pathogenesis of Infectious Diseases" (Cold Spring Harbor, NY)

Canberra Hospital (Canberra, Australia)
Columbia Univ. Microbiology, College of Physicians & Surgeons (New York)
Conference on Statistics and Applied Math -Rice University (Houston, TX)
Conference on Systemics (San Francisco, CA)
Dept. Microbiology, SUNY Buffalo
Developmental Biology of Sea Urchins (Woods Hole, MA)
Diagnostic Approaches for Infectious Disease (Orlando, FL)
Distinguished Lecture Series, Center for Disease Control (Atlanta, GA)
European Federation of Biotechnology (Copanello, Italy)
FEBS/PABMB (Lisbon, Portugal)
First Annual Molecular Genetics Symposium (Keynote, Galveston, TX)
First ASM International Conference on Enterococci (Banff, AB)
Frontiers of Genomics Symposium IV (Madison, WI)
Functional Genomics of Microbial Pathogens, Soc. Gen. Microbiol. (Dublin)
Genome Sequencing for Defense Workshop (Walter Reed Army Medical Center)
Genome Therapeutics Inc. (Waltham, MA)
Genome Therapeutics, Inc. (Waltham, MA)
Genomes 2000 Conference (Institut Pasteur, Paris, France)
Genomes 2004 (Sanger Institute, Hinxton, UK)
Genomics in Infectious Disease (Wurzburg, Germany)
Genomics Symposium, Microbial Diversity Course (Woods Hole, MA)
Genomics: Struct., Funct., Comp., and Evol. Approaches (Cargese, Corsica)
Gordon Research Conference on Biology of Spirochetes (Ventura, CA)
Gordon Research Conference on Periodontal Disease (Oxford, UK)
Gordon Research Conference on Spirochete Biology (Ventura, CA)
Grand Rounds, Dept. Pathol. & Lab. Med., M.D. Anderson Can. Cen. (Houston)
Grand Rounds, Dept. Pediatrics, Univ. Texas Houston Medical School
Houston Soc. for Engineering in Med. and Biol., Annual Conference (Houston)
Human Genome Conference (Texas Southern University, Houston, TX)
Insight Program on Impact of the Human Genome Project (San Diego, CA)
Institute for Molecular Bioscience (Brisbane, Australia)
Interagency Microbial Genome Working Group (Bethesda, MD)
International Workshop on Bovine Genomics (Montreal, Canada)
Keck Center for Computational Biology (Houston, TX)
Keck Center for Computational Biology (Rice University, Houston, TX)
Keystone Conf Strategies for Ident. Devel. Novel Antimicrob Agents (Santa Fe)
Los Alamos National Laboratory (Los Alamos, NM)
Medical College of Wisconsin (Milwaukee, WI)
Microbial Diversity Course (Woods Hole, MA)
Microbial Functional Genomics Conference, NIDCR, NIH (Bethesda, MD)
Molecular Analysis of Bacterial Pathogens Conference (Jamberoo, Australia)
Monash University (Victoria, Australia)
National Student Research Forum (Keynote, Galveston, TX)
NCCR Primate Genomics (San Antonio, TX)
NIH Bioengineering Consortium Annual Symposium (Bethesda, MD)
NSF Primate Genomics Workshop (Arlington, VA)
Oral Pathogens Sequence Database Annual Meeting (San Antonio, TX)
Pediatric Brain Tumor Consortium Annual Meeting (Houston, TX)
Prairie View A&M University (Prairie View, TX)
Rat Genomics and Models Conference (Cold Spring Harbor, NY)
SGM Symposium “Exploiting Genomes” (University of Manchester, UK)
Symposium on Livestock Genomes (Lake Conroe, TX)

The Institute for Genetic Research (Rockville, MD)
U.S. Genomics, Inc. (Woburn, MA)
Univ. Texas Houston Health Science Center, Dept. Health Informatics (Houston)
Univ. Texas Medical Branch, Galveston – Microbiology (Galveston, TX)
University of Georgia – Genetics (Athens, GA)
Yale University - Biochemistry and Biophysics (New Haven, CT)

2005-2009 Univ. Cal. San Diego Integrative Microbiol. Distinguished Lecturer (San Diego)
Los Alamos National Laboratory, Bioscience Division (Los Alamos)
Gordon Conf. on Chemical & Biological Terrorism Defense (Santa Barbara)
Univ. North Dakota Microbiology and Immunology (North Forks, ND)
Conference on Emerging and Re-emerging Infectious Diseases (Galveston)
13th Intl. Congress of Bacteriology and Applied Microbiology (San Francisco)
Developmental Biology of Sea Urchins (Woods Hole, MA)
USDA Distinguished Lecturer Series (Beltsville, MD)
Rice University Frontiers of Medicine (Houston)
Bovine Genome Project: The Next Phase, International Workshop (Houston)
Univ. Maryland Biotechnology Institute (Baltimore)
University of Uppsala (Sweden)
NATO Advanced Research Conf. on Molecular Biology of Spirochetes (Prague)
13th International Meeting on Microbial Genomes (Madison)
University of British Columbia (Vancouver)
Workshop on the Salmonid Genome (Norwegian Univ. of Life Sciences, Aas)
IBM Symposium on Information Based Translational Medicine (Houston)
Masaryk University, Faculty of Medicine (Brno, Czech Republic)
Vienna Biocenter (Austria)
M.D. Anderson Cancer Center, Genes & Devel. Program, Keynote (Houston)
Plant and Animal Genome XIV Conference (San Diego)
Genome Annotation Workshop (Naples, Italy)
Genomic Perspectives on Host-Pathogen Interactions (Sanger Institute, Hinxton)
Genetic Tools Optimizing Use of Rhesus Macaques for Transl. Research (NIH)
International Marine Genomics Conference Keynote Lecture (Sorrento, Italy)
16th Annual Keck Center Research Conference (Houston)
National Science Week Public Lecture (Melbourne)
2006 Emerging Technologies Conference (MIT)
International Conference on Genomics (Hangzhou, China)
Texas Branch, Amer. Soc. Microbiol. Annual Meeting (Galveston)
BARGEnv workshop (Sanger Institute, Hinxton, UK)
Gulf Coast Consortium Symposium on Bioinformatics (Houston)
Conf. on Honey Bee Genomics and Biology (Cold Spring Harbor)
Univ. North Carolina (Dept. Microbiol. Immunol.)
Amer. Soc. Microbiol. Biodefense Meeting (Washington DC)
Duke Univ (Genetics)
Biology of Genomes Conference (Cold Spring Harbor)
International Congress of Insect Biotechnology and Industry (Daegu, Korea)
Sequencing Technology Meeting (Marco Island)
EuroTools Meeting (Hinxton, UK)
Finishing in the Future Conference Keynote (Santa Fe)
American Society for Microbiology Annual Meeting (Toronto)
National Institute of Genetics (Mishima, Japan)
Marine Genomics Europe Exploratory Workshop (Roscoff, France)
National Advisory Council on Human Genome Research (NIH)

Interactome Mapping Workshop (Banbury Center, CSHL)
Primate Symposium (Wake Forest University)
15th Annual International Conference on Microbial Genomics (College Park)
2007 Emerging Technologies Conference (MIT)
RIKEN Genomic Sciences Center (Yokohama, Japan)
Baylor College of Medicine (Dept. Medicine Grand Rounds)
ORFeome Conference (Harvard Medical School, Boston)
Dept. Genetics, Washington University (St. Louis)
International Human Microbiome Consortium Meeting (Rockville, MD)
J. Craig Venter Institute (Rockville, MD)
Genomes 2008 Conference (Institut Pasteur, Paris)
UCLA Molecular Biology Institute
Indiana University
University of Iowa (Genetics)
University Texas Medical School (Houston, Dept. Biochem. Mol. Biol.)
Banbury Conference on Metagenomics (Cold Spring Harbor)
CDC Distinguished Lecture Series (Atlanta)
Dept. Molecular Microbiology (Wash. Univ.)
International Genomics Conference (Banjul, The Gambia)
Conference on Advances in qPCR (Stockholm)
Human Microbiome Project Workshop (NIH)
National Advisory Council on Human Genome Research (NIH)
Sixteenth International Microbial Genomics Conference (Lake Arrowhead)
Genomic Perspectives to Host Pathogen Interactions (Hinxton)
2nd Annual Conference of the Program in Quantitative Genomics (Harvard SPH)
MetaHIT/International Human Microbiome Consortium Meeting (Paris)
Pioneers in Genomic Biology (U. Illinois)
Annual Meeting, American Coll. Veterinary Pathologists, Keynote (San Antonio)
Bioinformatics Conf., American Academy of Microbiology (Washington, DC)
Workshop on Environmental Microbial Genomics (Changsha, China)
Roche Genome Sequencing FLX User Group Meeting (Keynote, New Haven)
International Human Microbiome Conference (Heidelberg)
Human Microbiome Colloquium, ASM Annual Meeting (Philadelphia)
DNA Sequencing Technology Colloquium, ASM Annual Meeting (Philadelphia)
8th International Workshop on Advanced Genomics (Tokyo)
4th European Conference on Prokaryotic Genomics (Gottingen)
Stanford Research Institute (Menlo Park)
Monterey Bay Aquarium Research Institute
Omics Science Center, Riken Yokohama Institute (Yokohama)
Univ. New Mexico (Albuquerque)
International Data Release Workshop (Toronto)
Human Microbiome Project Research Network Meeting (Gaithersberg, MD)
Molecular Diagnostics for Infectious Disease Conference (Washington, DC)
The Future of Science Conference on DNA (Venice)
ProkaGenomics Conference (Gottingen)
Yale University (New Haven)
Genome Standards Consortium Conference (Joint Genome Institute)
9th International Plant Molecular Biology Conference (St. Louis)
2nd Annual *Rendez-Vous* Génome Québec (Montreal)
Distinguished Lectures in Microbiology (Madison)
Medical College of Wisconsin (Milwaukee)
Centers for Disease Control (Atlanta)
Breast Cancer Seminar Series, Siteman Cancer Center (St. Louis)
University of Marburg (Germany)

John Innes Centre (Norwich, UK)

- 2010:
- International Human Microbiome Project Conference (Shenzhen)
 - 3rd International Conference on Enterococci (Portland, OR)
 - American Society for Microbiol. Annual Meeting (San Diego)
 - Frontiers in Life Sciences Lecture, Shanghai Jiao Tong University (China)
 - Université Laval (Quebec)
 - Procter & Gamble (Cincinnati)
 - Jeffrey L. Hout Lectures in Genome Sciences (Univ. N. Carolina)
 - Dept. Biological Sciences, Carnegie-Mellon University (Pittsburgh)
 - Metagenomics Conference (MoGene, St. Louis)
 - Illumina Sequencing Expert Panel (Toronto)
 - Petascale Computing and Personalized Medicine Workshop (Univ. Illinois)
 - Human Microbiome Research Conference (St. Louis)
 - Infectious Disease Genomics and Global Health (Sanger Institute, UK)
 - Lewis-Sigler Institute, Princeton Univ.
 - Illumina, Cambridge LTD
 - Inflammatory Bowel Disease Annual Workshop (Boston)
 - Microbial Forensics in the Era of Genomics (Cold Spring Harbor)
 - Roche-454 Life Sciences User Meeting (Chicago)
 - Adv. Sequencing Technologies & Applications Course (Cold Spring Harbor)
- 2011:
- International Human Microbiome Consortium Conference (Vancouver)
 - American Society for Microbiol. Annual Meeting (New Orleans)
 - Hematology/Oncology Grand Rounds (St. Louis)
 - Innovation in Science and Healthcare, Keynote (Boulder)
 - Center for Genomic Epidemiology (Copenhagen)
 - Broken Arrow Cystic Fibrosis Conference, Keynote (Quebec)
 - North American Congress of Epidemiology (Montreal)
 - European Molecular Biology Laboratory (Heidelberg)
 - Technology Summit (NuGEN, San Carlos)
 - Microbiome Symposium, Keynote (J&J, New Brunswick NJ)
 - Fungal Genome Initiative Symposium (Kunming, China)
 - Illumina Sequencing Expert Panel (Seattle)
 - International Genetic Epidemiological Society (Heidelberg)
 - Texas A&M University
 - White House workshop on Microbial Forensics (Washington DC)
 - NHLBI Workshop on The Human Microbiome (Rockville)
- 2012:
- The Microbiome: Role in Health and Disease Conference (Baeza, Spain)
 - DNA Sequencing, Microbes to Man (Featured Speaker, San Diego)
 - Global Health Genomics (CSH-Asia, Suzhou, China)
 - American Thoracic Society Annual Meeting (San Francisco)
 - Infectious Disease Genomics and Global Health (Sanger Institute, UK)
 - 5th Annual Dartmouth Integrative Biology Symposium (Keynote)
 - NGx: Applying Next-Generation Sequencing (Keynote, Providence)
 - Genome Canada Board of Directors (Ottawa)
 - 7th Annual Sequencing, Analysis, and Finishing in the Future Conference (Keynote, Santa Fe)
 - The Microbiome and Cancer Conference (Keynote, Birmingham AL)
 - IOM The Science and Applications of Microbial Genomics (Washington DC)
 - University of Waikato (Hamilton, NZ)
 - The Perfect Genome (OpGen Webinar)
 - Natl. Institute on Aging Workshop on Microbiome and Aging (Bethesda)
 - Biofutures Conference on Microbiomes (Virginia)
 - Science magazine live chat: The Bugs Inside of Us

Genomics of Common Diseases 2012 (Potomac)
bioMérieux (Durham)
NYU Immunology Club
Illumina User Conference
Institut Pasteur-INRA Microbiome Conference (Paris)

- 2013:
- Future of Genomic Medicine VI Conference (San Diego)
 - Human Genome Meeting/International Congress of Genetics 2013 (Singapore)
 - Molecular Genetics of Bacteria and Phages Meeting (Madison)
 - Dept. Microbiology, Univ. Georgia (Athens)
 - 60th Anniversary of DNA Structure Discovery (The Scientist, webinar)
 - Keystone Symp. Immunopathology of Type I Diabetes (Whistler)
 - 3rd Next-generation Sequencing Conference (Keynote, San Francisco)
 - High Throughput Sequencing Conf. (Keynote, Berlin)
 - Shanghai Jiao Tong University (Shanghai)
 - International Human Microbiome Consortium Conference (Hangzhou)
 - Jackson Laboratory Institute for Genomic Medicine (Farmington)
 - Jackson Laboratory (Bar Harbor)
 - Loyola University (Chicago)
 - Genome Institute of Singapore
 - Inventages' 2013 Summit: The changing landscape of medicine: intrigue of the Human Microbiome and its effect on lifestyle and disease outcome (Munich)
 - U.S. Food and Drug Administration (College Park, MD)
 - Infectious Disease Symposium (Iowa State Univ.)
 - 3rd Annual Illumina Scientific Summit (New Orleans)
 - Bill and Melinda Gates Foundation and Global Good (Seattle)
 - bioMérieux (Marcy l'Etoile, France)
 - bioMérieux (Grenoble, France)
 - bioMérieux (La Balme, France)
 - Clinical Genomics in the 21st Century (Jackson Lab, Farmington CT)
 - Roswell Park Cancer Institute (Buffalo, NY)
 - Badger Lecture in Network Medicine (Brigham & Women's Hospital, Boston)
 - Novartis Institute for Biomedical Research (Cambridge, MA)
 - Genome Center (Santiago, Chile)
 - 2nd Genomics in Medicine Symposium, Clínica Alemana de Santiago (Chile)
 - Root/Soil/Microbiome Systems Biology (Gates Foundation, Seattle)
 - Congress of the Chilean Society of Genetics (La Serena, Chile)
 - Pacific Biosciences Users Meeting (Palo Alto, CA)
 - Bioinformatics Workshop (Univ Conn, Storrs, CT)
 - Hong Kong University of Science and Technology
- 2014:
- Next Generation Microbial Genomics 2014 (Institut Pasteur)
 - Chronic Inflammatory Disease and the Microbiome (Royal Society, London)
 - Division of Laboratory & Genome Medicine (Washington Univ. St. Louis)
 - 4th ASM Conference on Enterococci (Cartagena, Columbia)
 - Max Planck Institute for Terrestrial Microbiology (Marburg, Germany)
 - Advances in Personal Genomics (Farmington, CT)
 - Canadian Microbiome Workshop (Keynote, Vancouver)
 - NY Genome Center, Metagenomics and Inf. Dis. Working Group
 - ICAAC (Washington, DC)
 - Connecticut Infectious Diseases Society (West Haven)
 - Jackson Laboratory for Genomic Medicine
 - Dept. Epidemiology, MD Anderson Cancer Center (Keynote, Houston)

Systems Medicine summer school (Kandersteg, Switzerland)
Innovative Approaches to Diabetes Research and Therapies (New Haven)
UK Genome Science Meeting (Keynote, Oxford)
4th Annual Next Generation Sequencing Conference (Keynote, San Diego)
Conference on Genes, Behaviors and Response to Weight Loss Interventions (NIH)
Illumina Discovery Symposium (Boston)
American Aging Association Annual Meeting (San Antonio)
GlaxoSmithKline (Collegeville, PA)
Genomics: The Power and The Promise (Ottawa)
New England Regional Genetics Group (Dartmouth)
2014 San Antonio Nathan Shock Center Conference on Aging (Bandera TX)
Gut Biology to Infection, Immune Tolerance & Disease Therapeutics (Keynote, Cambridge MA)
Immunogenomics 2014 (Farmington CT)
Jackson Laboratory Grand Opening Symposium (Farmington, CT)
Annual Symposium International Center for Microbial Genomics (Bogota)
Microbiology Symposium (University of Copenhagen)

International Human Microbiome Consortium (Luxembourg)

2015:

Distinguished Speaker, Nutritional Sci. Grad. Stud. Assoc., UTexas (Austin)
Advances in Next Gen Sequencing (Keynote, online)
Annual Retreat University of Massachusetts/Dana Farber CC (Cape Ann)

PROFESSIONAL SOCIETIES AND ORGANIZATIONS

American Academy of Microbiology (AAM)
American Association for the Advancement of Science (AAAS)
American Society for Biochemistry and Molecular Biology (ASBMB)
American Society of Human Genetics (ASHG)
American Society for Microbiology (ASM)
Association for Computing Machinery (ACM)
Federation of American Scientists (FAS)
Genetics Society of America (GSA)
Human Genome Organization International (HUGO)
Institute of Electrical and Electronics Engineers (IEEE)
Sigma Xi

EDITORIAL POSITIONS

1987-2006 Senior Editor, DNA and Cell Biology
1998-2004 Editorial Board, Journal of Bacteriology
2000 Guest Editor, Research in Microbiology, volume 151, Genomics issue
2002-2008 Editorial Board, Plasmid
2004-Present Advisory Board, Genome Biology
2005-Present Editorial Board, Genome Research
2005-Present Editorial Board, BMC-Genomics
2009-2013 Editorial Board, Genome Biology and Evolution
2010-2013 Encyclopedia of Genetics, Genomics Section Editor
2010 Guest Editor, Current Opinion in Microbiology, volume 13, issue 5, Genomics section

SYMPOSIA/CONFERENCES ORGANIZED:

1985 Lost Pines Molecular Biology Conference (Session Chair)
1990 Conference on "RecA and related proteins" (Gif-sur-Yvette, France; co-org)
1992 Am. Soc. Microbio. (co-org; Seminar on "Analysis of Prokaryotic Genomes")

- 1992 Conference on "Breakthroughs in Genetics" (Cold Spring Harbor Lab, NY)
- 1996 ASM Annual Meeting Colloquium on "Impact of Genome Sequencing"
- 1997 5th Annual Conference on "E. coli and other Small Genomes" (Snowbird, UT)
- 1998 6th Annual Conference on Small Genomes (Lake Arrowhead, CA)
- 2000 Genomes 2000 (Paris)
- 2000 Keck 2000 Symposium on Structural and Functional Genomics (Houston)
- 2001 ASM-TIGR Genome Conference (Monterey, CA)
- 2002 ASM-TIGR Genome Conference (Las Vegas)
- 2003 ASM-TIGR Genome Conference (New Orleans)
- 2004 Genomes 2004 Conference (Sanger Institute, UK)
- 2004 Functional Genomics of Host-Pathogen Interactions (Sanger Institute, UK)
- 2005 International Microbial Genome Conference 2005 (Halifax, Canada)
- 2006 Genomic Perspectives on Host-Pathogen Interactions (Sanger Institute, UK)
- 2006 Interpreting Functional Variation in the Human Genome (ASHG Annual Mtg)
- 2007 Genomes 2007 Conference (Sanger Institute, UK)
- 2007 Honey Bee Genomics and Biology (Cold Spring Harbor)
- 2007 Human Microbiome Project Workshop on Metagenomic Studies (NIH)
- 2007 15th Annual International Conf on Microbial Genomics (College Park, MD)
- 2008 Banbury Conference on Metagenomics (Cold Spring Harbor)
- 2008 Human Microbiome Project Community Outreach Workshop (NIH)
- 2008 Microbial Genome Conference 2008 (Paris)
- 2008-2010 Biology of Genomes Conference (Cold Spring Harbor)
- 2008 Genomic Perspectives to Host Pathogen Interactions (Hinxton)
- 2008 16th Annual Conference on Small Genomes (Lake Arrowhead, CA)
- 2009 Human Microbiome Colloquium, ASM Annual Meeting (Philadelphia)
- 2010 Infectious Disease Genomics and Global Health (Sanger Institute, UK)
- 2010 Human Microbiome Conference (St. Louis)
- 2011 International Human Microbiome Consortium Conference (Vancouver)
- 2011 State-of-the-Art Technology Colloquium, ASM Annual Meeting (New Orleans)
- 2011 Genome Canada Bioinformatics/Computational Biology Workshop (Toronto)
- 2012 International Human Microbiome Consortium Conference (Paris)
- 2012 Global Health Genomics (CSH-Asia, Suzhou, China)
- 2012 Infectious Disease Genomics and Global Health (Sanger Institute, UK)
- 2013 Infectious Disease Genomics and Global Health (Sanger Institute, UK)
- 2013 International Human Microbiome Consortium Conference (Hangzhou)
- 2014 Microbial Genomics Conference (Institut Pasteur)

CONTRACTS AND GRANTS

Project Status: Active

Project Number (Principal Investigator): U54 HG003079 (Richard K. Wilson, PI / Elaine Mardis, co-PI / George Weinstock, co-PI)

Funding Source: NIH-NHGRI

Title of Project (*and/or Subproject*): A Platform for Large-Scale Genomic Discovery

Dates of Approved/Proposed Project: 12/01/2011-11/30/2015

Total Costs: \$104,000,000

Percent Effort: 25%

Project Description: Support for the Genome Institute at Washington Univ.

