CURRICULUM VITAE

Eric Douglas Green

DATE: January 8, 2010

CONTACT INFORMATION:

National Human