Project Status: Active

Project Number (Principal Investigator): 1U54HG004968 (George Weinstock, PI)
Funding Source: NIH-NHGRI (Common Fund)
Title of Project (and/or Subproject): Sequencing the Human Microbiome
Dates of Approved/Proposed Project: 05/22/2009-04/30/2014
Total Costs: \$16,184,835
Percent Effort: 25%
Project Description: A portfolio of studies of the human microbiome in healthy individuals

Project Status: Active

Project Number (Principal Investigator): 1U54HG004968 04S1 (George Weinstock, PI)
Funding Source: NIH-NHGRI (Common Fund)
Title of Project (and/or Subproject): Sequencing the Human Microbiome
Dates of Approved/Proposed Project: 05/22/2009-04/30/2014
Total Costs: \$693,153
Percent Effort: 25%
Project Description: A portfolio of studies of the human microbiome in healthy individuals

Project Status: Active

Project Number (Principal Investigator): UH2 AI083265 (Phil Tarr, PI / George Weinstock Genomics PI)
Funding Source: NIH-NIAID (Common Fund)
Title of Project (*and/or Subproject*): The Neonatal Microbiome and Necrotizing Enterocolitis
Dates of Approved/Proposed Project: 04/01/09 – 03/31/15
Total Costs: \$4,409,580 (Genomics subproject)
Percent Effort: 3%
Project Description: Determining the role of the microbiome in necrotizing enterocolitis of premature infants

Project Status: Active

Project Number (Principal Investigator): 5UH3 AI09464104 (J. Dennis Fortenberry, PI)
Funding Source: NIH-NIDDK (Common Fund)
Title of Project (*and/or Subproject*): Urethral Microbiome of Adolescent Males
Dates of Approved/Proposed Project: 09/01/2010-08/31/2014
Total Costs: \$125,800
Percent Effort: 9%
Project Description: Study of the urethral Microbiome of Adolescent Males

Project Status: Active

Project Number (Principal Investigator): 1U01HL098960 (Homer Twigg PI, George Weinstock co-PI)
Funding Source: NIH
Title of Project (*and/or Subproject*): Lung Microbiome and Pulmonary Inflammation/Immunity in HIV Infection
Dates of Approved/Proposed Project: 10/01/09 – 09/30/14
Total Costs: \$1,138,446 (Genomics subproject)
Percent Effort: 1%

Project Description: Impact of HIV infection on the microbiome of the respiratory tract

Project Status: Active

Project Number (Principal Investigator): BMGF:01062000871 (George Weinstock, PI)

Funding Source: Bill and Melinda Gates Foundation

Title of Project (*and/or Subproject*): Vaccination and the pediatric microbiome

Dates of Approved/Proposed Project: 11/01/2011 – 06/30/2014

Total Costs: \$3,000,000

Percent Effort: 5%

Project Description: Effect of pneumococcus vaccination on the nasopharyngeal microbiome in infants in The Gambia and Bangladesh

Project Status: Active

Project Number (Principal Investigator): R01AI09721301 (Gregory Storch, PI)

Funding Source: NIH-NIAID

Title of Project (*and/or Subproject*): Defining the Human Virome in Immunocompromised Children

Dates of Approved/Proposed Project: 02/15/2012-01/31/2017

Total Costs: \$602,854

Percent Effort: 2%

Project Description: Discovery and analysis of viruses

Project Status: Active

Project Number (Principal Investigator): R01 HL116211 (Stephanie Davis, PI)

Funding Source: NIH-NHLBI

Title of Project (*and/or Subproject*): Viral Pathogenesis of Early Cystic Fibrosis Lung Disease

Dates of Approved/Proposed Project: 26/09/2012 – 30/06/2016

Total Costs: \$605,339

Percent Effort: 0

Project Description: Metagenomic analysis of CF infants

Project Status: Active

Project Number (Principal Investigator): R01 DK088831 (Nita Salzman, PI)

Funding Source: NIH-NIDDK

Title of Project (*and/or Subproject*): Intestinal Bacterial Metagenome in Pediatric NAFLD

Dates of Approved/Proposed Project: 15/09/2012 – 31/08/2017

Total Costs: \$1,499,969

Percent Effort: 2%

Project Description: Analysis of the human microbiome in children with fatty liver disease

Project Status: Active

Project Number (Principal Investigator): 1U54 DE023789 (Michael Snyder PI, George Weinstock co-PI)

Funding Source: NIH-NIDCR (Common Fund)

Title of Project (*and/or Subproject*): Longitudinal Multiomics Microbial Profiling in Healthy

	and Disease Individuals
Dates of Approved/Proposed Project:	09/26/2013-08/31/2016
Total Costs:	\$2,335,595
Percent Effort:	4%
Project Description:	Longitudinal study of microbiome in pre-diabetic adults
Project Status:	Active
Project Number (Principal Investigator):	5R21 HL10995502 (Ann Rowley, PI, George Weinstock co-PI)
Funding Source:	NIH-NIAID
Title of Project (<i>and/or Subproject</i>):	Deep Sequencing of Kawasaki Disease Tissues
Dates of Approved/Proposed Project:	06/01/2012-05/31/2014
Total Costs:	\$50,735
Percent Effort:	1%
Project Description:	Discovery of the Kawasaki Disease etiologic agent
Project Status:	Active
Project Number (Principal Investigator):	1U01HL121831 (Homer Twigg PI, George Weinstock co-PI)
Funding Source:	NIH-NHLBI
Title of Project (<i>and/or Subproject</i>):	Genomic Analysis of Immunity and Lung Inflammation in HIV Infection
Dates of Approved/Proposed Project:	09/01/2013-08/31/2018
Total Costs:	\$3,215,081
Percent Effort:	5%
Project Description:	Long term pulmonary follow up studies on HIV-infected subjects on antiretroviral treatment

PREVIOUS SUPPORT

1. "RecA Protein of *E. coli*", NIH BRSG, 10/84-8/85, \$9,000 (total costs).
2. "Genetic Analysis of the RecA Protein of *E. coli*", NIH, 8/30/85 - 7/31/88, \$319,293 (direct costs).
3. "Genetic Analysis of the RecA Protein of *E. coli*", NIH, 8/1/88 - 7/31/93, \$650,017 (direct costs).
4. "Isolation and Characterization of the Macrophage Specific Toxin Protein and Genes from *Pasteurella haemolytica*." Contract with Cactus Feeders, Inc., 6/1/85-10/31/89, \$498,461 (direct costs).
5. "Conference on RecA and related proteins", NSF, 7/1/90 - 9/1/91, \$10,000 (total costs).
6. "Isolation of a mutant of *Pasteurella haemolytica* that does not produce leukotoxin." Pfizer, Inc., 9/1/90 - 2/28/91, \$23,990 (direct costs).
7. "Isolation of a mutant of *Pasteurella haemolytica* that does not produce leukotoxin." Pfizer, Inc., 12/1/91 - 11/31/92, \$41,998 (direct costs).
8. "The application of genome sequence analysis to the prevention of infectious disease." Clayton Foundation, 1/1/92 - 12/31/96, \$1,250,000 (total award). Dr. S. Kaplan, P.I.
9. "Genetic organization of *Treponema pallidum*", NIH, 7/1/92-6/30/95, \$430,074 (direct costs), co-PI with Dr. S. Norris.
10. "Secreted antigens of *Pasteurella haemolytica*", Praxis Biologics, Inc., 6/15/93-6/14/94, \$49,345 (total award).
11. "Automation of DNA Sequencing", NIH, 10/1/93-9/30/94, \$35,300 (total costs).
12. "Genetic analysis of enterococci", NIH, 9/30/93-8/31/96, \$270,000 (total award), co-PI with Dr. B. Murray.
13. "Identification of a human retinitis pigmentosum gene on chromosome 8 using genomic DNA sequencing", UTHSC-H, 10/1/95-9/30/96, \$78,450 (total costs).
14. "Molecular analysis of microbes isolated from spacecraft and crew", Krug, Inc., 1996-1997, \$24,999 (total costs).
15. "Microbiology of space station spacecraft and crew", NASA NAG 9-903, 9/1/96-8/30/98, \$58,910 (total costs).
16. "Microbial interaction in the Mir space station environment", NASA NAS 9-19439, 7/17/95-2/15/1999, \$504,597 (total costs).
17. "Genetic organization of *Treponema pallidum*", NIH 1 R01 AI40390-01, 12/1/95-2/28/99, \$ 1,220,799 (total costs) (co-PI is Dr. Steve Norris).

18. "Genetic analysis of enterococci", NIH 2 R01 AI33516-04, 9/30/96-8/31/99, \$475,620 (total costs) (co-PI, with Dr. Barbara Murray)
19. "Microbial interactions in the space environment", Wyle Laboratories (NASA subcontractor), 07/01/98 - 06/30/00, \$30,000 (total costs)
20. "Generation of multiple MDR gene knockout mutations in *Enterococcus faecalis*", Phytera, Inc., 4/1/99-3/31/00, \$40,890 (total costs)
21. "Genetic Organization of *Treponema denticola*", NIH R01DE12488, \$1,541,931 (total costs), 7/1/1998 – 6/30/2001
22. "Microbial Genomics (*Fusobacterium nucleatum* genome sequence)", NIH 7R01DE013759, 9/21/2000 – 8/31/2003, \$705,644 (total costs)
23. "*Bacillus anthracis* clone set", NIH R41AI052522, 09/15/2002 – 08/31/2003, \$86,250 (total costs)
24. "Complete genome sequence of *Rickettsia typhi*", U01AI049040, 8/15/2000 – 7/31/2002, \$183,510 (total costs) (co-PI with Dr. David Walker)
25. "Draft sequence of the rat genome", NIH U54 HG02345, 02/27/01 to 02/26/03, \$10,976,914 (annual), (Richard Gibbs PI/George Weinstock Co-PI)
26. "The *Pasteurella (Mannheimia) haemolytica A-1* genome sequence", USDA/NRICGP 00-35204-9229, 9/1/00 - 8/31/02, \$220,083 (total costs) (co-PI with Dr. Sarah Highlander)
27. "Continuing megabase sequencing at the BCM-HGSC", NIH U01 HG02051, 3/8/99 - 10/31/03, \$14,643,348 annual (Richard Gibbs PI/George Weinstock Co-PI)
28. "Sequencing the mouse genome", NIH U54 HG02139, 10/01/99-9/30/02, \$4,753,407 annual, (Richard Gibbs PI/George Weinstock Co-PI)
29. "Sequencing, annotation and assembly of a second *Drosophila*", NIH U01HG002570, 5/10/2002 – 4/30/2003, \$3,336,211 (total costs) (Richard Gibbs PI/George Weinstock Co-PI)
30. "Itanium cluster equipment grant", Intel Corp., 1/1-2003 – 12/31/2003, \$150,000 (total costs).
31. "Bovine Genome Sequencing Project (BGSP)", USDA/CREES 59-0790-3-196, 9/01/03 - 9/30/05, \$878,050 (total costs) (Richard Gibbs PI/George Weinstock Co-PI)
32. "Genetic analysis of enterococci," NIH/NIAID 2 R01 AI 33516, 8/1/00-7/31/05, \$250,000 (total costs) (Barbara Murray PI)
33. "Clone pooling methods for physical mapping," NIH/NCRR 1 U01 RR18464, 9/30/02-8/31/05, \$206,693 (total costs) (A. Milosavljevic, PI)
34. "Clone-Array Pooled Shotgun Indexing," NIH HG02583, 07/19/02 – 03/31/06, \$328,418 (total costs) (A. Milosavljevic, PI)
35. "Large Scale Sequencing at BCM-HGSC," NIH 1 U01 HG02051, 11/10/03-10/31/06, \$21,028,110 annual (Richard Gibbs PI/George Weinstock Co-PI)
36. "Bovine Genome Sequencing Project," USDA, TEXR-2004-35216-14163, 12/01/03-11/31/06, \$3,879,953 annual (Richard Gibbs PI/George Weinstock Co-PI)
37. "Genome Sequencing of the Red Flour Beetle," USDA, 5805430-3-338, 09/29/03-09/28/06, \$175,500 annual (Richard Gibbs PI/George Weinstock Co-PI)
38. "Sequencing of the Honey Bee Bacterial Pathogen, *Paenibacillus larvae*," USDA 58-6204-3-024, 08/13/03-05/31/06, \$196,278 annual
39. "*Francisella* Genomics," NIAID R21 AI061106, 7/15/04–6/30/06, \$100,000 annual
40. "Genome Sequencing and Analysis of *Bacillus pumilis*," NSF EF-0414410, 7/1/2004 – 6/30/2007, \$194,511 (total costs) (G. Weinstock PI/S. Highlander Co-PI)
41. "Genome Sequencing and Analysis of *Pantoea stewartii* strain DC283," USDA 2004-35600-14174, 12/01/03 to 11/30/07, \$431,134 (total costs) (Nicole Perna PI /George Weinstock Co-PI)
42. "Genomes and Genetics at the BCM-HGSC, Human Microbiome Roadmap Project Supplement," NIH Roadmap Office, 12/1/2006 – 10/31/2007, \$2,285,000 (total costs) (Richard Gibbs, PI/George Weinstock Co-PI)
43. "Bovine Genome Sequencing Project (BGSP)," USDA TEXR-2003-05478, 12/01/03 to 11/30/07, \$9,790,034 annual, (Richard Gibbs, PI, George Weinstock, Co-PI)
44. "Genome comparison of Infectious Strains of *Enterococcus faecalis*," NIH 1 R21 AI064470, 4/1/2005 – 3/31/2008, \$371,243 (total costs) (George Weinstock PI)
45. "Genome sequence of *Ascospaera apis*," USDA 58-6204-0024, 8/13/2003 – 7/31/2008, \$624,258 (total costs) (George Weinstock PI)
46. "Comparative genomics of *Francisella*," NIH 1 R21 AI064369, 7/1/2005 – 6/30/2008, \$592,950 (total costs) (George Weinstock PI)
47. "*Staphylococcus aureus* antigens in human infections", Vivian Smith Foundation, 9/1/2006 – 8/31/2008, \$95,000, (Sheldon Kaplan Co-PI, George Weinstock Co-PI, Joe Petrosino Co-PI, Sarah Highlander Co-PI)
48. "Genomes and genetics at the BCM-HGSC", NIH 2U54 HG003273, 12/01/06 – 10/31/10, \$122,020,472, (Richard Gibbs PI, George Weinstock Co-PI)
49. "Probing the Human Virome for the Etiology of Kawasaki disease and other Febrile Illnesses", Gillson Longenbaugh Foundation, 7/01/07 – 6/30/08, \$60,000 (George Weinstock co-PI, Sheldon Kaplan co-PI)

50. "Disease-specific Virulence Factors of *Helicobacter pylori*", BCM Cen. Inf. Imm. Res., 4/1/07 – 3/31/09, \$70,000, (George Weinstock co-PI, David Graham co-PI).
51. "Revealing the Attenuating Mutations of *F. tularensis* LVS", NIH/NIAID U54 AI057156, 05/01/05 - 02/28/09, \$382,064 (George Weinstock, PI)
52. "Development of diagnostic reagents for the detection of *Francisella* and *Francisella* infection", NIH/NIAID U54 AI057156-04, 9/1/06 – 2/28/09, \$504,515, (George Weinstock PI)
53. "Genome sequencing of *Moraxella bovis*, the agent of bovine keratoconjunctivitis", USDA 2004-04989, 7/15/04-7/14/09, \$86,478, (Sarah Highlander PI/George Weinstock Co-PI)
54. "Genome sequencing of *Streptococcus iniae*, an emerging pathogen of aquaculture", USDA 0523776 (2006-35600-16569), 12/1/2005 – 11/30/2009, \$388,000, (Sarah Highlander, PI/George Weinstock, Co-PI)
55. "Vaccine for Epidemic Typhus", NIAID AI 1U01AI71283, 8/1/2006 – 7/31/2008, \$121,930, (David Walker PI/George Weinstock Co-PI)
56. "Complete genome sequencing of the chromatically adapting cyanobacterium *Fremyella diplosiphon*", NSF EF-0626927, 09/15/06 – 9/30/08, \$557,000, (George Weinstock PI/David Kehoe Co-PI)
57. "Comparative sequencing of social amoebae in the Dictyostelidae", NSF EF-0626963, 11/1/06 – 10/31/09, \$948,738, (Richard Gibbs PI, George Weinstock Co-PI, Adam Kuspa Co-PI)
58. "Complete genome sequencing of four nitrogen-fixing, plant-associated Burkholderias", NSF EF-0626896, 10/1/06 – 9/30/09, \$725,000, (George Weinstock PI/Ann Hirsch Co-PI).
59. "Frontiers in Metagenomics, Transcriptomics and Ocean Ecology", Gordon and Betty Moore Foundation, 12/1/2007 – 11/31/2009, \$312,436 (Alexandra Worden, PI/George Weinstock Co-PI)
60. "Metagenomic study of the human skin microbiome associated with acne", NIH-NIAID UH2 AR057503, 04/01/09 – 03/31/10, \$650,437, (Huiying Li PI / George Weinstock Genomics subcontract PI)
61. "Effect of Crohn's Disease Risk Alleles on Enteric Microbiota", NIH-NIDDK UH2 DK83994, 04/01/09 – 03/31/10, (Ellen Li, PI / George Weinstock, Genomics PI)
62. "The human virome in children and its relationship to febrile illness", NIH-NIAID UH2 AI083266, 04/01/09 – 03/31/10, (Greg Storch, PI / George Weinstock Genomics PI)
63. "Center for Large Scale Genome Sequencing and Sequence Analysis", NIH-NHGRI U54 HG003079, 12/01/06-10/31/11, \$30,401,888 direct costs yr 6, (Richard K. Wilson, PI / Elaine Mardis, co-PI / George Weinstock, co-PI)
64. "Center for Large Scale Genome Sequencing and Sequence Analysis", NIH-NHGRI U54 HG003079 07S1, \$1,000,000, 11/1/2009-10/31/2011, (Richard K. Wilson, PI / Elaine Mardis, co-PI / George Weinstock, co-PI)
65. "Sequencing the Microbiome in Two Primate Species Under Two Dietary Conditions", NIH-NCRR 3 P40 RR019963-05S2, 07/01/09 – 06/30/10, \$515,126, (Jay Kaplan, PI / George Weinstock, Genomics PI)
66. "Comparative Genomics in the Enterobacteriaceae", NIH-NIAID 5 R01 AI052237, 09/01/2008 - 08/31/2012, \$694,038, (George Weinstock, PI)
67. "Genetics of MRSA Infection", NIH-NHGRI RC2 HG005680, 09/30/09 – 09/29/12, \$2,000,000, (George Weinstock, PI)
68. "Sequencing & Phylogenomics of Food Animal & Community-acquired *Clostridium difficile*", USDA 2008-35600-04697, 09/01/08 - 12/31/12, \$184,262 (G. Songer, PI / George Weinstock, co-PI)
69. "Targeted High-Throughput Sequencing for Gene Discovery in Retinitis Pigmentosa", Foundation Fighting Blindness 01/06/2008 – 31/05/2013, \$1,450,000 (Steve Daiger, PI/George Weinstock, Co-PI)

TEACHING RESPONSIBILITIES

COURSES (hours taught):

UTHHSC Graduate School of Biomedical Sciences:	
Advanced Biochemistry 1985, 1987-1991	(1.5-4.5 hours)
Molecular Basis of Gene Action 1985-1997	(9 - 39 hours)
Macromolecular Structure and Function 1992	(2 hours)
Medical Microbiology 1992	(3 hours)
Current Methods in Biochemistry 1992-1999	(4 hours)
Toxicology 1993	(2 hours)
Computers in Molecular Biology 1993	(4 hours)

Laboratory Course in Recombinant DNA 1993	(45 hours)
Bacterial Genetics and Molecular Biology 1997, 1999	(10.5 hours)
Molecular Pathogenesis 1998	(1.5h)
Microbial Genetics 1998-2000	(20h)
Microbiology and Molecular Genetics 2000-2004	(12h)
UTHHSC School of Health Informatics: Short course on Health Informatics 2001-2003	(2h)
UTHHSC Medical School:	
Biochemistry 1985-1997	(8-16 hours)
Molecular Medicine 1995	(8 hours)
Microbiology 1998-2000	(11 hours)
Problem Based Learning 1999	(>80 hours)
BCM:	
Rearrangements in the Eukaryotic Genome 1987-1993	(2h)
Molecular Genetics of Procaryotes 1988-1997	(2h)
Advanced Genetics 1998-2002	(3h)
Method and Logic in Molecular Biology 2001	(6h)
Structural Basis of Human Disease 2001-2004	(2h)

EXTRAMURAL COURSES (hours taught):

1986-1990	Adv Bacterial Gen (3 weeks) at Cold Spring Harbor Lab, NY
1990	Molec Gen (2h) Univ Texas Health Science Center at Dallas
1990-1993	Bacterial Genetics and Pathogenesis (1 week) Intl Centre for Genetic Engineering and Biotechnology, Trieste, Italy

TRAINING OF CANDIDATES FOR POSTGRADUATE DEGREES:

1984-1988	Jane M. Weisemann (Ph.D. 1988; postdoc at USDA, Beltsville MD; NCBI)
1986-1990	Jesus Eraso (Ph.D. 1990; postdoc with Dr. S. Kaplan, Univ Texas Med. School)
1986-1992	Joe Don Heath (PHS trainee; Ph. D. 1992; postdoc with Dr. E. Nester, Univ. Washington; Incyte Pharmaceuticals)
1988-1992	Xiaomei Jin (CUSBEA Program; postdoc with Dr. B Murray, Univ. Texas Med. Sch.; Canji, Inc.)
1989-1993	Piero Bianco (postdoc with Dr. Steve Kowalczykowski, U. Asst. Prof. SUNY Buffalo)
1989-1990	Linda Oldham (M.S. 1990; community college science teacher)
1989-1993	Jeff Perkins (M.D./Ph.D. 1993; resident at Johns Hopkins)
1991-1993	Gang Zong (M.S. 1993; technician)
1992-1994	Yun You (M.S. 1994; technician biotechnology company)
1992-1995	C. Michael Jones (moved, University of Tennessee faculty)

	1993-1995	Xiaotao Li (M.S. 1995; technician; re-entered graduate school 1999)
A&M)	1993-1998	Yi Xu (Ph.D. 1998; postdoc with Dr. Magnus Hook, Texas
	1994-1995	Lingxia Jiang (moved to TIGR)
	1995-1997	Christian Brauning (M.S. 1997; non-science job in business)
UTHHSC)	1995-2000	Qin Xiang (Ph.D. 2000, postdoc with Barbara Murray,
British	1996-2003	Michael McLeod (Ph.D. 2003, postdoc with Julian Davies, U. Columbia)
UTHHSC)	1996-2001	Fang Teng (Ph.D. 2001, postdoc with Barbara Murray,
	1998-2000	Brandie Jonas (M.S., 2000, staff scientist at Lexicon, Inc.)
	1999-2004	Tom McNeill (Ph.D., 2004, staff programmer at Pioneer, Inc.)
	2000-2002	Solida Mak (transferred to School of Public Health)
	2001-2005	Yue Liu (Ph.D., 2005, postdoc at BCM-HGSC)
	2001	Guangwei Fan (returned to China)
	2001-2006	Sandor Karpathy (Ph.D., 2006, postdoc at CDC)
	2002-2006	Yufeng Shen (Ph.D., 2006, postdoc at HGSC)
	2002	Xi Zhou (transferred to M.D. Anderson)
2010	2004-2005, 2007-2009	Petra Matejkova (Masaryk Univ., Brno, Czech Republic), PhD
	2005-2006	Bingshan Li (transferred to Suzanne Leal lab), PhD 2008
MD/PhD)	2006-2010	Tiffany Williams (PhD 2010; in Medical School finishing
	2006	Brian McWilliams (transferred to Joe Petrosino lab)
	2006-2010	Lei Chen (PhD 2010; postdoc, Washington University)
	2007-2008	Jin Wei (returned to China)
	2013-2014	Mo Lee Villagran (MS, moved to industry)
	2014-Present	Xin Zhou

TRAINING OF POSTDOCTORAL FELLOWS AND VISITING SCIENTISTS (current position):

1982-1983	Dr. Stephen Wagner, Damon Runyon-Walter Winchell Cancer Fund Fellowship
1982-1983	Dr. Raymond Devoret, visiting Scientist from CNRF, Gif-sur-Yvette, France
1982-1984	Dr. Sandra Dusing (staff scientist, Miles Pharmaceuticals).
1985-1986	Dr. Bernard Salles, Fellow of the Association pour la Recherche sur le Cancer (CNRF, Toulouse, France).
1985	Dr. Kelly Hughes, National Res. Service Award (faculty Univ. Wash.)
1986-1987	Dr. Wu Ying, Visiting Scholar Program with China (Res. Assoc, BCM)
1986-1990	Dr. Sarah Highlander (faculty, BCM).
1989-1992	Dr. Baldev Sharma (Houston Police Dept. Crime Lab).
1990-1991	Dr. Michael Engler, visiting Professor, UTHHSC
1991-1992	Dr. Barbara Murray, visiting Professor, UTHHSC
1992-1996	Dr. R. Christopher MacKenzie, Clayton Fdn Fellow (Res. Assoc, UTHHSC)
1995-2000	Dr. Erica Sodergren, Research Assistant Professor (faculty, BCM)
1995-1999	Dr. John Hardham (staff scientist, Pfizer)
1998-2001	Dr. David Smajs (faculty Masaryk University, Brno, Czech Republic)
2000-2002	Dr. Sangita Pal (Research Assoc, BCM-HGSC)
2000-2002	Dr. Mulu Ayele (staff scientist, TIGR)
2000-2001	Dr. Carla Bidinost, visiting Professor, Argentina
2001-2003	Dr. Qin Xiang (Programmer, BCM-HGSC)
2001-2003	Dr. Henry Song (Programmer, BCM-HGSC)
2002	Dr. Richard Willson, visiting Professor, UH
2002-2003	Dr. George Fox, visiting Professor, UH

2002-2004	Dr. Kirt Martin (postdoc, M.D. Anderson Cancer Center)
2002-2004	Dr. Lisa D’Souza (raising family)
2002-2005	Dr. Zhengdong Zhang (postdoc, Yale University)
2003-2004	Dr. Joe Petrosino (faculty, BCM)
2005-2008	Dr. Yue Liu (staff, HGSC, BCM)
2005-2010	Dr. Shailaja Yerrapragada
2006	Dr. Yang Da, visiting Professor, U. Minn.
2006-2008	Dr. Jason Gioia (Zygen, Inc)
2006-2008	Dr. Yufeng Shen (postdoc, Columbia)
2007-2008	Dr. Carson Jiaxin Qu (staff, HGSC, BCM)
2007-2012	Darina Cejkova (Masaryk Univ., Brno, Czech Republic)
2008-2009	Dr. Kathie Mihindukulasuriya (staff, GC, WU)
2008-2012	Dr. Yanjiao Zhou (staff scientist, Wash. Univ.)
2009-2012	Michal Stouhal (Masaryk Univ., Brno, Czech Republic)
2009-2012	Guohui Yao (Information Technology, Shanghai)
2009-2013	Kristine Wylie (Instructor, Wash. Univ.)
2010, 2014-present	Brenda Kwanbana (MRC, The Gambia)
2012-2013	Lenka Mikalova
2012-2014	Maze Ndonwi
2014-Present	Blake Hanson
2014-Present	Yanwei Chen
2014-Present	Lauren Petersen
2014-Present	Samantha Smith
2014-Present	Eddy Bautista
2014-07-25	Laura Rojas
2014-Present	Dan Spakowicz

TRAINING OF UNDERGRADUATE STUDENTS:

1985	Adam Quarles
1992	Jennifer Reyna
1995	Jonathan Mathy
1996	Jeff Gralnick, Mack Kuo, Michelle Hibbard
2000	Patricia Jimenez, Susan Abramski
2003	Fanny Chautin
2004	Alexis Beraducci
2005	Alexis Beraducci
2013	Ying Xue (Zoey) Wang

STUDENT ADVISORY/EXAMINATION COMMITTEES:

Current Student Advisory Committees:

Xin Zhou

Previous Student Advisory Committees:

Sandeep Agarwal (M.D./Ph.D.)	Caleb Gonzalez	Jim Mullen
Michelle Agnew	Laura Gumbiner-Russo	Linda Oldham (M.S., mentor)
Lida Anestidou	Dawn Hancock (UTHHSC)	Jeanine Pennington
Lisa Armitige (M.D./Ph.D.)	Alan Harris	Jeff Perkins (MD/PhD, mentor)
Linda Bachinski	Sumera Hashem (UTHHSC)	Rebecca Ponder
Subeena Bacus (Biochemistry, BCM)	Albert He	Joye Purser (UTHHSC)
Wenlong Bai	Joe Don Heath (mentor)	Svetlana Rashkova
Katie Bellinghausen	Micheal Hebert (UTHHSC)	Dean Reardon
Art Bergh	Stephen Henry (Texas A&M)	Larry Reiter (CMB, BCM)
Piero Bianco (mentor)	Anne Hodgson	Jose Rivera
Matthew Blankschien	Alex Hoffmaster	Jill Roberts (MMG, UTHHSC)

Gabriela Bowden	Laura Houston	John Schwartz
Chris Brauning (mentor)	Bradley Johnson	Yufeng Shen (mentor, BCM)
Mark Brenneman (Biochemistry, BCM)	Brandie Jonas (mentor)	Bill Smith
Al Brenner	C. Michael Jones (mentor)	Monica Smith
Robert Britton (CMB, BCM)	Ken Kalafus	Anjana Srivatsan
Laura Caskey (Microbiology, BCM)	April Kilburn (Biochem, BCM)	Qin Sun
Anne Chang (M.D./Ph.D.)	David Kristensen	Fang Teng (mentor)
Shao-Chun Chang (M.D./Ph.D.)	Qiao-Xin Li	Brian Tseng (M.D./Ph.D.)
Paul Chastain (Texas A&M)	Amanda Jarolimek (M.D./Ph.D.)	Pablo Tsukayama (WUSTL)
Hong Chen (Cell Biology, BCM)	Rupashree Jayashankar	Jim Versalovic (CMB, BCM)
Lei Chen (mentor, SCBMC, BCM)	Lingxia Jiang (mentor)	Mo Villagran
Shahreen Chowdhury	Xiaomei Jin (mentor)	Dan Wagner
Duane Compton	Sandor Karpathy (mentor , UTHHSC)	Jian Wang
Karen Considine	Ann Kays	Jin Wei (mentor, MHG, BCM)
Susan Cooper	Matthew Lawrenz	Jane Weisemann (mentor)
Tony Costa	Bingshan Li	Brenda Whaley
Janet Craig	Song-Feng Li	Tiffany Williams (mentor, MD/PhD, TBMMP, BCM)
Stacey Davis		Hongyun Wu
Michael Dillon	Xiaotao Li (mentor)	Jiaqian Wu
Darrell Dotson	Yue Liu (mentor, SCBMB, BCM)	Qin Xiang (mentor)
Melissa Drysdale	Daniel Magner	Wenbing Xu
Joseph Duffy	Solida Mak (mentor, MMG)	Yi Xu (mentor)
Al Edwards (M.D./Ph.D., BCM)	Ann Marie Marciel (MVM, BCM)	Chun Yang
Mark Emmett	Michael Marsh (SCBMB, BCM)	Vivian Yang (Texas A&M)
Jesus Eraso (mentor)	Cristina Materon (Biochemistry, BCM)	Yun You (mentor)
Guangwei Fan (mentor, UTHHSC)	Gregory McKenzie (Genetics, BCM)	Farideh Zamaniyan
Terry Farmer	Matthew McKevitt (Biochem, BCM)	Wei Zhang
Natalie Fonville	Mike McLeod (mentor, Keck Fellow, UTHHSC)	Song Qing Zhao
Trent Fowler	Tom McNeill (mentor, UH)	Xiaoyan Zhao
Cindee Funk	Brian McWilliams	Zheng Zhou (Biochemistry, BCM)
Sonya Garza	Ana Moran	Gang Zong (mentor)
Jason Gioia	Julia Hsi Morris	Karen Zscheck
	Stacey Mueller	Zhongming Zhao
		Xi Zhou (mentor, UTHHSC)

LABORATORY TUTORIALS:

1984-1985	Jing-Shan Hu
1985-1986	Joe Don Heath, Jesus Eraso, Peggy Saydak, Karen Considine
1986-1987	Donald Mandel, Li Li, Farideh Zamaniyan
1987-1988	Xiao-Mei Jin, Laura Houston
1988-1989	Janet Craig, Anne Hodgson, Piero Bianco, Jeff Perkins
1989-1990	none (full lab)
1990-1991	Gang Zong, Ruo-Dan Zhang, Dan Wagner
1991-1992	Haiyan Ma
1992-1993	Svetlana Rashkova, Yi Xu, Xiaotao Li, Haiying Zhang
1993-1994	on sabbatical leave
1994-1995	Lingxia Jiang, Qin Xiang, Chris Brauning
1995-1996	Michael McLeod, Fang Teng, Manu Chakravarthy
1996-1997	William Shi, Jennifer Bieszke, Stacey Smith, Huy Phan

	1997-1998	Yufang Wu, Brandie Jonas, Matthew Lawrenz, Zhenming Yu
	1998-1999	Melissa Drysdale, Jennifer Givens, Tom McNeill
	1999-2000	Matthew Dooris, Xinpu Chen, Solida Mak
	2000-2001	Hui Yao (BCM), Sandor Karpathy (UTHHSC), Yue Liu
(BCM)	2001-2002	Xi Zhou (UTHHSC), Yufeng Shen (BCM)
	2002-2003	Christopher House, Dustin Edwards, Eryong Huang, Cui Xu
	2003-2004	Alan Harris, Matthew Ward,
	2004-2005	Anup Parikh, Bingshan Li
	2005-2006	April Burant, Jian Li, Tiffany Williams, Brian McWilliams,
Lei Chen	2006-2007	Katie Bellinghausen, Jin Wei, Nelson Hawkins
	2007-2008	Bryce Daines, Domink Satory, Christian Marin-Mueller
	2008-2009	(move to Washington University)
	2009-2010	Lala Motihabi
	2013	Mo Lee Villagran, Dongdong Han
	2014	Xin Zhou, Veneta Qendro

PATENTS

1. Michael L. Berman, Thomas J. Silhavy, George M. Weinstock. Open reading frame vectors. Litton Bionetics, Inc. Mar 05, 1985: US 4503142.
2. Peter Berget, Michael Engler, Sarah Highlander, George Weinstock. Pharmaceutical compositions of a 105 kD P. Haemolytica derived antigen useful for treatment of Shipping Fever. Board of Regents The University of Texas System Sep 18, 1990: US 4957739.
3. Peter Berget, Michael Engler, Sarah Highlander, George Weinstock. Methods and compositions for the treatment and diagnosis of shipping fever. Board of Regents The University of Texas System Aug 09, 1994: US 5336491.
4. Peter Berget, Michael Engler, Sarah Highlander, George Weinstock. Methods and compositions for the treatment and diagnosis of shipping fever. Board of Regents The University of Texas System Aug 03, 1999: US 5932705.
5. Steven J Norris, Jing-Ren Zhang, John M Hardham, Jerrilyn K Howell, Alan G Barbour, George M Weinstock. VMP-like sequences of pathogenic borrelia. Board of Regents The University of Texas System Aug, 20 2002: US 6437116.
6. Steven J Norris, Jing-Ren Zhang, John M Hardham, Jerrilyn K Howell, Alan G Barbour, George M Weinstock. VMP-like sequences of pathogenic Borrelia. Board of Regents The University of Texas System Mar, 27 2003: US 20030060618.
7. Steven J Norris, Jing-Ren Zhang, John M Hardham, Jerrilyn K Howell, Alan G Barbour, George M Weinstock. VMP-like sequences of pathogenic Borrelia. Board of Regents The University of Texas System May, 15 2003: US 20030092903.
8. Steven J Norris, Jing-Ren Zhang, John M Hardham, Jerrilyn K Howell, Alan G Barbour, George M Weinstock. Vmp-like sequences of pathogenic borrelia. Board of Regents The University of Texas System Mar, 4 2004: US 20040044192.
9. Steven J Norris, Jing-Ren Zhang, John M Hardham, Jerrilyn K Howell, Alan G Barbour, George M Weinstock. VMP-like sequences of pathogenic Borrelia. Board of Regents The University of Texas System Apr, 13 2004: US 6719983.
10. Steven J Norris, Jing-Ren Zhang, John M Hardham, Jerrilyn K Howell, Alan G Barbour, George M Weinstock. VMP-like sequences of pathogenic borrelia. Board of Regents The University of Texas System May, 25 2004: US 6740744.
11. Steven J Norris, Jing-Ren Zhang, John M Hardham, Jerrilyn K Howell, Alan G Barbour, George M Weinstock. VMP-like sequences of pathogenic Borrelia. Oct, 28 2004: US 20040214225.
12. Steven J Norris, Jing-Ren Zhang, John M Hardham, Jerrilyn K Howell, Alan G Barbour, George M Weinstock. Vmp-like sequences of pathogenic Borrelia. Board of Regents The University of Texas System Apr, 12 2005: US 6878816.
13. Rebecca L Rich, Bernd Kriekemeyer, Rick T Owens, Magnus Hook, Barbara E Murray, Sreedhar R Nallapareddy, George M Weinstock. Collagen-binding proteins from enterococcal bacteria. The Texas A&M University System Jun, 21 2005: US 6908994.
14. Rebecca L Rich, Bernd Kriekemeyer, Rick T Owens, Magnus Hook, Barbara E Murray, Sreedhar R Nallapareddy, George M Weinstock. Collagen-binding proteins from Enterococcal bacteria. Aug, 18 2005: US 20050180986.

15. Steven J Norris, Jing-Ren Zhang, John M Hardham, Jerrilyn K Howell, Alan G Barbour, George M Weinstock. VMP-like sequences of pathogenic *Borrelia*. Board of Regents The University of Texas System Nov, 14 2006: US 7135176.
16. Steven J Norris, Jing-Ren Zhang, John M Hardham, Jerrilyn K Howell, Alan G Barbour, George M Weinstock. VMP-like sequences of pathogenic *Borrelia*. May, 24 2007: US 20070117970.
17. Rebecca L Rich, Bernd Kriekemeyer, Rick T Owens, Magnus Hook, Barbara E Murray, Sreedhar R Nallapareddy, George M Weinstock. Collagen-binding proteins from enterococcal bacteria. The Texas A & M University System Dec, 29 2009: US 7638135.
18. Steven J Norris, Jing-Ren Zhang, John M Hardham, Jerrilyn K Howell, Alan G Barbour, George M Weinstock. VMP-like sequences of pathogenic *Borrelia*. Board of Regents The University of Texas System Aug, 31 2010: US 7785597.
19. Steven J Norris, Jing-Ren Zhang, John M Hardham, Jerrilyn K Howell, Alan G Barbour, George M Weinstock. VMP-Like Sequences Of Pathogenic *Borrelia*. Dec, 16 2010: US 20100317026.
20. Steven J Norris, Jing-Ren Zhang, John M Hardham, Jerrilyn K Howell, Alan G Barbour, George M Weinstock. VMP-like sequences of pathogenic *Borrelia*. Board of Regents The University of Texas System Dec, 6 2011: US 8071109.
21. Steven J Norris, Jing-Ren Zhang, John M Hardham, Jemlyn K Howell, Alan G Barbour, George M Weinstock. VMP-Like Sequences of Pathogenic *Borrelia*. May, 17 2012: US 20120122238.

BIBLIOGRAPHY:

1. Weinstock, G.M.: Ph.D. Thesis, Genetic and physical studies of bacteriophage P22 genomes containing translocatable drug resistance elements. Massachusetts Institute of Technology. 1977.
22. Botstein, D., Weinstock, G., Kleckner, N. Specificity of translocatable drug-resistance elements. *Hoppe-seyler's Zeitschrift Fur Physiologische Chemie* 358: 419, 1977.
23. Weinstock, G.M., Susskind, M.M., and Botstein, D.: Regional specificity of illegitimate recombination by the translocatable ampicillin-resistance element Tn1 in the genome of phage P22. *Genetics* 92:685-710, 1979.
24. Weinstock, G.M. and Botstein, D.: Regional specificity of illegitimate recombination associated with the translocatable ampicillin-resistance element Tn1. *Cold Spring Harbor Symp. Quant. Biol.* 43:1209-1215, 1979.
25. McEntee, K., Weinstock, G.M.: The recA protein of *E. coli*: Regulation and function in recombination and repair. In: *Proceedings of Stadler Symposium Volume II, Columbia, MO.* 1979.
26. Weinstock, G.M., McEntee, K., and Lehman, I.R.: ATP-dependent renaturation of DNA catalyzed by the recA protein of *Escherichia coli*. *Proc. Natl. Acad. Sci. USA* 76:126-130, 1979.
27. McEntee, K., Weinstock, G.M., Lehman, I.R.: Initiation of general recombination catalyzed in vitro by the recA protein of *Escherichia coli*. *Proc. Natl. Acad. Sci. USA* 76:2615-2619, 1979.
28. McEntee, K., Weinstock, G.M., and Lehman, I.R.: RecA protein-catalyzed strand assimilation: Stimulation by *Escherichia coli* single-stranded DNA binding protein. *Proc. Natl. Acad. Sci. USA* 77:857-861, 1980.
29. Shortle, D., Koshland, D., Weinstock, G.M., and Botstein, D.: Segment directed mutagenesis: Construction in vitro of point mutations limited to a small predetermined region of a circular DNA molecule. *Proc. Natl. Acad. Sci. USA* 77:5375-5379, 1980.
30. Weinstock, G.M., Riggs, P.D., and Botstein, D.: Genetics of bacteriophage P22. III. The late operon. *Virology* 106:82-91, 1980.
31. Weinstock, G.M. and Botstein, D.: Genetics of bacteriophage P22. IV. Correlation of genetic and physical map using translocatable drug-resistance elements. *Virology* 106:92-99, 1980.
32. McEntee, K., Weinstock, G.M. and Lehman, I.R.: Binding of the recA protein of *Escherichia coli* single and double-stranded DNA. *J. Biol. Chem.* 256:8835-8844, 1981.
33. Weinstock, G.M., McEntee, K., and Lehman, I.R.: Hydrolysis of nucleoside triphosphates catalyzed by the recA protein of *Escherichia coli*. Characterization of ATP hydrolysis. *J. Biol. Chem.* 256:8829-8834, 1981.
34. Weinstock, G.M., McEntee, K., and Lehman, I.R.: Hydrolysis of nucleoside triphosphates catalyzed by the recA protein of *Escherichia coli*. Steady-state kinetic analysis of ATP hydrolysis. *J. Biol. Chem.* 256:8845-8849, 1981.
35. Weinstock, G.M., McEntee, K., and Lehman, I.R.: Hydrolysis of nucleoside triphosphates catalyzed by the recA protein of *Escherichia coli*. Hydrolysis of UTP. *J. Biol. Chem.* 256:8856-8858, 1981.
36. Weinstock, G.M., McEntee, K., and Lehman, I.R.: Interaction of the recA protein of *Escherichia coli* with adenosine 5'-0-(3 thiotriphosphate). *J. Biol. Chem.* 256:8850-8855, 1981.
37. Weinstock, G.M. and McEntee, K.: RecA protein dependent proteolysis of bacteriophage lambda repressor: Characterization of the reaction and stimulation by DNA binding proteins. *J. Biol. Chem.* 256:10883-10888, 1981.

38. McEntee, K. and Weinstock, G.M.: The *tif-1* mutation alters polynucleotide recognition by the *recA* protein of *Escherichia coli*. *Proc. Natl. Acad. Sci. USA.* 78:6061-6065, 1981.
39. McEntee, K., and Weinstock, G.M.: The *recA* enzyme of *Escherichia coli* and recombination assays. In: *The Enzymes*. P.D. Boyer, ed. Academic Press, N.Y. 3rd edition, Vol. XIV., Part A, Pp. 445-470, 1981.
40. McEntee, K., Weinstock, G.M., and Lehman, I.R.: DNA and nucleoside triphosphate binding properties of *recA* protein from *Escherichia coli*. In: *Progress in Nucleic Acid Research and Molecular Biology*. W.E. Cohn, ed., Academic Press, N.Y. Pp. 265-279, 1981.
41. Weinstock, G.M.: Enzymatic activities of the *recA* protein of *Escherichia coli*. *Biochimie.* 63:611-616, 1982.
42. Weinstock, G.M., McEntee, K., and Lehman, I.R.: Stimulation of *recA* protein dependent strand assimilation and DNA complex formation by single-stranded DNA binding proteins. In: *New Approaches in Eukaryotic DNA Replication*. A.M. deRecondo, ed. Plenum Press, N.Y. Pp. 333-341, 1983.
43. Weinstock, G.M., Ap Rhys, C., Berman, M.L., Hampar, B., Jackson, D., Silhavy, T.J., Weisemann, J., and Zweig, M.: ORF expression vectors: A general method for antigen production in *Escherichia coli* using protein fusions to *b-galactosidase*. *Proc. Natl. Acad. Sci. USA.* 80:4432-4436, 1983.
44. Weinstock, G.M., Berman, M.L., and Silhavy, T.J.: Chimeric genetics with *b-galactosidase*. In: *Gene Amplification and analysis*. Vol. 3 Expression of cloned genes in prokaryotic and eukaryotic cells. Elsevier Science Publishing Co., Inc., N.Y. Pp. 27-64, 1983.
45. Bremer, E., Silhavy, T.J., Weisemann, J., and Weinstock, G.M.: Lambda *placMu*: A transposable derivative of bacteriophage lambda for creating *lacZ* protein fusions in a single step. *J. Bacteriol.* 158:1084-1093, 1984.
46. Weisemann, J.M., Funk, C., and Weinstock, G.M.: Measurement of *in vivo* expression of the *recA* gene of *Escherichia coli* by using *lacZ* gene fusions. *J. Bacteriol.* 160:112-121, 1984.
47. Weisemann, J.M. and Weinstock, G.M.: Use of transcription and translation signals from the colicin E1 gene (*cea*) to express DNA sequences in *Escherichia coli*. *Gene Analy. Tech.* 2:9-16, 1984.
48. Weinstock, G.M.: Vectors for expressing open reading frame DNA in *Escherichia coli* using *lacZ* gene fusions. In: *Genetic Engineering*. J.K. Setlow and A. Hollaender, eds. Plenum Press, N.Y. Vol. 6, pp. 31-48, 1984.
49. Bremer, E., Silhavy, T.J., and Weinstock, G.M.: Transposable lambda *placMu* phages for creating *lacZ* operon fusions and kanamycin-resistant insertions in *Escherichia coli*. *J. Bacteriol.* 162:1092-1099, 1985.
50. Weisemann, J.M. and Weinstock, G.M.: Direct selection for mutations reducing transcription or translation of the *recA* gene of *Escherichia coli* with a *recA-lacZ* protein fusion. *J. Bacteriol.* 163:748-755, 1985.
51. Salles, B., Weisemann, J.M., and Weinstock, G.M.: Temporal control of colicin E1 induction. *J. Bacteriol.* 169:5028-5034, 1987
52. Weinstock, G.M.: Review of Genetics and Molecular Biology by R. Schlieff. *Quarterly Rev. Biol.* 62:69, 1987.
53. Weinstock, G.M.: Use of open reading frame expression vectors. In: *Methods in Enzymology: Recombinant DNA*, Part E. R. Wu and L. Grossman, eds. Academic Press, Orlando, Florida. vol.154, pp.156-163, 1987.
54. Weinstock, G.M.: General recombination in *Escherichia coli*. In: *Escherichia coli and Salmonella typhimurium: Cellular and Molecular Biology*. J.L. Ingraham, K. Brooks Low, Boris Magasanik, Frederick C. Neidhardt, Moselio Schaechter, and H. Edwin Umbarger, eds. American Society for Microbiology, Washington D.C., pp. 1034-1043, 1987.
55. Leibowitz, J.L., Perlman, S., Weinstock, G., DeVries, J.R., Budzilowicz, C., Weisemann, J. M. and Weiss, S.R.: Detection of a murine coronavirus nonstructural protein encoded in a downstream open reading frame. *Virol.* 164:156-164, 1988.
56. Weisemann, J.M. and Weinstock, G.M.: Mutations at the cysteine codons of the *recA* gene of *Escherichia coli*. *DNA* 7:389-398, 1988.
57. Bremer, E., Silhavy, T.J., and Weinstock, G.M.: Transposition of lambda *placMu* is mediated by the A protein altered at its carboxy-terminal end. *Gene* 71:177-186, 1988.
58. Salles, B. and Weinstock, G.M.: Mutation of the promoter and LexA binding sites of *cea*, the gene encoding colicin E1. *Mol.Gen.Genet.* 215:483-489, 1989.
59. Salles, B. and Weinstock, G.M.: Interaction of the CRP-cAMP complex with the *cea* regulatory region. *Mol.Gen.Genet.* 215:537-542, 1989.
60. Highlander, S.K., Chidambaram, M., Engler, M.J., and Weinstock, G.M.: DNA sequence of the *Pasteurella haemolytica* leukotoxin gene cluster. *DNA* 8:15-28,
61. Zoltick, P.W., Leibowitz, J.L., DeVries, J.R., Weinstock, G.M., and Weiss, S.R.: A general method for the induction and screening of antisera for cDNA- encoded polypeptides: antibodies specific for a coronavirus putative polymerase-encoding
62. Highlander, S.K., Engler, M.J., and Weinstock, G.M.: Secretion and expression of the *Pasteurella haemolytica* leukotoxin. *J. Bacteriol.* 172:2343-2350, 1990.

63. Murray, B.E., Singh, K.V., Heath, J.D., Sharma, B., and Weinstock, G.M.: Comparison of Genomic DNA of Different Enterococcal Isolates Using Restriction Endonucleases with Infrequent Recognition Sites. *J. Clin. Micro.* 28:2059-2063, 1990.
64. Heath, J.D. and Weinstock, G.M.: Tandem duplications in the lac region of the Escherichia coli chromosome. *Biochimie* 73:343-352, 1991
65. Weinstock, G.M.: Transduction in Gram-negative bacteria. In: *Modern Microbial Genetics*. U.N. Streips and R.E. Yasbin, eds. Alan Liss Inc., N.Y. 1991, p. 253-270
66. Weisemann, J.M. and Weinstock, G.M.: The promoter of the recA gene of Escherichia coli. *Biochimie* 73:457-470, 1991
67. Murray, B.E., Singh, K.V., Markovitz, S.M., Lopardo, H.A., Patterson, J.E., Zervos, M.J., Ruboglio, E., Eliopoulos, G.M., Rice, L.B., Goldstein, S.W., Jenkins, S.G., Caputo, G.M., Nasnas, R., Moore, L.S., Wong, E.S., and Weinstock, G.M.: Evidence for clonal spread of a single strain of b-lactamase-producing Enterococcus (Streptococcus) faecalis to six hospitals in five states. *J. Inf. Dis.* 163:780-785, 1991.
68. Devoret, R. and Weinstock, G.M. (editors) *RecA and related proteins: From Recombination to SOS* Elsevier, Paris, 1991.
69. Ku, C.Y., Lu, Q., Ussuf, K.K., Weinstock, G.M., and Sanborn, B.M.: Hormonal regulation of cytochrome oxidase subunit mRNAs in rat Sertoli cells. *Molecular Endocrinology* 5:1669-1676, 1991.
70. Weinstock, G.M.: Review of the conference on RecA and Related Proteins. *The New Biologist* 3:126-129, 1991
71. Weinstock, G.M. and Highlander, S. K.: Bacterial virulence factors as targets for chemotherapy. In: *Emerging Targets in Antibacterial and Antifungal Chemotherapy*. J. A. Sutcliffe and N. H. Georgopapadakou, eds. Chapman and Hall, Inc., N.Y., pp.323-346, 1992.
72. Heath, J.D., Perkins, J., Sharma, B., and Weinstock, G.M.: NotI genomic cleavage map of Escherichia coli K-12 strain MG1655. *J. Bacteriol.* 174:558-567, 1992.
73. Perkins, J., Heath, J.D., and Weinstock, G.M.: SfiI genomic cleavage map of Escherichia coli K-12 strain MG1655. *Nucl. Acids Res.* 20:1129-1137, 1992
74. Eraso, J.M. and Weinstock, G.M.: Anaerobic control of colicin E1 production. *J. Bacteriol.* 174:5101-5109, 1992.
75. Lupski, J.R. and Weinstock, G.M.: Short, interspersed repetitive DNA sequences in prokaryotic genomes. *J. Bacteriol.* 174:4525-4529, 1992.
76. Perkins, J., Heath, J.D., Sharma, B., and Weinstock, G.M.: XbaI genomic cleavage map of Escherichia coli K-12 strain MG1655 and comparative analysis of other strains. *J. Mol. Biol.* 232:419-445, 1993.
77. Highlander, S.K., Wickersham, E.A., Garza, O., and Weinstock, G.M.: Expression of the Pasteurella haemolytica leukotoxin is inhibited by a locus that encodes an ATP-binding cassette homologue. *Infect. Immun.* 61:3942-3951, 1993.
78. Murray, B.E., Singh, K.V., Ross, R.P., Heath, J.D., Dunny, G.M., and Weinstock, G.M.: Generation of restriction map of Enterococcus faecalis strain OG1 and investigation of growth requirements and regions encoding biosynthetic function. *J. Bacteriol.* 175:5216-5223, 1993.
79. Highlander, S.K. and Weinstock, G.M.: Static DNA bending and protein interactions within the Pasteurella haemolytica leukotoxin promoter region. Development of an activation model for leukotoxin transcriptional control. *DNA and Cell Biol.* 13:171-181, 1994.
80. Weinstock, G.M.: Bacterial genomes: Mapping and stability. *ASM News* 60:73-78, 1994.
81. Norris, S., Walker, E., Heath, J.D., Howell, J., Chidambaram, M., and Weinstock, G.M.: Physical map of the chromosome of Treponema pallidum. *J. Bacteriol.* 177:1797-1804, 1994.
82. Bianco, P.R. and Weinstock, G.M.: Automation of the assay for β -galactosidase. *BioTechniques* 17:974-980, 1994.
83. Choudhary, M., Mackenzie, C., Nereng, K.S., Sodergren, E., Weinstock, G.M., and Kaplan, S.: Multiple chromosomes in bacteria: Structure and function of chromosome II of Rhodobacter sphaeroides 2.4.1T. *J. Bacteriol.* 176:7694-7702, 1994.
84. Walker, E.M., Weinstock, G.M., and Norris, S.J.: Genetics of Treponema pallidum. Chapter 3 in E.W. Hook III and S.A. Lukehart (eds.), *Syphilis*. Blackwell Publishing, New York. 1995.
85. Chidambaram, M., Sharma, B., Petras, S.F., Reese, C.P., Froshauer, S., and Weinstock, G.M., and: Isolation of Pasteurella haemolytica leukotoxin mutants. *Infect. Immun.* 63:1027-1032, 1995.
86. Petras, S.F., Chidambaram, M., Illyes, E.F., Froshauer, S., Weinstock, G.M., and Reese, C.P.: Antigenic and virulence properties of Pasteurella haemolytica leukotoxin mutants. *Infect. Immun.* 63:1033-1039, 1995.
87. Mackenzie, C., Chidambaram, M., Sodergren, E., Kaplan, S., and Weinstock, G.M.: DNA repair mutants of Rhodobacter sphaeroides 2.4.1. *J. Bacteriol.* 177:3027-3035, 1995.
88. Li, X., Weinstock, G.M., and Murray, B.E.: Generation of auxotrophic mutants of Enterococcus faecalis. *J. Bacteriol.* 177:6866-6873, 1995.
89. Karlin, S., Weinstock, G.M., and Brendel, V.: Bacterial classifications derived from RecA protein sequence comparisons. *J. Bacteriol.* 177:6881-6893, 1995.

90. Eraso, J.M., Chidambaram, M., and Weinstock, G.M.: Increased production of colicin E1 in stationary phase. *J. Bacteriol.* 178:1928-1935, 1996.
91. You, Y., Elmore, S., Colton, L., Mackenzie, C., Stoops, J.K., Weinstock, G.M., and Norris, S.J.: Characterization of the cytoplasmic filament protein gene (cfpA) of *Treponema pallidum* subsp. *pallidum*. *J. Bacteriol.* 178:3177-3187, 1996.
92. Froshauer, S., Silvia, A.M., Chidambaram, M., Sharma, B., and Weinstock, G.M.: Sensitization of bacteria to danofloxacin by temperate prophages. *Antimicrobiol. Agents Chemother.* 40:1561-1563, 1996.
93. Bianco, P.R. and Weinstock, G.M.: Interaction of the RecA protein of *Escherichia coli* with single-stranded oligodeoxyribonucleotides. *Nucl. Acids Res.* 24:4933-4939, 1996.
94. Pierson, D.L., Chidambaram, M., Heath, J.D., Mallary, L., Mishra, S.K., Sharma, B., and Weinstock, G.M.: Epidemiology of *Staphylococcus aureus* During Space Flight. *FEMS Microbiol. Immunol.* 16:273-281, 1996.
95. Lupski, J.R., Roth, J.R., and Weinstock, G.M.: Chromosomal duplications in bacteria, fruitflies, and humans. *Am. J. Hum. Gen.* 58:21-27, 1996.
96. Hardham, J.M., Stamm, L.V., Porcella, S., Frye, J.G., Barnes, N.Y., Howell, J.K., Mueller, S.L., Radolf, J.D., Weinstock, G.M., and Norris, S.J.: Identification and transcriptional analysis of a *Treponema pallidum* operon encoding a putative ABC transport system, an iron-activated repressor protein homolog, and a glycolytic pathway enzyme homolog. 1997. *Gene* 197:47-64.
97. Sohocki, M.M., Sullivan, L.S., Harrison, W.R., Sodergren, E.J., Elder, F.F.B., Weinstock, G.M., Tanase, S., and Daiger, S.P.: Human glutamate pyruvate transaminase (GPT): Localization to 8q24.3, cDNA and genomic sequences, and polymorphic sites. *Genomics* 40:247-252. 1997.
98. Xu, Y., Jiang, L., Murray, B.E., and Weinstock, G.M.: *Enterococcus faecalis* antigens in human infection. *Infect. Immun.* 65:4207-4215, 1997
99. Choudhary, M., Mackenzie, C., Nereng, K., Sodergren, E., Weinstock, G.M., and Kaplan, S.: Low-resolution sequencing of *Rhodobacter sphaeroides* 2.41T: chromosome II is a true chromosome. *Microbiology* 143:3085-3099, 1997.
100. de Bruijn, F.J., Lupski, J.R., and Weinstock, G.M. (editors): *Bacterial Genomes: Physical Structure and Analysis* Chapman & Hall, New York, 1998.
101. Mackenzie, C., Choudhary, M., Nereng, K.S., Sodergren, E., Chidambaram, M., Weinstock, G.M., and Kaplan, S.: *Rhodobacter sphaeroides* 2.4.1T. in deBruijn, F.J., Lupski, J.R., and Weinstock, G.M. (eds.): *Bacterial Genomes: Physical Structure and Analysis*. Chapman & Hall, New York, 1998, pp. 729-731.
102. Murray, B.E., Singh, K.V., Jiang, L., Li, X., Heath, J.D., and Weinstock, G.M.: *Enterococcus faecalis*. in deBruijn, F.J., Lupski, J.R., and Weinstock, G.M. (eds.) *Bacterial Genomes: Physical Structure and Analysis*. Chapman & Hall, New York, 1998, pp. 649-650.
103. Norris, S.J., Walker, E.M., Howell, J.K., You, Y., Hoffmaster, A.R., Heath, J.D., Chidambaram, M., and Weinstock, G.M.: *Treponema pallidum* subsp *pallidum* (Nichols)Physical. in deBruijn, F.J., Lupski, J.R., and Weinstock, G.M. (eds.) *Bacterial Genomes: Physical Structure and Analysis*. Chapman & Hall, New York, 1998, pp. 773-774.
104. Weinstock, G.M.: *Escherichia coli*. in deBruijn, F.J., Lupski, J.R., and Weinstock, G.M. (eds.) *Bacterial Genomes: Physical Structure and Analysis*. Chapman & Hall, New York, 1998, pp. 651-653.
105. Mackenzie, C., Chidambaram, M., Choudhary, M., Nereng, K.S. Kaplan, S., and Weinstock, G.M.: Sequence skimming of chromosome II of *Rhodobacter sphaeroides* 2.4.1T. in deBruijn, F.J., Lupski, J.R., and Weinstock, G.M. (eds.) *Bacterial Genomes: Physical Structure and Analysis*. Chapman & Hall, New York, 1998, pp. 541-551.
106. Weinstock, G.M.: Resources for the *Escherichia coli* genome project. in deBruijn, F.J., Lupski, J.R., and Weinstock, G.M. (eds.) *Bacterial Genomes: Physical Structure and Analysis*. Chapman & Hall, New York, 1998, pp. 489-497.
107. Malathum, K., Singh, K.V., Weinstock, G.M., and Murray, B.E. REP-PCR versus pulsed field gel electrophoresis in the epidemiologic evaluation of *Enterococcus faecalis*. *J. Clin. Micro.* 36:211-215, 1998.
108. Teng, F., Murray, B.E., and Weinstock, G.M.: Conjugal transfer of plasmid DNA from *Escherichia coli* to enterococci: a method to make insertion mutations. *Plasmid* 39:182-186, 1998.
109. Bianco, P.R. and Weinstock, G.M.: Characterization of RecA1332 in vivo and in vitro. A role for α -helix as a liaison between the subunit interface and the DNA and ATP binding domains of RecA protein. *Genes to Cells* 3: 79-97, 1998.
110. Bianco, P.R. and Weinstock, G.M.: UTP is a cofactor for the DNA strand exchange reaction performed by the RecA protein of *Escherichia coli*. *Biochemistry* 37:7313-7320, 1998.
111. Qin, X., Singh, K.V., Xu, Y., Weinstock, G.M., and Murray, B.E.: Effect of disruption of a gene encoding an autolysin of *Enterococcus faecalis* OG1RF. *Antimicrob. Ag. Chemoth.* 42:2883-2888, 1998.
112. Fraser, C.M., Norris, S.J., Weinstock, G.M., White, O., Sutton, G.G., Dodson, R., Gwinn, M., Hickey, E.K., Clayton, R., Ketchum, K.A., Sodergren, E., Hardham, J.M., McLeod, M.P., Salzberg, S., Peterson, J., Khalak, H., Richardson, D., Howell, J.K., Chidambaram, M., Utterback, T., McDonald, L., Artiach, P., Bowman, C., Cotton, M.D., Fujii, C., Garland, S., Hatch, B., Horst, K., Roberts, K., Watthey, L., Weidman,

- J., Smith, H.O., and Venter, J.C.: Complete genome sequence of *Treponema pallidum*, the syphilis spirochete. *Science* 281:375-388, 1998.
113. Xiao, J., Höök, M., Weinstock, G.M., and Murray, B.E.: Conditional adherence of *Enterococcus faecalis* to extracellular matrix proteins. *FEMS Immunol. Med. Microbiol.* 21:287-295, 1998.
114. Xu, Y., Murray, B.E., and Weinstock, G.M.: A cluster of genes for polysaccharide biosynthesis in *Enterococcus faecalis* strain OG1RF. *Infect. Immun.* 66: 4313-4323, 1998.
115. Singh, K.V., Qin, X., Weinstock, G.M., and Murray, B.E.: Generation and testing of mutants of *Enterococcus faecalis* in a mouse peritonitis model. *J. Inf. Dis.* 178:1416-1420, 1998.
116. Singh, K.V., Weinstock, G.M., and Murray, B.E.: In vivo testing of an *Enterococcus faecalis* efaA mutant and use of efaA homologs for species identification. *FEMS Immunol. Med. Microbiol.* 21:323-331, 1998.
117. Palzkill, T., Huang, W., and Weinstock, G.M.: Mapping protein-ligand interactions using whole genome phage display libraries. *Gene* 221:79-83, 1998.
118. Xu, Y., Jiang, L., Jin, X., Murray, B.E., and Weinstock, G.M.: Isolation of antigen-encoding genes from genomic libraries of enterococcal DNA. *Methods in Cell Science* 20:95-106, 1998
119. Xiang, Q., Teng, F., Xu, Y., Weinstock, G.M., and Murray, B.E.: Targeted mutagenesis of enterococcal genes. *Methods in Cell Science* 20:21-33, 1998.
120. Norris, S.J., Fraser, C.M., and Weinstock, G.M.: Illuminating the agent of syphilis: the *Treponema pallidum* genome project. *Electrophoresis* 19:551-553, 1998
121. Weinstock, G.M., Hardham, J.M., McLeod, M.P., Sodergren, E.J., and Norris, S.J.: The genome of *Treponema pallidum*: new light on the agent of syphilis. *FEMS Microbiological Reviews* 22:323-332, 1998.
122. Coque, T.M., Singh, K.V., Weinstock, G.M., and Murray, B.E.: Characterization of dihydrofolate reductase genes from trimethoprim-susceptible and trimethoprim-resistant strains of *Enterococcus faecalis*. *Antimicrob. Agents Chemother.* 43:141-147 1999.
123. Rich, R. L., B. Kreikemeyer, R. T. Owens, S. LaBrenz, S. V. Narayana, G. M. Weinstock, B. E. Murray, and M. Hook. Ace is a collagen-binding MSCRAMM from *Enterococcus faecalis*. *J. Biol. Chem.* 274:26939-26945. 1999.
124. Murray, B.E. and Weinstock, G.M.: Enterococci: new aspects of an old organism. *Proc. Assoc. Am. Physicians* 111:328-334. 1999.
125. Xu, Y., Singh, K.V., Qin, X., Murray, B.E., and Weinstock, G.M.: Analysis of a gene cluster of *Enterococcus faecalis* involved in polysaccharide biosynthesis. *Inf. Immun.* 68:815-823, 2000.
126. Qin, X., Singh K.V., Weinstock, G.M., and Murray, B.E.: Effects of *Enterococcus faecalis* fsr genes on production of gelatinase and a serine protease and virulence. *Infect. Immun.* 68:2579-2586, 2000
127. Weinstock, G.M., Norris, S.J., Sodergren, E.J., and Smajs, D.: Identification of virulence genes in silico: Infectious disease genomics. In: *Virulence Mechanisms of Bacterial Pathogens*, 3rd Edition. K.A. Brogden et al. (eds.), ASM Press, Washington, DC, pp. 251-261, 2000.
128. Adams, M.D., et al.: The genome sequence of *Drosophila melanogaster*. *Science* 287:2185-2195, 2000.
129. Nallapareddy, S., Qin, X., Weinstock, G.M., Hook, M., and Murray, B.E.: *Enterococcus faecalis* adhesin, Ace, mediates attachment to extracellular matrix proteins collagen type IV and laminin as well as collagen type I. *Infect. Immun.* 68:5218-5224, 2000
130. Nallapareddy, S., Singh, K.V., Duh, R.-W., Weinstock, G.M., and Murray, B.E.: Diversity of ace, a gene encoding a microbial surface component recognizing adhesive matrix molecules, from different strains of *Enterococcus faecalis* and evidence for production of Ace during human infections. *Infect. Immun.* 68:5210-5217, 2000
131. Norris, S.J. and Weinstock, G.M.: The genome sequence of *Treponema pallidum*, the syphilis spirochete: will clinicians benefit?. *Curr. Opin. Inf. Dis.* 13:29-36, 2000.
132. Weinstock, G.M., Smajs, D., Hardham, J., and Norris, S.J.: From microbial genome sequence to applications. *Res. Microbiol.* 151:151-158, 2000
133. Norris, S.J.; Cox, D.L.; Weinstock, G.M.: Biology of *Treponema pallidum*: correlation of functional activities with genome sequence data. *J. Mol. Microbiol. Biotechnol.* 3:37-62, 2001.
134. International Human Genome Sequencing Consortium: Initial sequencing and analysis of the human genome. *Nature* 409: 860-921, 2001.
135. Davis, D.R., McAlpine, J.B., Pazoles, C.J., Talbot, M.K., Alder, E.A., White, A.C., Jonas, B.M., Murray, B.E., Weinstock, G.M., and Rogers, B.L.: *Enterococcus faecalis* Multi-Drug Resistance Transporters: Application for Antibiotic Discovery. *J. Molec. Microbiol. Biotechnol.* 3:179-184, 2001.
136. Weinstock, G.M.: Genomics and bacterial pathogenesis. *Emerg. Inf. Dis.* 6:496-504, 2001.
137. Norris, S.J., Cox, D.L., and Weinstock, G.M.: Biology of *Treponema pallidum*: Correlation of Functional Activities With Genome Sequence Data. In: *The Spirochetes: Molecular and Cellular Biology*. M.H. Saier Jr. and J. Garcia-Lara (eds.), Horizon Press, Norfolk UK, Ch. 18, 2001.
138. Qin, X., Singh K.V., Weinstock, G.M., and Murray, B.E.: Characterization of fsr, a Regulator Controlling the Expression of Gelatinase and Serine Protease in *Enterococcus faecalis* OG1RF. *J. Bacteriol.* 183:3372-3382, 2001.

139. Smajs, D. and Weinstock, G.M.: Genetic organization of colicin Js activity, immunity and release genes on pColJs and toxic activity of colicin Js polypeptide. *J. Bacteriol.* 183:3949-3957, 2001
140. Smajs, D. and Weinstock, G.M.: The iron- and virB-regulated cjrABC operon of *Shigella* and enteroinvasive *Escherichia coli* strains codes for colicin Js receptor. *J. Bacteriol.* 183:3958-3966, 2001.
141. Jonas, B.M., Murray, B.E., and Weinstock, G.M.: Characterization of emeA, a norA homolog and a multidrug resistance efflux pump in *Enterococcus faecalis*. *Antimicrob. Agents Chemother.* 45:3574-9, 2001.
142. Chen, R., Bouck, J.B., Weinstock, G.M., and Gibbs, R.G.: Comparing vertebrate whole genome shotgun reads to the human genome. *Gen. Res.* 11:1807-16, 2001.
143. Smajs, D., McKeivitt, M., Wang, L., Howell, J.K., Norris, S.J., Palzkill, T., and Weinstock, G.M. BAC library of *Treponema pallidum* DNA in *E. coli*. *Gen. Res.* 12:515-22, 2002.
144. Teng, F., Wang, L., Singh, K.V., Murray, B.E., and Weinstock, G.M.: Involvement of PhoP-PhoS homologs in *Enterococcus faecalis* virulence. *Infect. Immun.* 70:1991-6, 2002.
145. Davis, D.R., McAlpine, J.B., Pazoles, C.J., Talbot, M.K., Alder, E.A., White, A.C., Jonas, B.M., Murray, B.E., Weinstock, G.M., and Roger, B.L. *Enterococcus faecalis* multi-drug resistance transporters: Application for antibiotic discovery. In: *Microbial Multidrug Efflux*. I.T. Paulsen and K.Lewis (eds.), Horizon Scientific Press, Norfolk, England. pp83-98, 2002.
146. Teng F, Jacques-Palaz KD, Weinstock GM, Murray BE. Evidence that the enterococcal polysaccharide antigen gene (epa) cluster is widespread in *Enterococcus faecalis* and influences resistance to phagocytic killing of *E. faecalis*. *Infect Immun.* 70:2010-5, 2002.
147. Smajs D, Karpathy S, Smarda J, Weinstock GM. Colicins produced by the *Escherichia fergusonii* strains closely resemble colicins encoded by *Escherichia coli*. *FEMS Microbiol Lett.* 208:259-62, 2002.
148. Singh, K.V., Weinstock, G.M., and Murray, B.E. An *Enterococcus faecalis* species specific ABC homologue (Lsa) is required for the resistance of this species to clindamycin and quinupristin-dalfopristin. *Antimicrob. Ag. Chemother.* 46:1845-50, 2002.
149. Celniker, S.E., Wheeler, D.A., Kronmiller, B., Carlson, J.W., Halpern, A., Patel, S., Adams, M., Champe, M., Dugan, S.P., Frise, E., Hodgson, A., George, R.A., Hoskins, R.A., Laverty, T., Muzny, D.M., Nelson, C.R., Pacleb, J.M., Park, S., Pfeiffer, B.D., Richards, S., Sodergren, E.J., Svirskas, R., Tabor, P.E., Wan, K., Scherer, S.E., Stapleton, M., Sutton, G.G., Venter, C., Weinstock, G., Myers, E.W., Gibbs, R.A., and Rubin, G.M. Finishing a whole genome shotgun: Release 3 of the *Drosophila melanogaster* euchromatic genome sequence. *Gen. Biol.* 3: research0079.1-0079.14, 2002.
150. Teng, F., Kawalec, M., Weinstock, G.M., Hryniewicz, W., and Murray, B.E. An *Enterococcus faecium* secreted antigen, SagA, exhibits broad-spectrum binding to extracellular matrix (ECM) proteins and appears essential for *E. faecium* growth. *Inf. Immun.* 71:5033-5041 2003.
151. McKeivitt, M.; Patel, K.; Smajs, D.; Marsh, M.; McLoughlin, M.; Norris, S.J.; Weinstock, G.M.; Palzkill, T. Systematic cloning of *Treponema pallidum* open reading frames for protein expression and antigen discovery. *Genome Res.* 13:1665-1674, 2003.
152. Šmajs, D, Šmarda, J, and Weinstock, G.M. The *Escherichia fergusonii* iucABCD iutA genes are located within a larger chromosomal region similar to pathogenicity Islands. *Folia Microbiol (Praha)*.48:139-47, 2003.
153. Nallapareddy, S.R., Weinstock, G.M., and Murray, B.E. Clinical isolates of *Enterococcus faecium* exhibit strain-specific collagen binding mediated by Acm, a new member of the MSCRAMM family. *Mol Microbiol.* 47:1733-47, 2003.
154. Milosavljevic, A., M. Csuros, Weinstock, G.M et al. Shotgun sequencing, clone pooling, and comparative strategies for mapping and sequencing. *Targets*, 2(6):245-252, 2003.
155. The International HapMap Consortium: The International HapMap Project. *Nature* 426, 789 – 796, 2003.
156. Gibbs, R.A. and Weinstock, G.M. Evolving methods for the assembly of large genomes. *Cold Spring Harbor Symp. Quant. Biol.*, Cold Spring Harbor Press, Cold Spring Harbor, NY, Vol. LXVIII, pp. 189-194, 2003.
157. Chen, R., Sodergren, E., Weinstock, G. M., & Gibbs, R. A. Dynamic building of a BAC clone tiling path for the Rat Genome Sequencing Project. *Genome Res.* 14, 679-684, 2004.
158. Gibbs, R. A. et al. Genome sequence of the Brown Norway rat yields insights into mammalian evolution. *Nature* 428, 493-521, 2004.
159. Havlak, P. et al. The Atlas genome assembly system. *Genome Res.* 14, 721-732 (2004).
160. Seshadri, R. et al. Comparison of the genome of the oral pathogen *Treponema denticola* with other spirochete genomes. *Proc. Natl. Acad. Sci. U.S.A* 101, 5646-5651, 2004.
161. Zeng, J., Teng, F., Weinstock, G. M., & Murray, B. E. Translocation of *Enterococcus faecalis* strains across a monolayer of polarized human enterocyte-like T84 cells. *J. Clin. Microbiol.* 42, 1149-1154, 2004.
162. Zhang, Z. et al. Genomic analysis of the nuclear receptor family: new insights into structure, regulation, and evolution from the rat genome. *Genome Res.* 14, 580-590, 2004.
163. Smajs, D., Norris, S.J., and Weinstock, G.M.: Construction of small genome BAC library for functional and genomic applications. In: *Methods in Molecular Biology* vol. 255: Bacterial Artificial Chromosomes

- Vol. 1: Library Construction, Physical Mapping, and Sequencing. S. Zhao and M. Stodolsky (eds), Humana Press Inc., Totowa, NJ, p. 47-56, 2004.
164. Pal, S., Mak, S., and Weinstock, G.M.: Preparation of BAC libraries from bacterial genomes by in vitro packaging. In: Methods in Molecular Biology vol. 255: Bacterial Artificial Chromosomes Vol. 1: Library Construction, Physical Mapping, and Sequencing. S. Zhao and M. Stodolsky (eds), Humana Press Inc., Totowa, NJ., p. 57-68, 2004.
165. International HapMap Consortium: Integrating ethics and science in the International HapMap project. *Nat. Gen.* 5:467-75, 2004.
166. McLeod, M., Qin, X., Karpathy, S., Gioia, J., Highlander, S., Fox, G.E., McNeill, T.Z., Jiang, H., Muzny, D., Jacob, L., Hawes, A.C., Sodergren, E., Gill, R., Hume, J., Morgan, M., Fan, G., Amin, A.G., Gibbs, R.A., Hong, C., Yu, X., Walker, D.H., and Weinstock, G.M.: Complete Genome Sequence of *Rickettsia typhi* and Comparison with Sequences of Other *Rickettsiae*. *J. Bacteriol.* 186:5842-55, 2004.
167. International Human Genome Sequencing Consortium. Finishing the euchromatic sequence of the human genome. *Nature* 431:931-45, 2004.
168. RL Alford, C Summers, S Wright, K Henderson, C Maxwell, D Gassmann, K Ghonima, K Bradley, H Valdes, N Greig, J Wise, D Van Tuerenhout, DM Brooks, D Temple, KE Morris, CM Rives, SE Scherer, G Weinstock, RA Gibbs, R McDonald. The Living Genome: Reading the Book of Life-- A Model for Community-Based Genetics Education. *Biology Digest* 2004 Nov;31(3):10-17.
169. Richards, S., Liu, Y., Bettencourt, B.R., Hradecky, P., Letovsky, S., Nielsen, R., Thornton, K., Todd, M.J., Chen, R., Meisel, R.P., Couronne, O., Hua, S., Smith, M.A., Zhang, P., Liu, J., Bussemaker, H.J., van Batenburg, M.F., Howells, S.L., Scherer, S.E., Sodergren, E., Matthews, B.B., Crosby, M.A., Schroeder, A.J., Ortiz-Barrientos, D., Rives, C.R., Metzker, M.L., Muzny, D.M., Scott, G., Steffen, D., Wheeler, D.A., Worley, K.C., Havlak, P., Durbin, K.J., Egan, A., Gill, R., Hume, J., Morgan, M.B., Miner, G., Hamilton, C., Huang, Y., Waldron, L., Verduzco, D., Clerc-Blankenburg, K.P., Dubchak, I., Noor, M.A.F., Anderson, W., White, K.P., Clark, A.G., Schaeffer, S.W., Gelbart, W., Weinstock, G.M., and Gibbs, R.A. Comparative genome sequencing of *Drosophila pseudoobscura*: Chromosomal, gene and cis-element evolution. *Genome Research* 15:1-18, 2005.
170. Milosavljevic, A., Harris, R.A., Sodergren, E.J., Jackson, A.R., Kalafus, K.J., Hodgson, A., Cree, A., Dai, W., Csuros, M., Zhu, B., de Jong, P.J., Weinstock, G.M., and Gibbs, R.A. Pooled Genomic Indexing of Rhesus Macaque. *Genome Research* 15:292-301, 2005.
171. Smajs, D. McKevitt, M., Howell, J.K., Norris, S.J., Cai, W.-W., Palzkill, T., and Weinstock, G.M. Transcriptome of *Treponema pallidum*: Gene Expression Profile during Experimental Rabbit Infection. *J. Bacteriol.* 187:1866-1874, 2005.
172. Ross, M.T., et al. The DNA sequence of the human X chromosome. *Nature* 434:325-337, 2005
173. L. Eichinger, J.A. Pachebat, G. Glöckner, M.-A. Rajandream, R. Sugang, M. Berriman, J. Song, R. Olsen, K. Szafranski, Q. Xu, B. Tunggal, S. Kummerfeld, M. Madera, B. A. Konfortov, P. Farbrother, A. T. Bankier, R. Lehmann, N. Hamlin, R. Davies, P. Gaudet, P. Fey, K. Pilcher, G. Chen, D. Saunders, E. Sodergren, P. Davis, A. Kerhornou, X. Nie, N. Hall, C. Anjard, L. Hemphill, N. Bason, F. Rivero, B. Desany, E. Just, T. Morio, R. Rost, C. Churcher, J. Cooper, S. Haydock, N. van Driessche, A. Cronin, I. Goodhead, D. Muzny, T. Mourier, A. Pain, M. Lu, D. Harper, R. Lindsay, H. Hauser, K. James, M. Quiles, M. B. Mohan, T. Saito, C. Buchrieser, A. Wardroper, M. Felder, M. Thangavelu, D. Johnson, A. Knights, H. Loulseged, K. Mungall, K. Oliver, C. Price, M.A. Quail, H. Urushihara, J. Hernandez, E. Rabbinowitsch, D. Steffen, M. Sanders, J. Ma, Y. Kohara, S. Sharp, M. Simmonds, S. Spiegler, A. Tivey, S. Sugano, B. White, D. Walker, J. Woodward, T. Winckler, Y. Tanaka, G. Shaulsky, M. Schleicher, G. Weinstock, A. Rosenthal, E.C. Cox, R. L. Chisholm, R. Gibbs, W. F. Loomis, M. Platzter, R. R. Kay, J. Williams, P. H. Dear, A. A. Noegel, B. Barrell and A. Kuspa. The genome of the social amoeba *Dictyostelium discoideum*. *Nature* 435:43-57, 2005.
174. Alford, R.L., Summers, C., Valdes, H., Belcher, M., Ghonima, K., Law, C., Reiff, P., Morris, K.E., Rives, C.M., Scherer, S.E., Weinstock, G., Gibbs, R.A.. Genetic testing, biotechnology, and GMO's: A snapshot of public opinion 2003-2004. *Genet.Med.* 7: 454-455 (2005)
175. McKevitt, M.; Brinkman, M.B.; McLoughlin, M.; Perez, C.; Howell, J.K.; Weinstock, G.M.; Norris, S.J.; and Palzkill, T. Genome scale identification of *Treponema pallidum* antigens. *Infect. Immun.* 73:4445-4450, 2005
176. Siepel, A., Bejerano, G., Pedersen, J.S., Hinrichs, A., Hou, M., Rosenbloom, K., Clawson, H., Spieth, J., Hillier, L.W., Richards, S., Weinstock, G.M., Wilson, R.K., Gibbs, R.A., Kent, W.J., Miller, W., and Haussler, D. Evolutionarily Conserved Elements in Vertebrate, Fly, Worm, and Yeast Genomes. *Gen. Res.* 15:1034-1050, 2005.
177. Nallapareddy S.R., Wenxiang H., Weinstock G.M., and Murray B.E. Molecular characterization of a widespread, pathogenic, and antibiotic resistance-receptive *Enterococcus faecalis* lineage and dissemination of its putative pathogenicity island. *J Bacteriol.* 2005 187:5709-18.
178. Brettin, T., Altherr, M.R., Du, Y., Mason, R., Friedrich, A., Potter, L., Langford, C., Keller, T.J., Jens, J., Howie, H., Weyands, N., Clary, S., Prichard, K., Wachocki, S., Sodergren, E., Dillard, J.P., Weinstock, G.,

- So, M., and Arvidson, C.G. Expression capable library for studies of *Neisseria gonorrhoeae*, version 1.0. *BMC Microbiology* 2005, 5:50.
179. International HapMap Consortium. A haplotype map of the human genome. *Nature* 437:1299-1320, 2005
180. Martin KA, Siefert JL, Yerrapragada S, Lu Y, McNeill TZ, Moreno PA, Weinstock GM, Widger WR, Fox GE. Cyanobacterial signature genes. *Photosynth Res.* 75:211-21, 2005
181. Brinkman, M.B.; McKeivitt, M.; McLoughlin, M.; Perez, C.; Howell, J.K.; Weinstock, G.M.; Norris, S.J.; and Palzkill, T. Reactivity of antibodies from syphilis patients to a protein array representing the *Treponema pallidum* proteome. *J. Clin. Microbiol.* 44:888-891 2006.
182. Scherer, S., et al. The finished DNA sequence of human chromosome 12. *Nature* 440:346-351, 2006.
183. Childers, C.P., Newkirk, H.L., Honeycutt, D.A., Ramlachan, N., Muzney, D.M., Sodergren, E., Gibbs, R.A., Weinstock, G.M., Womack, J.E., and Skow, L.C. Comparative analysis of the bovine MHC class IIb sequence identifies inversion breakpoints and three unexpected genes. *Animal Gen.* 37:121-129, 2006.
184. Smajs, D., Matejkova, P., and Weinstock, G.M. Recognition of a pore-forming colicin Y by its cognate immunity protein. *FEMS Microbiol. Lett.* 258:108-113, 2006.
185. Highlander, S.K., Weissenberger, S., Alvarez, L.E., Weinstock, G.M., and Berget, P.B. Complete nucleotide sequence of a P2 family lysogenic bacteriophage, varphiMhaA1-PHL101, from *Mannheimia haemolytica* serotype A1. *Virology* 350:79-89, 2006.
186. Muzny, D.M., et al. The DNA sequence, annotation and analysis of human chromosome 3. *Nature* 440:1194-1198, 2006.
187. Norris, S.J. and Weinstock, G.M. Comparative Genomics of Spirochetes. In *Pathogenic Treponema Molecular and Cellular Biology*. J.D. Radolf and S.A. Lukehart, eds. Caister Academic Press, Norwich, UK. 2006.
188. Petrosino, J., Xiang, Q., Karpathy, S.E., Jiang, H., Yerrapragada, S., Liu, Y., Gioia, J., Hemphill, L., Gonzalez, A., Raghavan, T. M., Uzman, A., Fox, G.E., Highlander, S., Reichard, M., Morton, R.J., Clinkenbeard, K.D., and Weinstock, G.M. Chromosome Rearrangement and Diversification of *Francisella tularensis* Revealed by the Type B (OSU18) Genome Sequence. *J. Bacteriol.*, 188:6977-6985, 2006.
189. Savard, J., Tautz, D., Richards, S., Weinstock, G.M., Gibbs, R.A., Werren, J.H., Tettelin, H., Leaf, D., and Lercher, M.J. Phylogenomic analysis reveals bees and wasps (Hymenoptera) at the base of the radiation of holometabolous insects. *Genome Res.* 16:1334-1338, 2006.
190. Gioia, J., Qin, X., Jiang, H., Clinkenbeard, K., Lo, R., Liu, Y., Fox, G.E., McLeod, M.P., McNeill, T.Z., Hemphill, L., Sodergren, E., Weinstock, G.M., and Highlander, S.K. The genome sequence of *Mannheimia haemolytica* A1: insights into virulence, natural competence and Pasteurellaceae phylogeny. *J. Bacteriol.* 188:7257-7266, 2006.
191. Elsik, C.G., Worley, K.C., Zhang, L., Milshina, N.V., Jiang, H., Reese, J.T., Childs, K.L., Venkatraman, A., Dickens, C.M., Weinstock, G.M., and Gibbs, R.A. Community annotation: procedures, protocols, and supporting tools. *Genome Res.* 16:1329-1333, 2006.
192. Robinson, G.E., Evans, J.D., Maleszka, R., Robertson, H.M., Weaver, D.B., Worley, K., Gibbs, R.A., and Weinstock, G.M. Sweetness and Light: Illuminating the Honey Bee Genome. *Insect Mol. Biol.* 15:535-539, 2006.
193. Qin, X., Evans, J.D., Aronstein, K.A., Murray, D., and Weinstock, G.M. Genome sequences of the honey bee pathogens *Paenibacillus larvae* and *Ascosphaera apis*. *Insect Molec. Biol.* 15:715-718, 2006.
194. Honey bee genome sequencing consortium. Insights into social insects from the genome of the honey bee *Apis mellifera*. *Nature* 443:931-949, 2006.
195. Weinstock, G.M., Smajs, D., Matejkova, P., Strouhal, M., Albert, T.J., Norris, S.J., Palzkill, T., and Sodergren, E.J. *Treponema* Genomics. In *Molecular Biology of Spirochetes*, pp. 96-100. F.C. Cabello, D. Hulinska, and H.P. Godfrey (eds.) NATO Science Series: Life and Behavioural Sciences, vol. 373. IOS Press, Amsterdam. 2006.
196. Sea Urchin Genome Sequencing Consortium. The genome of the sea urchin *Strongylocentrotus purpuratus*. *Science* 314:941-952, 2006.
197. Sodergren, E., Shen, Y., Song, X., Zhang, L., Gibbs, R.A., and Weinstock, G.M. Shedding genetic light on Aristotle's lantern. *Developmental Biol.* 300:2-8, 2006.
198. Elsik, C.G., Mackey, A.J., Reese, J.T., Milshina, N.V., Roos, D.S., and Weinstock, G.M. Creating a honey bee consensus gene list. *Genome Biol.* 8:R13, 2006.
199. Solignac, M., Zhang, L., Mougel, F., Li, B., Vautrin, D., Monnerot, M., Cornuet, J.-M., Worley, K.C., Weinstock, G.M., and Gibbs, R.A. The genome of *Apis mellifera*: dialog between linkage mapping and sequence assembly. *Genome Biol.* 8:403.1-403.4, 2007.
200. The Rhesus Macaque Genome Sequencing and Analysis Consortium, Gibbs RA, Rogers J, Katze MG, Bumgarner R, Weinstock GM, Mardis ER, Remington KA, Strausberg RL, Venter JC, Wilson RK, Batzer MA, Bustamante CD, Eichler EE, Hahn MW, Hardison RC, Makova KD, Miller W, Milosavljevic A, Palermo RE, Siepel A, Sikela JM, Attaway T, Bell S, Bernard KE, Buhay CJ, Chandrabose MN, Dao M, Davis C, Delehaunty KD, Ding Y, Dinh HH, Dugan-Rocha S, Fulton LA, Gabisi RA, Garner TT, Godfrey J, Hawes AC, Hernandez J, Hines S, Holder M, Hume J, Jhangiani SN, Joshi V, Khan ZM, Kirkness EF,

- Cree A, Fowler RG, Lee S, Lewis LR, Li Z, Liu YS, Moore SM, Muzny D, Nazareth LV, Ngo DN, Okwuonu GO, Pai G, Parker D, Paul HA, Pfannkoch C, Pohl CS, Rogers YH, Ruiz SJ, Sabo A, Santibanez J, Schneider BW, Smith SM, Sodergren E, Svatek AF, Utterback TR, Vattathil S, Warren W, White CS, Chinwalla AT, Feng Y, Halpern AL, Hillier LW, Huang X, Minx P, Nelson JO, Pepin KH, Qin X, Sutton GG, Venter E, Walenz BP, Wallis JW, Worley KC, Yang SP, Jones SM, Marra MA, Rocchi M, Schein JE, Baertsch R, Clarke L, Csuros M, Glasscock J, Harris RA, Havlak P, Jackson AR, Jiang H, Liu Y, Messina DN, Shen Y, Song HX, Wylie T, Zhang L, Birney E, Han K, Konkel MK, Lee J, Smit AF, Ullmer B, Wang H, Xing J, Burhans R, Cheng Z, Karro JE, Ma J, Raney B, She X, Cox MJ, Demuth JP, Dumas LJ, Han SG, Hopkins J, Karimpour-Fard A, Kim YH, Pollack JR, Vinar T, Addo-Quaye C, Degenhardt J, Denby A, Hubisz MJ, Indap A, Kosiol C, Lahn BT, Lawson HA, Marklein A, Nielsen R, Vallender EJ, Clark AG, Ferguson B, Hernandez RD, Hirani K, Kehrer-Sawatzki H, Kolb J, Patil S, Pu LL, Ren Y, Smith DG, Wheeler DA, Schenck I, Ball EV, Chen R, Cooper DN, Giardine B, Hsu F, Kent WJ, Lesk A, Nelson DL, O'Brien WE, Pruffer K, Stenson PD, Wallace JC, Ke H, Liu XM, Wang P, Xiang AP, Yang F, Barber GP, Haussler D, Karolchik D, Kern AD, Kuhn RM, Smith KE, Zweig AS. The Rhesus Macaque Genome Sequence Informs Biomedical and Evolutionary Analyses. *Science* 316:222-234, 2007.
201. Weinstock, G.M. ENCODE: More empowerment through genomics. *Genome Research* 17:667-668, 2007.
202. Weinstock, G.M. Genomes for the masses. *Technology Review* 110:32-33, 2007.
203. Margulies, E.H., et al. Relationship between evolutionary constraint and genome function in 1% of the human genome. *Genome Research*, 17:760-774, 2007.
204. The ENCODE Project Consortium. The ENCODE pilot project: identification and analysis of functional elements in 1% of the human genome. *Nature* 447:799-816, 2007.
205. Weinstock, G.M., Smajs, D., Palzkill, T., and Norris, S.J. Comparative pathogenomics of spirochetes. In *Pathogenomics*, M.J. Pallen, K.E. Nelson, and G.M. Preston, eds. American Society for Microbiology Press, Washington, D.C. pp.141-159, 2007.
206. Karpathy, S.E., Xiang, Q., Gioia, J., Jiang, H., Liu, Y., Petrosino, J.F., Yerrapragada, S., Fox, G.E., Haake, S.K., Weinstock, G.M., and Highlander, S.K. Genome sequence of *Fusobacterium nucleatum* subspecies *polymorphum* - a genetically tractable Fusobacterium. *PLOS One* 2: e659, 2007.
207. Gioia, J., Yerrapragada, S., Qin, X., Jiang, H., Igboeli, O.C., Muzny, D., Dugan-Rocha, S., Ding, Y., Hawes, A., Liu, W., Perez, L., Kovar, C., Dinh, H., Lee, S., Nazareth, L., Blyth, P., Holder, M., Buhay, C., Tirumalai, M.R., Liu, Y., Dasgupta, I., Bokhetache, L., Fujita, M., Karouia, F., Moorthy, P.E., Siefert, J., Uzman, A., Buzumbo, P., Verma, A., Zwiya, H., McWilliams, B.D., Olowu, A., Clinkenbeard, K.D., Newcombe, D., Golebiewski, L., Petrosino, J.F., Highlander, S.K., Nicholson, W.L., Fox, G.E., Venkateswaran, K., and Weinstock, G.M. Paradoxical DNA repair and peroxide resistance gene conservation in *Bacillus pumilis*. *PLOS One* 2:e928 2007.
208. The International HapMap Consortium. A second generation human haplotype map of over 3.1 million SNPs. *Nature* 449: 851-862, 2007.
209. Sabeti, P.C., Varilly, P., Fry, B., Lohmueller, J., Hostetter, E., Cotsapas, C., Xie, X., Byrne, E.H., McCarroll, S.A., Gaudet, R., Schaffner, S.F., Lander, E.S., and The International HapMap Consortium. Genome-wide detection and characterization of positive selection in human populations. *Nature* 449: 913-918, 2007.
210. Weir, B.A., Woo, M.S., Getz, G., Perner, S., Ding, L., Beroukhim, R., Lin, W.M., Province, M.A., Kraja, A., Johnson, L., Shah, K., Thomas, R.K., Barletta, J.A., Borecki, I.B., Broderick, S., Chang, A.C., Chiang, D.Y., Chirieac, L.R., Cho, J., Fujii, Y., Gazdar, A., Giordano, T., Greulich, H., Johnson, B.E., Kris, M.G., Lash, A., Lin, L., Lindeman, N., Mardis, E.R., McPherson, J.D., Minna, J., Morgan, M.B., Nadel, M., Orringer, M.B., Osborne, J.R., Ozenberger, B., Ramos, A.H., Robinson, J., Roth, J.A., Rusch, V., Sasaki, H., Sato, M., Shepard, F., Spitz, M.R., Tsao, M.-S., Twomey, D., Verhaak, R., Weinstock, G.M., Wheeler, D.A., Winckler, W., Yoshizawa, A., Yu, S., Zakowski, M.F., Zhang, Q., Beer, D.G., Wistuba, I.I., Watson, M.A., Garraway, L.A., Ladanyi, M., Travis, W., Pao, W., Rubin, M.A., Gabriel, S., Gibbs, R., Varmus, H., Wilson, R.K., Lander, E., and Meyerson, M. Characterizing the cancer genome in lung adenocarcinoma. *Nature* 450:893-898, 2007.
211. Miller, W., Rosenbloom, K., Hardison, R.C., Hou, M., Taylor, J., Raney, B., Burhans, R., King, D.C., Baertsch, R., Blankenberg, D., Kosakovsky, S.L., Nekrutenko, A., Giardine, B., Harris, R.S., Tyekucheva, S., Diekhans, M., Pringle, T.H., Murphy, W.J., Lesk, A., Weinstock, G.M., Lindblad-Toh, K., Gibbs, R.A., Lander, E.S., Siepel, A., Haussler, D., Kent, W.J. 28-Way Vertebrate Alignment and Conservation Track in the UCSC Genome Browser. *Gen. Res.* 17:1797-1808, 2007.
212. Strouhal, M., Šmajš, D., Matějková, P., Sodergren, E., Amin, A., Howell, J.K., Norris, S.J., and Weinstock, G.M. Genome differences between *Treponema pallidum* subsp. *pallidum* strain Nichols and *T. paraluiscuniculi* strain Cuniculi A. *Inf. Immun.* 75:5859-5866, 2007.
213. Albert, T.J., Molla, M.N., Muzny, D.M., Nazareth, L., Wheeler, D., Song, X., Richmond, T.A., Middle, C.M., Rodesch, M.J., Packard, C.J., Weinstock, G.M., and Gibbs, R.A. Direct selection of human genomic loci by microarray hybridization. *Nat. Methods* 4:903-905, 2007.

214. Highlander, S.K., Hultén, K.G., Qin, X., Jiang, H., Yerrapragada, S., Mason, E.O. Jr., Shang, Y., Williams, T., Fortunov, Régine, M., Liu, Y., Igboeli, O.C., Petrosino, J., Tirumalai, M.R., Uzman, A., Fox, G.E., Cardenas, A.M., Muzny, D., Hemphill, L., Ding, Y., Dugan-Rocha, S., Blyth, P., Buhay, C., Dinh, H., Hawes, A., Holder, M., Kovar, C., Lee, S., Liu, W., Nazareth, L., Wang, Q., Zhou, J., Kaplan, S.L., and Weinstock, G.M. Subtle genetic changes enhance virulence of methicillin resistant and sensitive *Staphylococcus aureus*. *BMC Microbiol.* 7:99 2007
215. Aronstein, K.A., Murray, K.D., de Leon, J.H., Qin, X., and Weinstock, G.M. High mobility group (HMG-box) genes in the honey bee fungal pathogen *Ascosphaera apis*. *Mycologia* 99:553-561, 2007.
216. Zhang, Z.D., Cayting, P., Weinstock, G.M., and Gerstein, M. Analysis of nuclear receptor pseudogenes in vertebrates: How the silent tell their stories. *Molec. Biol. Evol.* 25:131-143, 2008.
217. Durfee T, Nelson R, Baldwin S, Plunkett G 3rd, Burland V, Mau B, Petrosino JF, Qin X, Muzny DM, Ayele M, Gibbs RA, Csorgo B, Pósfai G, Weinstock GM, and Blattner FR. The complete genome sequence of *Escherichia coli* DH10B: Insights into the biology of a laboratory workhorse. *J. Bacteriol.* 190:2597-2606, 2008
218. *Tribolium* Genome Sequencing Consortium. The first genome sequence of a beetle, *Tribolium castaneum*, a model for insect development and pest biology. *Nature* 452:949-955 2008.
219. Park, Y., Aikins, J., Wang, L.J., Beeman, R.W., Oppert, B., Lord, J.C., Brown, S.J., Lorenzen, M.D., Richards, S., Weinstock, G.M., and Gibbs, R.A. Analysis of transcriptome data in the red flour beetle, *Tribolium castaneum*. *Insect Biochem. Mol. Biol.* 38:380-386, 2008.
220. Worley, K.C., Weinstock, G.M., and Gibbs, R.A. Rats in the Genomic Era. *Physiol. Genomics.* 32:273-282, 2008.
221. Twigger, S.N., Pruitt, K.D., Fernandez-Suarez, X.M., Karolchik, D., Worley, K., Maglott, D., Brown, G., Weinstock, G., Gibbs, R., Birney, E., Kent, J., and Jacob, H.J. What everybody should know about the Rat Genome and its online resources. *Nature Gen.* 40:523-527, 2008.
222. Brinkman, M.B.; Petterson, J.; McGill, M.; Rodgers, A.; Matějková, P.; Šmajš, D.; Weinstock, G.M.; Norris, S.J.; and Palzkill, T. A novel *Treponema pallidum* antigen, TP0136, is an outer membrane protein that binds human fibronectin. *Infect. Immun.* 76:1848-1857, 2008.
223. Wheeler, D.A., Srinivasan, M., Egholm, M., Shen, Y., Chen, L., McGuire, A., He, W., Chen, Y.-J., Makhijani, V., Roth, G.T., Gomes, X., Tartaro, K., Niazi, F., Turcotte, C.L., Irzyk, G.P., Lupski, J.R., Chinault, A.C., Song, X.-Z., Liu, Y., Yuan, Y., Nazareth, L., Qin, Xiang., Muzny, D.M., Margulies, M., Weinstock, G.M., Gibbs, R.A., Rothberg, J.M. The complete genome of an individual by massively parallel DNA sequencing. *Nature* 452:872-876, 2008.
224. Matějková, P., Strouhal, M., Šmajš, D., Norris, S.J., Palzkill, T., Petrosino, J., Sodergren, E., Norton, J., Singh, J., Richmond, T.A., Molla, M., Albert, T.J., and Weinstock, G.M. Complete genome sequence of *Treponema pallidum* ssp. *pallidum* strain SS14 determined with oligonucleotide arrays. *BMC Microbiology* 8:76. 2008.
225. Zhang, Z.D., Weinstock, G.M., and Gerstein, M. Rapid evolution by positive Darwinian selection in T-cell antigen CD4 in primates. *J. Mol. Evol.* 66:446-456, 2008.
226. Anim, B.N., Mohapatra, B., Vatta, M., Murray, D., Weinstock, G., and Gibbs, R. Role of the beta-adrenergic receptors in the cardiac response to beta-blocker therapy. *FASEB J.* 22:1046.4, 2008.
227. Gao H., Pattison D., Yan T., Klingeman D.M., Wang X., Petrosino J., Hemphill L., Wan X., Leapart A.B., Weinstock G.M., Palzkill T., Zhou J... Generation and Validation of a *Shewanella oneidensis* MR-1 Clone Set for Protein Expression and Phage Display. *PLoS ONE* 3:e2983, 2008.
228. Sillanpää, J., Nallapareddy, S.R., Prakash, V.P., Qin, X., Höök, M., Weinstock, G.M., and Murray, B.E. Identification and phenotypic characterization of a second collagen adhesin, Scm, and genome-based identification and analysis of 13 other predicted MSCRAMMs, including four distinct pilus loci, in *Enterococcus faecium*. *Microbiol.* 154:3199-3211, 2008.
229. Wang, X., Gao, H., Shen, Y., Weinstock, G.M., Zhou, J., and Palzkill, T. A High-throughput Percentage-of-Binding Strategy to Measure Binding Energy in DNA-Protein Interactions: Application to Genome Scale Site Discovery. *Nucl. Acids Res.* 36:4863-4871, 2008.
230. Bourgogne, A., Garsin, D.A., Qin, X., Singh, K.V., Sillanpää, J., Yerrapragada, S., Ding, Y., Dugan-Rocha, S., Buhay, C., Shen, H., Chen, G., Williams, G., Muzny, D., Maadani, A., Fox, K.A., Gioia, J., Chen, L., Shang, Y., Arias, C.A., Nallapareddy, S.R., Zhao, M., Prakash, V.P., Chowdhury, S., Jiang, H., Gibbs, R.A., Murray, B.E., Highlander, S.K., and Weinstock, G.M. Large scale variation in *Enterococcus faecalis* illustrated by the genome analysis of strain OG1RF. *Genome Biol.* 9:R110, 2008. PMC 2530867
231. The Cancer Genome Atlas Research Network. Comprehensive genomic characterization defines human glioblastoma genes and core pathways. *Nature* 455:1061-1068, 2008.
232. Ding L, Getz G, Wheeler DA, Mardis ER, McLellan MD, Cibulskis K, Sougnez C, Greulich H, Muzny DM, Morgan MB, Fulton L, Fulton RS, Zhang Q, Wendl MC, Lawrence MS, Larson DE, Chen K, Dooling DJ, Sabo A, Hawes AC, Shen H, Jhangiani SN, Lewis LR, Hall O, Zhu Y, Mathew T, Ren Y, Yao J, Scherer SE, Clerc K, Metcalf GA, Ng B, Milosavljevic A, Gonzalez-Garay ML, Osborne JR, Meyer R, Shi X, Tang Y, Koboldt DC, Lin L, Abbott R, Miner TL, Pohl C, Fewell G, Haipek C, Schmidt H, Dunford-

- Shore BH, Kraja A, Crosby SD, Sawyer CS, Vickery T, Sander S, Robinson J, Winckler W, Baldwin J, Chirieac LR, Dutt A, Fennell T, Hanna M, Johnson BE, Onofrio RC, Thomas RK, Tonon G, Weir BA, Zhao X, Ziaugra L, Zody MC, Giordano T, Orringer MB, Roth JA, Spitz MR, Wistuba II, Ozenberger B, Good PJ, Chang AC, Beer DG, Watson MA, Ladanyi M, Broderick S, Yoshizawa A, Travis WD, Pao W, Province MA, Weinstock GM, Varmus HE, Gabriel SB, Lander ES, Gibbs RA, Meyerson M, Wilson RK. Somatic mutations affect key pathways in lung adenocarcinoma. *Nature* 455:1069-1075, 2008. PMID: 18948947.
233. Bovine Genome Sequencing and Analysis Consortium, Elsik CG, Tellam RL, Worley KC, Gibbs RA, Muzny DM, Weinstock GM, Adelson DL, Eichler EE, Elnitski L, Guigó R, Hamernik DL, Kappes SM, Lewin HA, Lynn DJ, Nicholas FW, Reymond A, Rijnkels M, Skow LC, Zdobnov EM, Schook L, Womack J, Alioto T, Antonarakis SE, Astashyn A, Chapple CE, Chen HC, Chrast J, Câmara F, Ermolaeva O, Henrichsen CN, Hlavina W, Kapustin Y, Kiryutin B, Kitts P, Kokocinski F, Landrum M, Maglott D, Pruitt K, Sapojnikov V, Searle SM, Solovyev V, Souvorov A, Ucla C, Wyss C, Anzola JM, Gerlach D, Elhaik E, Graur D, Reese JT, Edgar RC, McEwan JC, Payne GM, Raison JM, Junier T, Kriventseva EV, Eyras E, Plass M, Donthu R, Larkin DM, Reecy J, Yang MQ, Chen L, Cheng Z, Chitko-McKown CG, Liu GE, Matukumalli LK, Song J, Zhu B, Bradley DG, Brinkman FS, Lau LP, Whiteside MD, Walker A, Wheeler TT, Casey T, German JB, Lemay DG, Maqbool NJ, Molenaar AJ, Seo S, Stothard P, Baldwin CL, Baxter R, Brinkmeyer-Langford CL, Brown WC, Childers CP, Connelley T, Ellis SA, Fritz K, Glass EJ, Herzig CT, Iivanainen A, Lahmers KK, Bennett AK, Dickens CM, Gilbert JG, Hagen DE, Salih H, Aerts J, Caetano AR, Dalrymple B, Garcia JF, Gill CA, Hiendleder SG, Memili E, Spurlock D, Williams JL, Alexander L, Brownstein MJ, Guan L, Holt RA, Jones SJ, Marra MA, Moore R, Moore SS, Roberts A, Taniguchi M, Waterman RC, Chacko J, Chandrabose MM, Cree A, Dao MD, Dinh HH, Gabisi RA, Hines S, Hume J, Jhangiani SN, Joshi V, Kovar CL, Lewis LR, Liu YS, Lopez J, Morgan MB, Nguyen NB, Okwuonu GO, Ruiz SJ, Santibanez J, Wright RA, Buhay C, Ding Y, Dugan-Rocha S, Herdandez J, Holder M, Sabo A, Egan A, Goodell J, Wilczek-Boney K, Fowler GR, Hitchens ME, Lozado RJ, Moen C, Steffen D, Warren JT, Zhang J, Chiu R, Schein JE, Durbin KJ, Havlak P, Jiang H, Liu Y, Qin X, Ren Y, Shen Y, Song H, Bell SN, Davis C, Johnson AJ, Lee S, Nazareth LV, Patel BM, Pu LL, Vattathil S, Williams RL Jr, Curry S, Hamilton C, Sodergren E, Wheeler DA, Barris W, Bennett GL, Eggen A, Green RD, Harhay GP, Hobbs M, Jann O, Keele JW, Kent MP, Lien S, McKay SD, McWilliam S, Ratnakumar A, Schnabel RD, Smith T, Snelling WM, Sonstegard TS, Stone RT, Sugimoto Y, Takasuga A, Taylor JF, Van Tassell CP, Macneil MD, Abatepaulo AR, Abbey CA, Ahola V, Almeida IG, Amadio AF, Anatriello E, Bahadue SM, Biase FH, Boldt CR, Carroll JA, Carvalho WA, Cervelatti EP, Chacko E, Chapin JE, Cheng Y, Choi J, Colley AJ, de Campos TA, De Donato M, Santos IK, de Oliveira CJ, Deobald H, Devinoy E, Donohue KE, Dovc P, Eberlein A, Fitzsimmons CJ, Franzin AM, Garcia GR, Genini S, Gladney CJ, Grant JR, Greaser ML, Green JA, Hadsell DL, Hakimov HA, Halgren R, Harrow JL, Hart EA, Hastings N, Hernandez M, Hu ZL, Ingham A, Iso-Touru T, Jamis C, Jensen K, Kapetis D, Kerr T, Khalil SS, Khatib H, Kolbehdari D, Kumar CG, Kumar D, Leach R, Lee JC, Li C, Logan KM, Malinverni R, Marques E, Martin WF, Martins NF, Maruyama SR, Mazza R, McLean KL, Medrano JF, Moreno BT, Moré DD, Muntean CT, Nandakumar HP, Nogueira MF, Olsaker I, Pant SD, Panzitta F, Pastor RC, Poli MA, Poslusny N, Rachagani S, Ranganathan S, Razpet A, Riggs PK, Rincon G, Rodriguez-Osorio N, Rodriguez-Zas SL, Romero NE, Rosenwald A, Sando L, Schmutz SM, Shen L, Sherman L, Southey BR, Lutzow YS, Sweedler JV, Tammen I, Telugu BP, Urbanski JM, Utsunomiya YT, Verschoor CP, Waardenberg AJ, Wang Z, Ward R, Weikard R, Welsh TH Jr, White SN, Wilming LG, Wunderlich KR, Yang J, Zhao FQ. The genome sequence of taurine cattle: A window to ruminant biology and evolution. *Science* 324:522-528, 2009. PMID: 19390049.
234. Bovine HapMap Consortium, Gibbs RA, Taylor JF, Van Tassell CP, Barendse W, Eversole KA, Gill CA, Green RD, Hamernik DL, Kappes SM, Lien S, Matukumalli LK, McEwan JC, Nazareth LV, Schnabel RD, Weinstock GM, Wheeler DA, Ajmone-Marsan P, Boettcher PJ, Caetano AR, Garcia JF, Hanotte O, Mariani P, Skow LC, Sonstegard TS, Williams JL, Diallo B, Hailemariam L, Martinez ML, Morris CA, Silva LO, Spelman RJ, Mulatu W, Zhao K, Abbey CA, Agaba M, Araujo FR, Bunch RJ, Burton J, Gorni C, Olivier H, Harrison BE, Luff B, Machado MA, Mwakaya J, Plastow G, Sim W, Smith T, Thomas MB, Valentini A, Williams P, Womack J, Woolliams JA, Liu Y, Qin X, Worley KC, Gao C, Jiang H, Moore SS, Ren Y, Song XZ, Bustamante CD, Hernandez RD, Muzny DM, Patil S, San Lucas A, Fu Q, Kent MP, Vega R, Matukumalli A, McWilliam S, Sclep G, Bryc K, Choi J, Gao H, Grefenstette JJ, Murdoch B, Stella A, Villa-Angulo R, Wright M, Aerts J, Jann O, Negrini R, Goddard ME, Hayes BJ, Bradley DG, Barbosa da Silva M, Lau LP, Liu GE, Lynn DJ, Panzitta F, Dodds KG. The genetic history of cattle. *Science* 324:528-532, 2009. PMID: 19390050.
235. Liu, Y., Qin, X., Song, X.-Z., Jiang, H., Shen, Y., Durbin, K.J., Lien, S., Kent, M.P., Sodeland, M., Ren, Y., Zhang, L., Sodergren, E., Havlak, P., Worley, K.C., Weinstock, G., Gibbs, R.A. *Bos taurus* genome assembly. *BMC Genomics* 10:180, 2009. PMID: 19393050.
236. Matějková, P., Flasarová, M., Zákoucká, H., Bořek, M., Křemenová, S., Arenberger, P., Woznicová, V., Weinstock, G.M., Šmajš, D. Macrolide treatment failure in the case of secondary syphilis: a novel A2059G

- mutation in the 23S rRNA gene of *Treponema pallidum* subsp. *pallidum*. J. Clin. Micro. 58:832-836, 2009. PMID: 19429763.
237. Church DM, Goodstadt L, Hillier LW, Zody MC, Goldstein S, and the Mouse Genome Sequencing Consortium. Lineage-specific biology revealed by a finished genome assembly of the mouse. PLOS Biology 7:e1000112, 2009. PMID: 19468303.
238. Koboldt DC, Chen K, Wylie T, Larson DE, McLellan MD, Mardis ER, Weinstock GM, Wilson RK, Ding L. VarScan: Variant detection in massively parallel sequencing of individuals and pooled samples. Bioinformatics 25:2283-2285, 2009. PMID: 19542151.
239. Loman NJ, Snyder LA, Linton JD, Langdon R, Lawson AJ, Weinstock GW, Wren BW, Pallen MJ. Genome sequence of the emerging pathogen *Helicobacter canadensis*. J Bacteriol. 191:5566-7, 2009. PMID: 19542273.
240. Sillanpää, J., Nallapareddy, S.R., Qin, X., Singh, K.V., Muzny, D.M., Kovar, C.L., Nazareth, L.V., Gibbs, R.A., Ferraro, M.J., Steckelberg, J.M., Weinstock, G.M., and Murray, B.E. A collagen-binding adhesin, Acb, and 10 other putative MSCRAMM and pilus family proteins of *Streptococcus gallolyticus* subsp. *gallolyticus* (*S. bovis* biotype 1). J. Bacteriol. 191:6643-6653, 2009. PMID: 19717590.
241. Toronto International Data Release Workshop Authors, Birney E, Hudson TJ, Green ED, Gunter C, Eddy S, Rogers J, Harris JR, Ehrlich SD, Apweiler R, Austin CP, Berglund L, Bobrow M, Bountra C, Brookes AJ, Cambon-Thomsen A, Carter NP, Chisholm RL, Contreras JL, Cooke RM, Crosby WL, Dewar K, Durbin R, Dyke SO, Ecker JR, El Emam K, Feuk L, Gabriel SB, Gallacher J, Gelbart WM, Granell A, Guarner F, Hubbard T, Jackson SA, Jennings JL, Joly Y, Jones SM, Kaye J, Kennedy KL, Knoppers BM, Kyrpidis NC, Lowrance WW, Luo J, MacKay JJ, Martín-Rivera L, McCombie WR, McPherson JD, Miller L, Miller W, Moerman D, Mooser V, Morton CC, Ostell JM, Ouellette BF, Parkhill J, Raina PS, Rawlings C, Scherer SE, Scherer SW, Schofield PN, Sensen CW, Stodden VC, Sussman MR, Tanaka T, Thornton J, Tsunoda T, Valle D, Vuorio EI, Walker NM, Wallace S, Weinstock G, Whitman WB, Worley KC, Wu C, Wu J, Yu J. Prepublication Data Sharing. Nature 461:168-170, 2009. PMID: 19741685.
242. Chain PS, Grafham DV, Fulton RS, Fitzgerald MG, Hostetler J, Muzny D, Ali J, Birren B, Bruce DC, Buhay C, Cole JR, Ding Y, Dugan S, Field D, Garrity GM, Gibbs R, Graves T, Han CS, Harrison SH, Highlander S, Hugenholtz P, Khouri HM, Kodira CD, Kolker E, Kyrpidis NC, Lang D, Lapidus A, Malfatti SA, Markowitz V, Metha T, Nelson KE, Parkhill J, Pitluck S, Qin X, Read TD, Schmutz J, Sozhamannan S, Sterk P, Strausberg RL, Sutton G, Thomson NR, Tiedje JM, Weinstock G, Wollam A; Genomic Standards Consortium Human Microbiome Project Jumpstart Consortium, Detter JC. Genomics. Genome project standards in a new era of sequencing. Science 326:236-237, 2009. PMID: 19815760
243. Salzman NH, Hung K, Haribhai D, Chu H, Karlsson-Sjöberg J, Amir E, Teggatz P, Barman M, Hayward M, Eastwood D, Stoel M, Zhou Y, Sodergren E, Weinstock GM, Bevins CL, Williams CB, Bos NA. Enteric defensins are essential regulators of intestinal microbial ecology. Nat. Immunol. 11:76-83, 2010. PMID: 19855381.
244. Shen Y, Wan Z, Coarfa C, Drabek R, Chen L, Ostrowski EA, Liu Y, Weinstock GM, Wheeler DA, Gibbs RA, Yu F. A SNP discovery method to assess variant allele probability from next-generation resequencing data. Genome Res. 20:273-80, 2010. PMID: 20019143.
245. Snyder LA, Loman NJ, Linton JD, Langdon R, Weinstock GM, Wren BW, Pallen MJ. Simple sequence repeats in *Helicobacter canadensis* and their role in phase variable expression and C-terminal sequence switching. BMC Genomics. 11:67, 2010. PMID: 20105305
246. Daiger, S.P., Sullivan, L.S., Bowne, S.J., Birch, D.G., Heckenlively, J.R., Pierce, E.A., and Weinstock, G.M. Targeted High-Throughput DNA Sequencing for Gene Discovery in Retinitis Pigmentosa. Adv. Exp. Med. Biol. Vol. 664: Retinal Degenerative Diseases: Laboratory and Therapeutic Investigations, Anderson, Hollyfield, and LaVail eds., Springer (New York), pp 325-331, 2010. PMID: 20238032.
247. Lewis, T, Loman, NJ, Bingle, L, Jumaa P, Weinstock, GM, Mortiboy, D, Pallen, MJ. Use of high-throughput whole-genome sequencing to dissect the epidemiology of *Acinetobacter baumannii* isolates from a hospital outbreak. J. Hosp. Inf. 75:37-41, 2010. PMID: 20299126.
248. Ding L, Ellis MJ, Li S, Larson DE, Chen K, Wallis JW, Harris CC, McLellan MD, Fulton RS, Fulton LL, Abbott RM, Hoog J, Dooling DJ, Koboldt DC, Schmidt H, Kalicki J, Zhang Q, Chen L, Lin L, Wendl MC, McMichael JF, Magrini VJ, Cook L, McGrath SD, Vickery TL, Appelbaum E, Deschryver K, Davies S, Guintoli T, Lin L, Crowder R, Tao Y, Snider JE, Smith SM, Dukes AF, Sanderson GE, Pohl CS, Delehaunty KD, Fronick CC, Pape KA, Reed JS, Robinson JS, Hodges JS, Schierding W, Dees ND, Shen D, Locke DP, Wiechert ME, Eldred JM, Peck JB, Oberkfell BJ, Lolofie JT, Du F, Hawkins AE, O'Laughlin MD, Bernard KE, Cunningham M, Elliott G, Mason MD, Thompson DM Jr, Ivanovich JL, Goodfellow PJ, Perou CM, Weinstock GM, Aft R, Watson M, Ley TJ, Wilson RK, Mardis ER. Genome remodelling in a basal-like breast cancer metastasis and xenograft. Nature. 464(7291):999-1005, 2010. PMID: 20393555.
249. The Human Microbiome Jumpstart Reference Strains Consortium, Nelson KE, Weinstock GM, Highlander SK, Worley KC, Creasy HH, Wortman JR, Rusch DB, Mitreva M, Sodergren E, Chinwalla AT, Feldgarden M, Gevers D, Haas BJ, Madupu R, Ward DV, Birren BW, Gibbs RA, Methe B, Petrosino JF, Strausberg RL, Sutton GG, White OR, Wilson RK, Durkin S, Giglio MG, Gujja S, Howarth C, Kodira CD, Kyrpidis

- N, Mehta T, Muzny DM, Pearson M, Pepin K, Pati A, Qin X, Yandava C, Zeng Q, Zhang L, Berlin AM, Chen L, Hepburn TA, Johnson J, McCarrison J, Miller J, Minx P, Nusbaum C, Russ C, Sykes SM, Tomlinson CM, Young S, Warren WC, Badger J, Crabtree J, Markowitz VM, Orvis J, Cree A, Ferriera S, Fulton LL, Fulton RS, Gillis M, Hemphill LD, Joshi V, Kovar C, Torralba M, Wetterstrand KA, Abouelleil A, Wollam AM, Buhay CJ, Ding Y, Dugan S, Fitzgerald MG, Holder M, Hostetler J, Clifton SW, Allen-Vercoe E, Earl AM, Farmer CN, Liolios K, Surette MG, Xu Q, Pohl C, Wilczek-Boney K, Zhu D. A Catalog of Reference Genomes from the Human Microbiome. *Science*. 328:994-999, 2010. PMID: 20489017
250. Marri, P.R., Paniscus, M., Weyand, N.J., Rendon, M.A., Calton, C.M., Hernandez, D.R., Higashi, D.L., Sodergren, E., Weinstock, G.M., Rounsley, S. and So, M. Genome Sequencing Reveals Widespread Virulence Gene Exchange Among Human *Neisseria* Species. *PLoS ONE* 5(7): e11835, 2010. PMID: 20676376
251. Peter H. Sudmant, Jacob O. Kitzman, Francesca Antonacci, Can Alkan, Maika Malig, Anya Tsalenko, Nick Sampas, Laurakay Bruhn, Jay Shendure, 1000 Genomes Project, Evan E. Eichler. Diversity of Human Copy Number Variation and Multicopy Genes. *Science* 330:641-646, 2010. PMID: 21030649
252. The 1000 Genomes Project Consortium. A map of human genome variation from population-scale sequencing. *Nature* 467:1061-1073, 2010. PMID: 20981092
253. Dougan, G. and Weinstock, G.M. A new era in the genomics of bacteria. *Curr. Opin. Microbiol.* 13:616-618, 2010. PMID: 20846901
254. Tarr, P.I., Warner, B., Sodergren, E., Shannon, W., Hamvas, A., Magrini, V. & Weinstock, G. The Neonatal Microbiome and Necrotizing Enterocolitis. *Nature Precedings* doi:10.1038/npre.2010.5285.1, 2010.
255. Storch, G.A., Weinstock, G.M., Sodergren, E.J., Wylie, K.M., Arens, M.Q., Buller, R.S., Jaffe, D.M. & Muenzer, J.T. The Human Virome in Children and its Relationship to Febrile Illness. *Nature Precedings* doi:10.1038/npre.2010.5319.1, 2010.
256. Li, E., Sodergren, E., Weinstock, G., Stappenbeck, T., Frank, D., Robertson, C., Pace, N., Zhu, W., Boedeker, E., Sartor, R.B., Tarr, P., Mayer, L. & Dietz, D. Effect of Crohn's Disease Risk Alleles on Enteric Microbiota Marker Paper. *Nature Precedings* doi:10.1038/npre.2010.4975.1, 2010.
257. Nelson, D.E., Van Der Pol, B., Dong, Q., Revanna, K.V., Fan, B., Easwaran, S., Sodergren, E., Weinstock, G.M., Diao, L. and Fortenberry, J.D. Characteristic Male Urine Microbiomes Associate with Asymptomatic Sexually Transmitted Infection. *PLoS ONE* 5: e14116, 2010. doi:10.1371/journal.pone.0014116.
258. Mikalová L, Strouhal M, Čejková D, Zobaníková M, Pospíšilová P, Norris SJ, Sodergren E, Weinstock GM, Šmajš D. Genome Analysis of *Treponema pallidum* subsp. *pallidum* and subsp. *pertenue* Strains: Most of the Genetic Differences Are Localized in Six Regions. *PLoS One* 5:e15713, 2010. PMID: 21209953.
259. Haas BJ, Gevers D, Earl A, Feldgarden M, Ward DV, Giannokous G, Ciulla D, Tabbaa D, Highlander SK, Sodergren E, Methe B, Desantis TZ, The Human Microbiome Consortium, Petrosino JF, Knight R, Birren BW. Chimeric 16S rRNA sequence formation and detection in Sanger and 454-pyrosequenced PCR amplicons. *Gen. Res.* 2011. doi:10.1101/gr.112730.110. PMID: 21212162
260. Mikalová L, Strouhal M, Čejková D, Zobaníková M, Pospíšilová P, Norris SJ, Sodergren E, Weinstock GM, Šmajš D. Genome analysis of *Treponema pallidum* subsp. *pallidum* and subsp. *pertenue* strains: most of the genetic differences are localized in six regions. *PLoS One*. 2010 Dec 29;5(12):e15713. PMID: 21209953
261. Bowne, S.J., Sullivan, L.S., Koboldt, D.C., Ding, L., Fulton, R., Abbott, R.M., Sodergren, E.J., Birch, D.G., Wheaton, D.H., Heckenlively, J.R., Liu, Q., Pierce, E.A., Weinstock, G.M., Daiger, S.P. Identification of Disease-Causing Mutations in Autosomal Dominant Retinitis Pigmentosa (adRP) Using Next-Generation Sequencing. *Invest. Ophthalmol. Vis. Sci.* 52:494-503, 2011. PMID: 20861475
262. Tianyi Zhang, Robert A DeSimone, Hongyan Chen, Christina M Hamm, Jeffrey Yuan, Qing Qing Gong, Steven R Hunt, Themistocles Dassopoulos, Rodney D Newberry, Daniel N Frank, Charles E Robertson, Norman R Pace, Erica Sodergren, George Weinstock, Xiangmin Jiao, Wei Zhu, and Ellen Li. Cluster analysis of genome-wide expression differences in disease-unaffected ileal mucosa in inflammatory bowel diseases. 2011 IEEE 1st International Conference on Computational Advances in Bio and Medical Sciences (ICCBMS), pp 220-225. 2011.
263. Locke, D.P., Hillier, L.W., Warren, W.C., Worley, K.C., Nazareth, L.V., Muzny, D.M., Yang, S.-P., Wang, Z., Chinwalla, A.T., Minx, P., Mitreva, M., Cook, L., Delehaunty, K.D., Fronick, C., Fulton, L., Fulton, R.S., Nelson, J.O., Magrini, V., Pohl, C., Graves, T.A., Markovic, C., Cree, A., Dinh, H.H., Hume, J., Kovar, C.L., Fowler, G.R., Lunter, G., Meader, S., Heger, A., Ponting, C.P., Marques-Bonet, T., Alkan, C., Chen, L., Cheng, Z., Kidd, J.M., Eichler, E.E., White, S., Searle, S., Vilella, A.J., Flicek, P., Ma, J., Raney, B., Suh, B., Burhans, R., Herrero, J., Haussler, D., Faria, R., Fernando, O., Darré, F., Farré, D., Gazave, E., Oliva, M., Navarro, A., Roberto, R., Capozzi, O., Archidiacono, N., Della Valle, G., Purgato, S., Rocchi, M., Konkel, M.K., Walker, J.A., Ullmer, B., Batzer, M.A., Smit, A.F.A., Hubley, R., Casola, C., Schrider,

- D.R., Hahn, M.W., Quesada, V., Puente, X.S., Ordoñez, G.R., López-Otín, C., Vinar, T., Brejova, B., Ratan, A., Harris, R.S., Miller, W., Kosio, C., Lawson, H.A., Taliwal, V., Martins, A.L., Siepel, A., RoyChoudhury, A., Ma, X., Degenhardt, J., Bustamante, C.D., Gutenkunst, R.N., Mailund, T., Dutheil, J.Y., Hobolth, A., Schierup, M.H., Chemnick, L., Ryder, O.A., Yoshinaga, Y., de Jong, P.J., Weinstock, G.M., Rogers, J., Mardis, E.R., Gibbs, R.A., and Wilson, R.K. Comparative and demographic analysis of orangutan genomes. *Nature* 469:529-533, 2011. PMID: 21270892.
264. Mills RE, Walter K, Stewart C, Handsaker RE, Chen K, Alkan C, Abyzov A, Yoon SC, Ye K, Cheetham RK, Chinwalla A, Conrad DF, Fu Y, Grubert F, Hajirasouliha I, Hormozdiari F, Iakoucheva LM, Iqbal Z, Kang S, Kidd JM, Konkel MK, Korn J, Khurana E, Kural D, Lam HY, Leng J, Li R, Li Y, Lin CY, Luo R, Mu XJ, Nemesh J, Peckham HE, Rausch T, Scally A, Shi X, Stromberg MP, Stütz AM, Urban AE, Walker JA, Wu J, Zhang Y, Zhang ZD, Batzer MA, Ding L, Marth GT, McVean G, Sebat J, Snyder M, Wang J, Ye K, Eichler EE, Gerstein MB, Hurler ME, Lee C, McCarroll SA, Korbel JO; 1000 Genomes Project. Mapping copy number variation by population-scale genome sequencing. *Nature* 470:59-65, 2011. PMID: 21293372.
265. Suen, G., Teiling, C., Li, L., Holt, C., Abouheif, E., Bornberg-Bauer, E., Bouffard, P., Caldera, E.J., Cash, E., Cavanaugh, A., Denas, O., Elhaik, E., Favé, M.-J., Gadau, J., Gibson, J.D., Graur, D., Grubbs, K.J., Hagen, D.E., Harkins, T.T., Helmkampf, M., Hu, H., Johnson, B.R., Kim, J., Marsh, S.E., Moeller, J.A., Muñoz-Torres, M.C., Murphy, M.C., Naughton, M.C., Nigam, S., Overson, R., Rajakumar, R., Reese, J.T., Scott, J.J., Smith, C.R., Tao, S., Tsutsui, N.D., Viljakainen, L., Wissler, L., Yandell, M.D., Zimmer, F., Taylor, J., Slater, S.C., Clifton, S.W., Warren, W.C., Elsik, C.G., Smith, C.D., Weinstock, G.M., Gerardo, N.M., and Currie, C.R. The Genome Sequence of the Leaf-cutter Ant *Atta cephalotes* Reveals Insights into its Obligate Symbiotic Lifestyle. *PLoS Genetics* 7:e1002007, 2011. PMID: 21347285.
266. Ye L, Hillier LW, Minx P, Thane N, Locke D, Martin JC, Chen L, Mitreva M, Miller JR, Haub KV, Dooling D, Mardis ER, Wilson RK, Weinstock GM, Warren WC. A vertebrate case study of the quality of assemblies derived from next-generation sequences. *Genome Biology* 12:R31, 2011. PMID: 21453517.
267. Nallapareddy SR, Sillanpää J, Mitchell J, Singh KV, Chowdhury SA, Weinstock GM, Sullam PM, Murray BE. Conservation of Ebp-type Pilus Genes among Enterococci and Demonstration of Their Role in Adherence of *Enterococcus faecalis* to Human Platelets. *Infect. Immun.* 79:2911-2920, 2011. PMID: 21502588.
268. Yilmaz P, Kottmann R, Field D, Knight R, Cole JR, Amaral-Zettler L, Gilbert JA, Karsch-Mizrachi I, Johnston A, Cochrane G, Vaughan R, Hunter C, Park J, Morrison N, Rocca-Serra P, Sterk P, Arumugam M, Bailey M, Baumgartner L, Birren BW, Blaser MJ, Bonazzi V, Booth T, Bork P, Bushman FD, Buttigieg PL, Chain PS, Charlson E, Costello EK, Huot-Creasy H, Dawyndt P, DeSantis T, Fierer N, Fuhrman JA, Gallery RE, Gevers D, Gibbs RA, San Gil I, Gonzalez A, Gordon JI, Guralnick R, Hankeln W, Highlander S, Hugenholtz P, Jansson J, Kau AL, Kelley ST, Kennedy J, Knights D, Koren O, Kuczynski J, Kyrpides N, Larsen R, Lauber CL, Legg T, Ley RE, Lozupone CA, Ludwig W, Lyons D, Maguire E, Methé BA, Meyer F, Muegge B, Nakielný S, Nelson KE, Nemergut D, Neufeld JD, Newbold LK, Oliver AE, Pace NR, Palanisamy G, Peplies J, Petrosino J, Proctor L, Pruesse E, Quast C, Raes J, Ratnasingham S, Ravel J, Relman DA, Assunta-Sansone S, Schloss PD, Schriml L, Sinha R, Smith MI, Sodergren E, Spo A, Stombaugh J, Tiedje JM, Ward DV, Weinstock GM, Wendel D, White O, Whiteley A, Wilke A, Wortman JR, Yatsunenko T, Glöckner FO. Minimum Information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MlxS) specifications. *Nat. Biotechnol.* 29:415-420, 2011. PMID: 21552244.
269. Weinstock, G.M. The volatile microbiome. *Genome Biol.* 12:114, 2011. PMID: 21635714.
270. Danecek P, Auton A, Abecasis G, Albers CA, Banks E, DePristo MA, Handsaker RE, Lunter G, Marth GT, Sherry ST, McVean G, Durbin R; 1000 Genomes Project Analysis Group. The variant call format and VCFtools. *Bioinformatics.* 27:2156-2158, 2011. PMID: 21653522.
271. Sara J. Bowne, Marian M. Humphries, Lori S. Sullivan, Paul F. Kenna, Lawrence C.S. Tam, Anna Sophia Kiang, Matthew Campbell, George M. Weinstock, Daniel C. Koboldt, Li Ding, Robert S. Fulton, Erica J. Sodergren, Denis Alman, Sophia Millington-Ward, Arpad Palfi, Alex McKee, Susan H. Blanton, Susan Slifer, Ioanna Konidari, G. Jane Farrar, Stephen P. Daiger and Peter Humphries. A Dominant Mutation in RPE65 Identified by Whole-Exome Sequencing Causes Retinitis Pigmentosa with Choroidal Involvement. *Eur. J. Hum. Gen.* 2011. doi: 10.1038/ejhg.2011.86. PMID: 21654732.
272. Smajs D, Zbaniková M, Strouhal M, Cejková D, Dugan-Rocha S, Pospíšilová P, Norris SJ, Albert T, Qin X, Hallsworth-Pepin K, Buhay C, Muzny DM, Chen L, Gibbs RA, Weinstock GM. Complete Genome Sequence of *Treponema paraluis-cuniculi*, Strain Cuniculi A: The Loss of Infectivity to Humans Is Associated with Genome Decay. *PLoS One.* 6:e20415, 2011. PMID: 21655244.
273. Conrad DF, Keebler JE, DePristo MA, Lindsay SJ, Zhang Y, Casals F, Idaghdour Y, Hartl CL, Torroja C, Garimella KV, Zilversmit M, Cartwright R, Rouleau GA, Daly M, Stone EA, Hurler ME, Awadalla P; 1000 Genomes Project. Variation in genome-wide mutation rates within and between human families. *Nat. Gen.* 43:712-714, 2011. doi: 10.1038/ng.862. PMID: 21666693.

274. The Cancer Genome Atlas Research Network. Integrated genomic analyses of ovarian carcinoma. *Nature*. 474:609-615, 2011. doi: 10.1038/nature10166. PMID: 21720365.
275. Gravel S, Henn BM, Gutenkunst RN, Indap AR, Marth GT, Clark AG, Yu F, Gibbs RA; The 1000 Genomes Project, Bustamante CD. Demographic history and rare allele sharing among human populations. *Proc Natl Acad Sci U S A*. 108:11983-8, 2011. PMID: 21730125.
276. Church DM, Schneider VA, Graves T, Auger K, Cunningham F, Bouk N, Chen HC, Agarwala R, McLaren WM, Ritchie GR, Albracht D, Kremitzki M, Rock S, Kotkiewicz H, Kremitzki C, Wollam A, Trani L, Fulton L, Fulton R, Matthews L, Whitehead S, Chow W, Torrance J, Dunn M, Harden G, Threadgold G, Wood J, Collins J, Heath P, Griffiths G, Pelan S, Grafham D, E Eichler E, Weinstock G, Mardis ER, Wilson RK, Howe K, Flicek P, Hubbard T. Modernizing reference genome assemblies. *PLoS Biol*. 2011 Jul;9(7):e1001091. doi: 10.1371/journal.pbio.1001091. PMID: 21750661.
277. Renfree MB, Papenfuss AT, Deakin JE, Lindsay J, Heider T, Belov K, Rens W, Waters PD, Pharo EA, Shaw G, Wong ES, Lefevre CM, Nicholas KR, Kuroki Y, Wakefield MJ, Zenger KR, Wang C, Ferguson-Smith M, Nicholas FW, Hickford D, Yu H, Short KR, Siddle HV, Frankenberg SR, Chew KY, Menzies BR, Stringer JM, Suzuki S, Hore TA, Delbridge ML, Mohammadi A, Schneider NY, Hu Y, O'Hara W, Al Nadaf S, Wu C, Feng ZP, Cocks BG, Wang J, Flicek P, Searle SM, Fairley S, Beal K, Herrero J, Carone DM, Suzuki Y, Sagano S, Toyoda A, Sakaki Y, Kondo S, Nishida Y, Tatsumoto S, Mandiou I, Hsu A, McColl KA, Landsell B, Weinstock G, Kuczek E, McGrath A, Wilson P, Men A, Hazar-Rethinam M, Hall A, Davies J, Wood D, Williams S, Sundaravadanam Y, Muzny DM, Jhangiani SN, Lewis LR, Morgan MB, Okwuonu GO, Ruiz SJ, Santibanez J, Nazareth L, Cree A, Fowler G, Kovar CL, Dinh HH, Joshi V, Jing C, Lara F, Thornton R, Chen L, Deng J, Liu Y, Shen JY, Song XZ, Edson J, Troon C, Thomas D, Stephens A, Yapa L, Levchenko T, Gibbs RA, Cooper DW, Speed TP, Fujiyama A, Graves JA, O'Neill RJ, Pask AJ, Forrest SM, Worley KC. Genome sequence of an Australian kangaroo, *Macropus eugenii*, provides insight into the evolution of mammalian reproduction and development. *Genome Biology* 12:414, 2011. PMID: 22212627.
278. Arias CA, Panesso D, McGrath DM, Qin X, Mojica MF, Miller C, Diaz L, Tran TT, Rincon S, Barbu EM, Reyes J, Roh JH, Lobos E, Sodergren E, Pasqualini R, Arap W, Quinn JP, Shamoo Y, Murray BE, Weinstock GM. Genetic basis for in vivo daptomycin resistance in enterococci. *New Engl. J. Med*. 365:892-900, 2011. PMID: 21899450.
279. Weinstock, G.M. The Human Microbiome Project. In *Handbook of Molecular Microbial Ecology I: Metagenomics and Complementary Approaches* (Wiley/Blackwell), F. De Bruijn, ed., pp. 307-312, 2011.
280. Weinstock, G.M. The impact of next-generation sequencing technologies on metagenomics. In *Handbook of Molecular Microbial Ecology I: Metagenomics and Complementary Approaches* (Wiley/Blackwell), F. De Bruijn, ed., pp. 143-147, 2011.
281. Weinstock, G. (2011), "The human microbiome project", in Finlay, B. (ed.), *Microbiota: Agents for Health and Disease*, The Biomedical & Life Sciences Collection, Henry Stewart Talks Ltd, London (online at <http://hstalks.com/?t=BL1323009-Weinstock>)
282. David Šmajš, Lenka Mikalová, Darina Čejková, Michal Strouhal, Marie Zobaníková, Petra Pospíšilová, Steven J. Norris, and George M. Weinstock. Whole genome analyses of treponemes: new targets for strain- and subspecies-specific molecular diagnostics. In *Syphilis – Recognition, Description and Diagnosis*, pp. 19-34, Neuzha S. Sato, ed. InTech (Rijeka, Croatia). 2011.
283. Monier A, Welsh RM, Gentemann C, Weinstock G, Sodergren E, Armbrust EV, Eisen JA & AZ Worden. Phosphate transporters in marine phytoplankton and their viruses: cross-domain commonalities in viral-host gene exchanges. *Environ. Microbiol. 'Omics Driven Microbial Ecology' Special Issue*. 2011. doi: 10.1111/j.1462-2920.2011.02576.x. PMID: 21914098.
284. Lori R. Holtz, Kristine M. Wylie, Erica Sodergren, Yanfang Jiang, Carl J. Franz, George M. Weinstock, Gregory A. Storch, and David Wang . Astrovirus MLB2 Viremia in a Febrile Child. *Emerg. Inf. Dis*. 17:2050-2052, 2011. PMID: 22099095.
285. Marth GT, Yu F, Indap AR, Garimella K, Gravel S, Leong WF, Tyler-Smith C, Bainbridge M, Blackwell T, Zheng-Bradley X, Chen Y, Challis D, Clarke L, Ball EV, Cibulskis K, Cooper DN, Fulton B, Hartl C, Koboldt D, Muzny D, Smith R, Sougnez C, Stewart C, Ward A, Yu J, Xue Y, Altshuler D, Bustamante CD, Clark AG, Daly M, DePristo M, Flicek P, Gabriel S, Mardis E, Palotie A, Gibbs R; 1000 Genomes Project. The functional spectrum of low-frequency coding variation. *Genome Biol*. 12:R84, 2011.
286. Kerstin Lindblad-Toh, Manuel Garber, Or Zuk, Michael F. Lin, Brian J. Parker, Stefan Washietl, Pouya Kheradpour, Jason Ernst, Gregory Jordan, Evan Mauceli, Lucas D. Ward, Craig B. Lowe, Alisha K. Holloway, Michele Clamp, Sante Gnerre, Jessica Alfoldi, Kathryn Beal, Jean Chang, Hiram Clawson, Federica Di Palma, Stephen Fitzgerald, Paul Flicek, Mitchell Guttman, Melissa J Hubisz, David B. Jaffe, Irwin Jungreis, Dennis Kostka, Marcia Lara, Andre L Martins, Tim Massingham, Ida Moltke, Brian J. Raney, Matthew D. Rasmussen, Alexander Stark, Albert J. Vilella, Jiayu Wen, Xiaohui Xie, Michael C. Zody, Broad Institute Sequencing Platform and Whole Genome Assembly Team, Kim C. Worley, Christie L. Kovar, Donna M. Muzny, Richard A. Gibbs, Baylor College of Medicine Human Genome Sequencing

- Center, Wesley C. Warren, Elaine R Mardis, George M. Weinstock, Richard K. Wilson, Washington University Genome Center, Ewan Birney, Elliott H. Margulies, Javier Herrero, Eric D. Green, David Haussler, Adam Siepel, Nick Goldman, Katherine S. Pollard, Jakob S. Pedersen, Eric S. Lander, Manolis Kellis. A high-resolution map of human evolutionary constraint using 29 mammals. *Nature*. 478:476-482, 2011. PMID: 21993624.
287. Guohui Yao, Liang Ye*, Hongyu Gao, Patrick Minx, Wesley C. Warren, George M. Weinstock. Graph accordance of next-generation sequence assemblies. *Bioinformatics* 28:13-16, 2012. PMID: 22025481
288. Darina Čejková, Marie Zbaníková, Lei Chen, Petra Pospíšilová, Michal Strouhal, Xiang Qin, Lenka Mikalová, Steven J. Norris, Donna M. Muzny, Richard A. Gibbs, Lucinda L. Fulton, Erica Sodergren, George M. Weinstock, and David Šmajš. Whole Genome Sequences of Three *Treponema pallidum* ssp. pertenue Strains: Yaws and Syphilis *Treponemes* Differ in Less than 0.2% of the Genome Sequence. *PLoS Neg. Trop. Dis.* 6:e1471, 2012. PMID: 22292095.
289. Collaborative Cross Consortium. The Genome Architecture of the Collaborative Cross Mouse Genetic Reference Population. *Genetics* 190(2): 389–401, 2012. PMC3276630
290. 1000 Genomes Project Consortium, Abecasis GR, Auton A, Brooks LD, DePristo MA, Durbin RM, Handsaker RE, Kang HM, Marth GT, McVean GA. An integrated map of genetic variation from 1,092 human genomes. *Nature*. 491:56-65, 2012. doi:10.1038/nature11632. PMID: 23128226
291. Clarke L, Zheng-Bradley X, Smith R, Kulesha E, Xiao C, Toneva I, Vaughan B, Preuss D, Leinonen R, Shumway M, Sherry S, Flicek P; 1000 Genomes Project Consortium. The 1000 Genomes Project: data management and community access. *Nat Methods*. 9:459-62, 2012. doi: 10.1038/nmeth.1974. PMID: 22543379
292. Jasinska, A.J., Lin, M.K., Service, S., Choi, O.-W., DeYoung, J., Grujic, O., Kong, S.-Y., Jung, Y., Jorgensen, M.J., Fairbanks, L.A., Turner, T., Cantor, R.M., Wasserscheid, J., Dewar, K., Warren, W., Wilson, R.K., Weinstock, G., Jentsch, J.D., Freimer, N.B. A non-human primate system for large-scale genetic studies of complex traits. *Hum. Molec. Gen.* 21:3307-3316, 2012. PMID: 22556363.
293. David Šmajš, Steven J. Norris, and George M. Weinstock. Genetic diversity in *Treponema pallidum*: implications for pathogenesis, evolution and molecular diagnostics of syphilis and yaws. *Infect Genet Evol.* 12:191-202, 2012. PMID: 22198325.
294. Li E, Hamm CM, Gulati AS, Sartor RB, Chen H, Wu X, Zhang T, Rohlf FJ, Zhu W, Gu C, Robertson CE, Pace NR, Boedeker EC, Harpaz N, Yuan J, Weinstock GM, Sodergren E, Frank DN. Inflammatory bowel diseases phenotype, *C. difficile* and NoD2 genotype are associated with shifts in human ileal mucosa-associated microbial composition. *PLoS ONE* 7: e26284, 2012. doi/10.1371/journal.pone.0026284. PMID: 22719818.
295. Wylie KM, Mihindukulasuriya KA, Sodergren E, Weinstock GM, Storch GA. Sequence analysis of the human virome in febrile and afebrile children. *PLoS ONE* 7(6): e27735, 2012. doi/10.1371/journal.pone.0027735. PMID: 22719819.
296. Zhang T, DeSimone RA, Jiao X, Rohlf FJ, Zhu W, Gong QQ, Hunt SR, Dassopoulos T, Newberry RD, Sodergren E, Weinstock G, Robertson CE, Frank DN, Li E. Host genes related to paneth cells and xenobiotic metabolism are associated with shifts in human ileum-associated microbial composition. *PLoS ONE* 7(6): e30044, 2012. doi:10.1371/journal.pone.0030044. PMID: 22719822.
297. Jumpstart Consortium Human Microbiome Project Data Generation Working Group. Evaluation of 16S rDNA-Based Community Profiling for Human Microbiome Research. *PLoS ONE* 7: e39315, 2012. doi:10.1371/journal.pone.0039315. PMID: 22720093.
298. Martin J, Sykes S, Young S, Kota K, Sanka R, Sheth N, Orvis J, Sodergren E, Wang Z, Weinstock GM, Mitreva M. Optimizing Read Mapping to Reference Genomes to Determine Composition and Species Prevalence in Microbial Communities. *PLoS ONE* 7: e36427, 2012. doi:10.1371/journal.pone.0036427. PMID: 22719831.
299. Nelson DE, Dong Q, Van der Pol B, Toh E, Fan B, Katz BP, Mi D, Rong R, Weinstock GM, Sodergren E, Fortenberry JD. Bacterial communities of the coronal sulcus and distal urethra of adolescent males. *PLoS One* 7:e36298, 2012. doi: 10.1371/journal.pone.0036298. PMID: 22606251
300. Wylie KM, Weinstock GM, Storch GA. Emerging view of the human virome. *Transl. Res.* 160:283-90, 2012. doi: 10.1016/j.trsl.2012.03.006. PMID: 22683423.
301. Human Microbiome Project Consortium. A framework for human microbiome research. *Nature* 486:215-221, 2012. doi: 10.1038/nature11209. PMID: 22699610.
302. Human Microbiome Project Consortium. Structure, function and diversity of the healthy human microbiome. *Nature* 486:207-214, 2012. doi: 10.1038/nature11234. PMID: 22699609.
303. Wylie KM, Truty RM, Sharpton TJ, Mihindukulasuriya KA, Zhou Y, Gao H, Sodergren E, Weinstock GM, Pollard KS. Novel Bacterial Taxa in the Human Microbiome. *PLoS ONE* 7: e35294, 2012. doi:10.1371/journal.pone.0035294. PMID: 22719826.
304. Qin X, Galloway-Pena JR, Sillanpaa J, Hyeob Roh J, Nallapareddy SR, Chowdhury S, Bourgogne A, Choudhury T, Munzy DM, Buhay CJ, Ding Y, Dugan-Rocha S, Liu W, Kovar C, Sodergren E, Highlander S, Petrosino JF, Worley KC, Gibbs RA, Weinstock GM, Murray BE. Complete genome sequence of

- Enterococcus faecium* strain TX16 and comparative genomic analysis of *Enterococcus faecium* genomes. BMC Microbiol. 12:135, 2012. doi: 10.1186/1471-2180-12-135. PMID: 22769602.
305. Weinstock GM. Genomic approaches to studying human microbiota. Nature 489:250-256, 2012. doi: 10.1038/nature11632. PMID: 23128226
306. Wendl MC, Kota K, Weinstock GM, Mitreva M. Coverage theories for metagenomic DNA sequencing based on a generalization of Stevens' theorem. J. Math. Bio. 67:1141-1161, 2013. doi: 10.1007/s00285-012-0586-x. PMID: 22965653.
307. McWilliams BD, Palzkill T, Weinstock GM, Petrosino JF. Identification of novel and cross-species seroreactive proteins from *Bacillus anthracis* using a ligation-independent cloning-based, SOS-inducible expression system. Microb. Pathog. 53:250-8, 2012. doi: 10.1016/j.micpath.2012.08.006. PMID: 22975444
308. Helena Pětrošová, Marie Zobaníková, Darina Čejková, Lenka Mikalová, Petra Pospíšilová, Michal Strouhal, Lei Chen, Xiang Qin, Donna M. Muzny, George M. Weinstock, and David Šmajš. Whole genome sequence of *Treponema pallidum* ssp. *pallidum*, strain Mexico A, suggests recombination between yaws and syphilis strains. PLoS Negl. Trop. Dis. 6: e1832, 2012. doi:10.1371/journal.pntd.0001832.
309. Clarke L, Zheng-Bradley X, Smith R, Kulesha E, Xiao C, Toneva I, Vaughan B, Preuss D, Leinonen R, Shumway M, Sherry S, Flicek P; 1000 Genomes Project Consortium. The 1000 Genomes Project: data management and community access. Nat Methods. 9:459-62, 2012. doi: 10.1038/nmeth.1974. PMID: 22543379. PMCID: PMC3340611.
310. Williams TM, Loman NJ, Ebruke C, Musher DM, Adegbola RA, Pallen MJ, Weinstock, GM, and Antonio, M. Genome Analysis of a Highly Virulent Serotype 1 Strain of *Streptococcus pneumoniae* from West Africa. PLoS ONE 7: e26742, 2012. doi:10.1371/journal.pone.0026742.
311. La Rosa PS, Shands B, Deych E, Zhou Y, Sodergren E, Weinstock G, and Shannon WD. Statistical Object Data Analysis of Taxonomic Trees from Human Microbiome Data. PLoS One 7:e48996, 2012. doi: 10.1371/journal.pone.0048996. PMID: 23152838.
312. Kontur WS, Schackwitz WS, Ivanova N, Martin J, Labutti K, Deshpande S, Tice HN, Pennacchio C, Sodergren E, Weinstock GM, Noguera DR, Donohue TJ. Revised Sequence and Annotation of the *Rhodobacter sphaeroides* 2.4.1 Genome. J Bacteriol. 194:7016-7, 2012. doi: 10.1128/JB.01214-12. PMID: 23209255
313. McElvania Tekippe E, Wylie KM, Deych E, Sodergren E, Weinstock G, Storch GA. Increased Prevalence of Anellovirus in Pediatric Patients with Fever. PLoS ONE 7:e50937, 2012. doi:10.1371/journal.pone.0050937. PMID: 23226428.
314. Colvin JM, Muenzer JT, Jaffe DM, Smason A, Deych E, Shannon WD, Arens MQ, Buller RS, Lee WM, Weinstock EJ, Weinstock GM, Storch GA. Detection of Viruses in Young Children with Fever without an Apparent Source. Pediatrics 130:e1455-62, 2012. doi: 10.1542/peds.2012-1391. PMID: 23129086
315. La Rosa PS, Brooks JP, Deych E, Boone EL, Edwards DJ, Wang Q, Sodergren E, Weinstock G, Shannon WD. Hypothesis testing and power calculations for taxonomic-based human microbiome data. PLoS ONE 7:e52078, 2012. doi: 10.1371/journal.pone.0052078. PMID: 23284876.
316. Schloissnig S, Arumugam M, Sunagawa S, Mitreva M, Tap J, Zhu A, Waller A, Mende DR, Kultima JR, Martin J, Kota K, Sunyaev SR, Weinstock GM, Bork P. Genomic variation landscape of the human gut microbiome: Individuality and temporal stability. Nature 493:45-50, 2013. doi: 10.1038/nature11711. PMID: 23222524.
317. Cejkova D, Zobanikova M, Pospisilova P, Strouhal M, Mikalova L, Weinstock GM, Smajs D. Structure of *rrn* operons in pathogenic non-cultivable treponemes: sequence but not genomic position of intergenic spacers correlates with classification of *Treponema pallidum* and *T. paraluisunculi* strains. J Med Microbiol. 62(Pt 2):196-207, 2013. doi: 10.1099/jmm.0.050658-0. PMID: 23082031
318. Tran TT, Panesso D, Gao H, Roh JH, Munita JM, Reyes J, Diaz L, Lobos EA, Shamoo Y, Mishra NN, Bayer AS, Murray BE, Weinstock GM, Arias CA. Whole-Genome Analysis of a Daptomycin-Susceptible *Enterococcus faecium* and Its Daptomycin-Resistant Variant Arising During Therapy. Antimicrob Agents Chemother. 57:261-8, 2013. doi: 10.1128/AAC.01454-12. PMID: 23114757.
319. Redel H, Gao Z, Li H, Alekseyenko AV, Zhou Y, Perez-Perez GI, Weinstock G, Sodergren E, Blaser MJ. Quantitation and composition of cutaneous microbiota in diabetic and non-diabetic men. J. Infect. Dis. 207:1105-1114, 2013. doi: 10.1093/infdis/jit005. PMID: 23300163.
320. Zhou Y, Gao H, Mihindukulasuriya KA, Rosa PS, Wylie KM, Vishnivetskaya T, Podar M, Warner B, Tarr PI, Nelson DE, Fortenberry JD, Holland MJ, Burr SE, Shannon WD, Sodergren E, Weinstock GM. Biogeography of the ecosystems of the healthy human body. Genome Biol. 14:R1. 2013. PMID: 23316946.
321. Fitz-Gibbon S, Tomida S, Chiu BH, Nguyen L, Du C, Liu M, Elashoff D, Erfe MC, Loncaric A, Kim J, Modlin RL, Miller JF, Sodergren E, Craft N, Weinstock GM, Li H. *Propionibacterium acnes* strain populations in the skin microbiome associated with acne. J. Invest. Dermatol. 133:2152-60, 2013. doi: 10.1038/jid.2013.21. PMID: 23337890.
322. Lozupone C, Cota-Gomez A, Palmer BE, Linderman DJ, Charlson ES, Sodergren E, Mitreva M, Abubucker S, Martin J, Yao G, Campbell TB, Flores SC, Ackerman G, Stombaugh J, Ursell L, Beck JM, Curtis JL, Young VB, Lynch SV, Huang L, Weinstock GM, Knox KS, Twigg H, Morris A, Ghedin E,

- Bushman FD, Collman RG, Knight R, Fontenot AP; for the Lung HIV Microbiome Project. Widespread Colonization of the Lung by *Tropheryma whippelii* in HIV Infection. *Am J Respir Crit Care Med*. 187:1110-7, 2013. doi: 10.1164/rccm.201211-2145OC2013. PMID: 23392441.
323. Zabaníková M, Mikolka P, Čejková D, Pospíšilová P, Chen L, Strouhal M, Qin X, Weinstock GM, Šmajš D. Complete genome sequence of *Treponema pallidum* subsp. *pallidum* strain DAL-1. *Standards Genomic Sci*. 7:12-21. doi: 10.4056/sigs.2615838. PMID: 23449808
324. Desai PT, Porwollik S, Long F, Cheng P, Wollam A, Bhonagiri-Palsikar V, Hallsworth-Pepin K, Clifton SW, Weinstock GM, McClelland M. Evolutionary Genomics of the *Salmonella enterica* subspecies. *mBio* 4:e00579-12, 2013. doi: 10.1128/mBio.00579-12. PMID: 23462113.
325. Morris A, Beck JM, Schloss PD, Campbell TB, Crothers K, Curtis JL, Flores SC, Fontenot AP, Ghedin E, Huang L, Jablonski K, Kleerup E, Lynch SV, Sodergren E, Twigg H, Young VB, Bassis CM, Venkataraman A, Schmidt TM, Weinstock GM; on behalf of the Lung HIV Microbiome Project. Comparison of the respiratory microbiome in healthy non-smokers and smokers. *Am. J. Resp. Crit. Care Med*. 187:1067-75, 2013. doi: 10.1164/rccm.201210-1913OC. PMID: 23491408
326. Zabaníková M, Strouhal M, Mikolka P, Čejková D, Ambrožová L, Pospíšilová P, Fulton LL, Chen L, Sodergren E, Weinstock GM, Šmajš D. Whole Genome Sequence of the *Treponema* Fribourg-Blanc: Unspecified Simian Isolate belongs to the Yaws Subspecies. *PLoS Negl. Trop. Dis*. 7: e2172, 2013. doi:10.1371/journal.pntd.0002172. PMID: 23638193.
327. Aylward FO, Burnum-Johnson KE, Tringe SG, Teiling C, Tremmel DM, Moeller JA, Scott JJ, Barry KW, Piehowski PD, Nicora CD, Malfatti SA, Monroe ME, Purvine SO, Goodwin LA, Smith RD, Weinstock GM, Gerardo NM, Suen G, Lipton MS, Currie CR. *Leucoagaricus gongylophorus* produces a diversity of enzymes for recalcitrant plant polymer degradation in leaf-cutter ant fungus gardens. *Appl. Environ. Microbiol*. 79:3770-8, 2013. doi: 10.1128/AEM.03833-12. PMID: 23584789.
328. Tomida S, Nguyen L, Chiu BH, Liu J, Sodergren E, Weinstock GM, Li H. Pan-genome and comparative genome analyses of *Propionibacterium acnes* reveal its genomic diversity in the healthy and diseased human skin microbiome. *MBio* 4:e00003-13, 2013. doi:pii: 10.1128/mBio.00003-13. PMID: 23631911.
329. Doolittle WF, Fraser P, Gerstein MB, Graveley BR, Henikoff S, Huttenhower C, Oshlack A, Ponting CP, Rinn JL, Schatz MC, Ule J, Weigel D, Weinstock GM. Sixty years of genome biology. *Gen. Biol*. 14:113, 2013. doi:10.1186/gb-2013-14-4-113. PMID: 23651518.
330. Angus AA, Lee A, Lum MR, Shehayeb M, Hessabi R, Fujishige NA, Yerrapragada S, Kano S, Song N, Yang P, Estrada de los Santos P, de Faria SM, Dakora FD, Weinstock G and Hirsch AM. Nodulation and Effective Nitrogen Fixation of *Macroptilium atropurpureum* (siratro) by *Burkholderia tuberum*, a Nodulating and Plant Growth Promoting Beta-Proteobacterium, Is Influenced by Environmental Factors. *Plant and Soil* 369:543-562, 2013. doi: 10.1007/s11104-013-1590-7.
331. Wylie KM, Weinstock GM, Storch GA. Virome genomics: a tool for defining the human virome. *Curr Opin Microbiol*. 16:479-84, 2013. doi: 10.1016/j.mib.2013.04.006. PMID: 23706900.
332. Tirumalai MR, Rastogi R, Zamani N, O'Bryant Williams, E, Allen S, Diouf F, Kwende S, Weinstock GM, Venkateswaran KJ, & Fox GE. Candidate genes that may be responsible for the unusual resistances exhibited by *B. pumilus* SAFR-032 spores *PLoS ONE* 8:e66012, 2013. doi:10.1371/journal.pone.00660122013. PMID: 23799069
333. Twigg HL 3rd, Morris A, Ghedin E, Curtis JL, Huffnagle GB, Crothers K, Campbell TB, Flores SC, Fontenot AP, Beck JM, Huang L, Lynch S, Knox KS, Weinstock G; Lung HIV Microbiome Project. Use of bronchoalveolar lavage to assess the respiratory microbiome: signal in the noise. *Lancet Respir Med*. 1:354-356, 2013. doi:10.1016/S2213-2600(13)70117-6. PMID: 24429191.
334. Lang GI, Rice DP, Hickman MJ, Sodergren E, Weinstock GM, Botstein D, Desai MM. Pervasive genetic hitchhiking and clonal interference in forty evolving yeast populations. *Nature* 500:571-4, 2013. doi: 10.1038/nature12344. PMID: 23873039.
335. Tran TT, Panesso D, Mishra NN, Mileykovskaya E, Guan Z, Munita JM, Reyes J, Diaz L, Weinstock GM, Murray BE, Shamoo Y, Dowhan W, Bayer AS, Arias CA. Daptomycin-Resistant *Enterococcus faecalis* Diverts the Antibiotic Molecule From the Division Septum and Remodels Cell Membrane Phospholipids. *MBio* 4:pii: e00281-13, 2013. doi:pii: e00281-13. 10.1128/mBio.00281-13. PMID:23882013.
336. Turabelidze G, Lawrence SJ, Gao H, Sodergren E, Weinstock G, Abubucker S, Wylie T, Mitreva M, Shaikh N, Gautom R, Tarr PI. Precise Dissection of an *Escherichia coli* O157:H7 outbreak by Single Nucleotide Polymorphism Analysis. *J. Clin. Microbiol*. 51:3950-3954, 2013. doi: 10.1128/JCM.01930-13. PMID: 24048526.
337. Pětrošová H, Pospíšilová P, Strouhal M, Čejková D, Zabaníková M, et al. Resequencing of *Treponema pallidum* ssp. *pallidum* Strains Nichols and SS14: Correction of Sequencing Errors Resulted in Increased Separation of Syphilis *Treponeme* Subclusters. *PLoS ONE* 8(9): e74319, 2013. doi:10.1371/journal.pone.0074319.
338. Kelly SA, Bell TA, Selitsky SR, Buus RJ, Hua K, Weinstock GM, Garland T Jr, Pardo-Manuel de Villena F, Pomp D. A novel intronic single nucleotide polymorphism in the myosin heavy polypeptide 4 gene is

- responsible for the mini-muscle phenotype characterized by major reduction in hind-limb muscle mass in mice. *Genetics*. 195:1385-95, 2013. doi: 10.1534/genetics.113.154476. PMID: 24056412
339. Khurana E, Fu Y, Colonna V, Mu XJ, Kang HM, Lappalainen T, Sboner A, Lochovsky L, Chen J, Harmanci A, Das J, Abyzov A, Balasubramanian S, Beal K, Chakravarty D, Challis D, Chen Y, Clarke D, Clarke L, Cunningham F, Evani US, Flicek P, Fragoza R, Garrison E, Gibbs R, Gümüs ZH, Herrero J, Kitabayashi N, Kong Y, Lage K, Liliashvili V, Lipkin SM, MacArthur DG, Marth G, Muzny D, Pers TH, Ritchie GR, Rosenfeld JA, Sisu C, Wei X, Wilson M, Xue Y, Yu F; 1000 Genomes Project Consortium, Dermitzakis ET, Yu H, Rubin MA, Tyler-Smith C, Gerstein M, Abecasis GR, Auton A, Brooks LD, DePristo MA, Durbin RM, Handsaker RE, McVean GA. Integrative annotation of variants from 1092 humans: application to cancer genomics. *Science* 342:1235587, 2013. doi: 10.1126/science.1235587. PMID: 24092746.
340. Davis C, Kota K, Baldhandapani V, Gong W, Abubucker S, et al. mblast: Keeping up with the Sequencing Explosion for (Meta) Genome Analysis. *J Data Mining Genomics Proteomics* 4:135, 2013. doi: 10.4172/2153-0602.1000135.
341. Snyder LA, Loman NJ, Faraj LA, Levi K, Weinstock G, Boswell TC, Pallen MJ, Ala'Aldeen DA. Epidemiological investigation of *Pseudomonas aeruginosa* isolates from a six-year-long hospital outbreak using high-throughput whole genome sequencing. *Euro Surveill*. 18(42):pii:20611, 2013. PMID: 24176582.
342. Jasinska AJ, Schmitt CA, Service SK, Cantor RM, Dewar K, Jentsch JD, Kaplan JR, Turner TR, Warren WC, Weinstock GM, Woods RP, Freimer NB. Systems biology of the vervet monkey. *ILAR J*. 54:122-43, 2013. doi: 10.1093/ilar/ilt049. PMID: 24174437.
343. Chen K, Chen L, Fan X, Wallis J, Ding L, Weinstock G. TIGRA: A Targeted Iterative Graph Routing Assembler for Breakpoint Assembly. *Genome Res*. 24:310-7, 2014. doi: 10.1101/gr.162883.113. PMID: 24307552. PMCID: PMC3912421.
344. Angus AA, Agapakis CM, Fong S, Yerrapragada S, Estrada-de Los Santos P, Yang P, Song N, Kano S, Caballero-Mellado J, de Faria SM, Dakora FD, Weinstock G, Hirsch AM. Plant-associated symbiotic burkholderia species lack hallmark strategies required in Mammalian pathogenesis. *PLoS ONE* 9: e83779, 2014. doi:10.1371/journal.pone.0083779. PMID: 24416172.
345. Benahmed FH, Gopinath GR, Wang H, Jean-Gilles Beaubrun J, Grim C, Cheng CM, McClelland M, Ayers S, Abbott J, Desai P, Frye JG, Weinstock G, Hammack TS, Hanes DE, Rasmussen MA, Davidson MK. Whole genome sequencing of *Salmonella enterica* subsp. *enterica* serovar *Cubana* strains isolated from agricultural sources. *Genome Announc*. 2: e01184-13, 2014. doi: 10.1128/genomeA.01184-13. PMID: 24459266. PMCID: PMC3900898.
346. Koboldt DC, Larson DE, Sullivan LS, Bowne SJ, Steinberg KM, Churchill JD, Buhr AC, Nutter N, Pierce EA, Blanton SH, Weinstock GM, Wilson RK, Daiger SP. Exome-Based Mapping and Variant Prioritization for Inherited Mendelian Disorders. *Am J Hum Genet*. 94:373-84, 2014. doi: 10.1016/j.ajhg.2014.01.016. PMID: 24560519.
347. Daiger SP, Bowne SJ, Sullivan LS, Blanton SH, Weinstock GM, Koboldt DC, Fulton RS, Larsen D, Humphries P, Humphries MM, Pierce EA, Chen R, Li Y. Application of Next-Generation Sequencing to Identify Genes and Mutations Causing Autosomal Dominant Retinitis Pigmentosa (adRP). *Adv Exp Med Biol*. 801:123-9, 2014. doi: 10.1007/978-1-4614-3209-8_16. PMID: 24664689.
348. Rossi F, Diaz L, Wollam A, Panesso D, Zhou Y, Rincon S, Narechania A, Xing G, Di Gioia TS, Doi A, Tran TT, Reyes J, Munita JM, Carvajal LP, Hernandez-Roldan A, Brandão D, van der Heijden IM, Murray BE, Planet PJ, Weinstock GM, Arias CA. Transferable vancomycin resistance in a community-associated MRSA lineage. *N Engl J Med*. 370:1524-31, 2014. doi: 10.1056/NEJMoa1303359. PMID: 24738669 [PubMed - in process]
349. Richards VP, Palmer SR, Pavinski Bitar PD, Qin X, Weinstock GM, Highlander SK, Town CD, Burne RA, Stanhope MJ. Phylogenomics and the dynamic genome evolution of the genus *Streptococcus*. *Genome Biol Evol*. 6: 741–753, 2014. doi: 10.1093/gbe/evu048. PMID: 24625962. PMCID: PMC4007547.
350. Beigelman A, Weinstock GM, Bacharier LB. The relationships between environmental bacterial exposure, airway bacterial colonization, and asthma. *Curr Opin Allergy Clin Immunol*. 14:137-42, 2014. doi: 10.1097/ACI.0000000000000036. PMID: 24451910.
351. Carl MA, Ndao IM, Springman AC, Manning SD, Johnson JR, Johnston BD, Burnham CA, Weinstock ES, Weinstock GM, Wylie TN, Mitreva M, Abubucker S, Zhou Y, Stevens HJ, Hall-Moore C, Julian S, Shaikh N, Warner BB, Tarr PI. Sepsis From the Gut: The Enteric Habitat of Bacteria That Cause Late-Onset Neonatal Bloodstream Infections. *Clin. Inf. Dis*. 58:1211-8, 2014. doi: 10.1093/cid/ciu084. 2014. PMID: 24647013.
352. Patricio S. La Rosa, Yanjiao Zhou, Erica Sodergren, George Weinstock, and William D. Shannon. Hypothesis Testing of Metagenomic Data. In “Metagenomics for Microbiology” eds. Jacques Izard and Maria Rivera (Academic Press). (in press) 2014.
353. Zhou Y, Mihindukulasuriya KA, Gao H, La Rosa PS, Wylie KM, Martin JC, Kota K, Shannon WD, Mitreva M, Sodergren E, Weinstock GM. Exploration of bacterial community classes in major human habitats. *Genome Biol*. 15:R66, 2014. doi:10.1186/gb-2014-15-5-r66. PMID: 24887286.

354. Diaz L, Tran TT, Munita JM, Miller WR, Rincon S, Carvajal LP, Wollam A, Reyes J, Panesso D, Rojas NL, Shamoo Y, Murray BE, Weinstock GM, Arias CA. Whole Genome Analyses of *Enterococcus faecium* with Diverse Daptomycin Minimal Inhibitory Concentrations. *Antimicrob Agents Chemother.* pii: AAC.02686-14, 2014. PMID: 24867964.
355. Somarajan SR, Roh JH, Singh KV, Weinstock GM, Murray BE. CcpA is Important for Growth and Virulence of *Enterococcus faecium*. *Infect Immun.* pii: IAI.01911-14, 2014. PMID: 24914215.
356. Sunagawa, S., Schloissnig, S., Arumugam, M., Forslund, K., Mitreva, M., Tap, J., Zhu, A., Waller, A., Mende, D.R., Kultima, J.R., Martin, J., Kota, K., Sunyaev, S.R., Typas, A., Weinstock, G.M., & Bork, P. (2014). Individuality and temporal stability of the human gut microbiome. *Central Asian Journal of Global Health, 2*.
357. The Marmoset Genome Sequencing and Analysis Consortium. The Common Marmoset Genome Provides Insight into Primate Biology and Evolution. *Nat Genet.* doi: 10.1038/ng.3042. [Epub ahead of print] 2014. PMID: 25038751.
358. La Rosa PS, Warner BB, Zhou Y, Weinstock GM, Sodergren E, Hall-Moore CM, Stevens HJ, Bennett WE Jr, Shaikh N, Linneman LA, Hoffmann JA, Hamvas A, Deych E, Shands BA, Shannon WD, Tarr PI. The Patterned Progression of Bacterial Populations in the Premature Infant Gut. *Proc. Natl. Acad. Sci. USA* (in press) 2014. PMID: 25114261.
359. Wang W, Zhang X, Xu Y, Weinstock GM, Di Bisceglie AM, Fan X. High-Resolution Quantification of Hepatitis C Virus Genome-Wide Mutation Load and Its Correlation with the Outcome of Peginterferon-Alpha2a and Ribavirin Combination Therapy. *PLoS ONE* 9: e100131, 2014. doi:10.1371/journal.pone.0100131
360. Johnson MD, Bell J, Clarke K, Chandler R, Pathak P, Xia Y, Marshall RL, Weinstock GM, Loman NJ, Winn PJ, Lund PA.. Characterisation of mutations in the PAS domain of the EvgS sensor kinase selected for in laboratory evolution for acid resistance in *Escherichia coli*. *Mol Microbiol.* 2014. doi: 10.1111/mmi.12704. PMID: 24995530.
361. Nikos C. Kyrpides, Philip Hugenholtz, Jonathan A. Eisen, Tanja Woyke, Markus Göker, Charles T. Parker, Rudolf Amann, Brian J. Beck, Patrick Chain, Jongsik Chun, Rita R. Colwell, Antoine Danchin, Peter Dawyndt, Tom Dedeurwaerdere, Edward F. DeLong, John C. Detter, Paul De Vos, Timothy J. Donohue, Xiu-Zhu Dong, Dusko S. Ehrlich, Claire Fraser, Richard Gibbs, Jack Gilbert, Paul Gilna, Frank Oliver Glöckner, Janet K. Jansson, Jay D. Keasling, Rob Knight, David Labeda, Alla Lapidus, Jung-Sook Lee, Wen-Jun Li, Juncai Ma, Victor Markowitz, Edward R.B. Moore, Mark Morrison, Folker Meyer, Karen E. Nelson, Moriya Ohkuma, Christos A. Ouzounis, Norman Pace, Julian Parkhill, Nan Qin, Ramon Rossello-Mora, Johannes Sikorski, David Smith, Mitch Sogin, Rick Stevens, Uli Stingl, Ken Suzuki, Dorothea Taylor, Jim M. Tiedje, Brian Tindall, Michael Wagner, George Weinstock, Jean Weissenbach, Owen White, Jun Wang, Lixin Zhang, Yu-Guang Zhou, Genomic Standards Consortium, Dawn Field, William B. Whitman, George M. Garrity, and Hans-Peter Klenk. Genomic Encyclopedia of Bacteria and Archaea: sequencing a myriad of type strains. *PLoS Biology* 12:e1001920, 2014. doi: 10.1371/journal.pbio.1001920. PMID: 25093819.
362. John P Didion, Andrew P Morgan, Petko M Petkov, Timothy A Bell, Daniel M Gatti, James J Crowley, David L Aylor, Ling Bai, Mark Calaway, Elissa J Chesler, John E French, Thomas R Geiger, Terry J Gooch, Alison H Harrill, Kent Hunter, Leonard McMillan, Darla R Miller, Deborah A O'Brien, Kenneth Paigen, Wenqi Pan, Lucy B Rowe, George M. Weinstock, Ginger D Shaw, Petr Simecek, Patrick F Sullivan, Karen L Svenson, David W Threadgill, Daniel Pomp, Gary A Churchill and Fernando Pardo-Manuel de Villena. R2d2 is a genetically regulated meiotic drive system associated with a 4.4 Mb copy number gain on mouse Chromosome 2. *PLoS Genetics* (in press) 2014.
363. Wylie, K.M., K.A. Mihindukulasuriya, Y.Zhou, E.Sodergren, G.A. Storch, G.M. Weinstock. Metagenomic analysis of double-stranded DNA viruses in healthy adults. *BMC Biology* 2014 Sep 10;12(1):71. PMID: 25212266.
364. Kristine M. Wylie, George M. Weinstock, Gregory A. Storch. Emergence of rotavirus G12P[8] in St. Louis in the 2012-2013 rotavirus season. *J. Ped. Inf. Dis. Soc.* (in press) 2014
365. Deng X, Desai PT, den Bakker HC, Mikoleit M, Tolar B, Trees E, Hendriksen RS, Frye JG, Porwollik S, Weimer BC, Wiedmann M, Weinstock GM, Fields PI, McClelland M. Genomic Epidemiology of *Salmonella enterica* Serotype Enteritidis based on Population Structure of Prevalent Lineages. *Emerg Infect Dis.* 20:1481-1489, 2014. doi: 10.3201/eid2009.131095. PMID: 25147968
366. Sullivan LS, Koboldt DC, Bowne SJ, Lang S, Blanton SH, Cadena EL, Avery CE, Lewis RA, Webb-Jones K, Wheaton DK, Birch DG, Coussa RG, Ren H, Lopez I, Chakarova CF, Koenekoop R, Garcia CA, Fulton RS, Wilson RK, Weinstock GM, Daiger SP. A dominant mutation in hexokinase 1 (HK1) causes retinitis pigmentosa. *Invest Ophthalmol Vis Sci.* pii: IOVS-14-15419, 2014. doi: 10.1167/iovs.14-15419. PMID: 25190649.
367. Sommovilla J, Zhou Y, Sun RC, Choi PM, Diaz-Miron J, Shaikh N, Sodergren E, Warner BB, Weinstock GM, Tarr PI, Warner BW. Small Bowel Resection Induces Long-Term Changes in the Enteric Microbiota of Mice. *J Gastrointest Surg.* Sept 3, 2014. PMID: 25183407.

Manuscripts under review

1. Jane C. Harrington, Sara H. Browne, David T. Pride, Michael J. Preziosi, George M. Weinstock, Steffen Porwollik, Prerak Desai, Michael McClelland, Donald G. Guiney, and Lars Eckmann. A distinct genetic polymorphism accounts for differential niche colonization of fecal and bloodstream isolates of the human enteric pathogen *Salmonella enterica* serovar Typhimurium. (in revision) 2014.
2. Yan Liu, Hongyu Gao, Bin Wu, George Weinstock, David H. Walker, and Xue-jie Yu. Inactivation of SAM-methyltransferase is the mechanism of attenuation of a historic live attenuated louse-borne typhus rickettsial vaccine. *Inf. Imm.* (submitted) 2014
3. Samuel Kimani, Jamie Rylance, Anstead Kankwatira, Kristina Crothers, David E Nelson, Evelyn Toh, Richard B Day, Huaiying Lin, Qunfeng Dong, Deming Mi, Barry Katz, Erica Sodergren, George M Weinstock, Stephen B Gordon, and Homer Twigg III. Significant differences in the respiratory microbiome exist between a U.S. and Malawian population. *PLoS ONE* 2014 (submitted).
4. Qunyuan Zhang, Haley Abel, Alan Wells, Petra Lenzini, Felicia Gomez, Michael A. Province, Alan A. Templeton, George M. Weinstock, Nita H. Salzman, Ingrid Borecki. Selection of Models for the Analysis of Risk-factor Trees: Leveraging biological knowledge to mine large sets of risk factors with application to microbiome data. *Bioinformatics* (submitted) 2014.
5. Paul J. Planet, Sergios-Orestis Kolokotronis, Apurva Narechania, Jinnethe Reyes, Galen Xing, Sandra Rincon, Hannah Smith, Diana Panesso, Chanelle Ryan, Lorena Diaz, Robert Sebra, Rathel L. Nolan, Fred C. Tenover, George M. Weinstock, D. Ashley Robinson, Cesar A. Arias. Pan-American Origins of the Community-Associated USA300 MRSA Epidemic. *Science* (submitted) 2014.
6. Yanjiao Zhou, Carey-Ann Burnham, Tiffany Hink, Lei Chen, Nurmohammad Shaikh, Aye Wollam, Erica Sodergren, George M. Weinstock, Philip I. Tarr, and Erik R. Dubberke. Phenotypic and genotypic analysis of *Clostridium difficile* isolates: a single center study. (submitted) 2014.
7. Yanjiao Zhou, Guru Shan, Phillip Tarr, Erica Sodergren, George M. Weinstock, W. Allan Walker, and Katherine E. Gregory. Longitudinal Analysis of Premature Infant Intestinal Microbiome Prior to Necrotizing Enterocolitis. *PLOS ONE* (submitted) 2014.
8. Yanjiao Zhou, Martin J. Holland, Pateh Makalo, Hassan Joof, Chrissy H. Roberts, David C. W. Mabey, Robin L. Bailey, Matthew J. Burton, George M. Weinstock, and Sarah E. Burr. The conjunctival microbiome in health and trachomatous disease: a case-control study. (submitted) 2014.
9. Yair Dorsett, Yanjiao Zhou, Anthony T. Tubbs, Bo-Ruei Chen, Caitlin Purman, Baek-Seung Lee, Rosmy George, Andrea L. Bredemeyer, Dale Dorsett, Ziva Misulovin, Erica Sodergren, George M. Weinstock, Alejandro Reyes, Jacqueline E. Payton, and Barry P. Sleckman. HCoDES reveals chromosomal DNA ends structures with single nucleotide resolution. (submitted) 2014.
10. Baochen Shi, Michaela Chang, John Martin, Makedonka Mitreva, Renate Lux, Perry Klokkevold, Erica Sodergren, George M. Weinstock, Susan K. Haakeb, Huiying Li. Dynamic Changes in the Subgingival Microbiome Associated with Periodontitis. (submitted) 2014.
11. The Integrative HMP (iHMP) Research Network Consortium. The Integrative Human Microbiome Project (iHMP): Dynamic Analysis of Microbiome-Host Omics Profiles During Periods of Human Health and Disease. *Cell Host-Microbe* (submitted) 2014
12. Xue-jie Yu, Bin Wu, George Weinstock, David H Walker and Yan Liu. Inactivation of SAM-methyltransferase is the mechanism of attenuation of an historic louse borne typhus vaccine strain. *PLOS ONE* (submitted) 2014.
13. Tangi Smallwood, Daniel M. Gatti, Pamela Quizon, George M. Weinstock, Kuo-Chen Jung, Liyang Zhao Hayworth, Kunjie Hua, Daniel Pomp Brian J. Bennett. High-Resolution Genetic Mapping of Atherosclerosis in the Diversity Outbred Mouse Population. *Genetics* (submitted) 2014.

Manuscripts in preparation

1. Yanjiao Zhou; Hongyu Gao; Kathie Mihindukulasuriya; Berkely Shands; Patricio S La Rosa; William D Shannon; Erica Sodergren; George M Weinstock. Defining Conserved Microbiota In A Large Cohort of Healthy Humans. *PLoS ONE* (in revision) 2013.
2. Yael R. Nobel, Alexander Alekseyenko, Isabel Teitler, Jennifer Chung, Francis Kirigin, Sahar Abubucker, Makedonka Mitreva, George M. Weinstock, Martin J. Blaser Early-life pulsed antibiotic treatment alters growth, intestinal microbiome composition, and metabolic gene prevalence in mice. (in preparation) 2014.
3. Shaila Yerrapragada, Animesh Shukla, Kymberlie Hallsworth-Pepin, Kwangmin Choi; Aye Wollam; Sandra Clifton; Xiang Qin; Donna Muzny; Sriram Raghuraman; Haleh Ashki; Akif Uzman; Sarah Highlander; Bart Fryszczyn, Brendon Bingwa, Catherine (Horton) Schaffer, George Fox, Madhan Tirumalai, Yamei Liu, Sun Kim; David M. Kehoe; George Weinstock. Extreme Sensory Complexity

- Encoded in the 10 Mb Draft Genome Sequence of the Chromatically Acclimating Cyanobacterium *Tolypothrix* sp. PCC 7601. (in preparation)
4. Animesh Shukla, Adam N. Bussell, Kwangmin Choi, Shaila Yerrapragada, Kymberlie Hallsworth-Pepin, Sandra Clifton, Sun Kim, George Weinstock, David M. Kehoe. Abundance, arrangement, and architecture of two component systems and light-sensing GAF domains in small and large bacterial genomes. (in preparation)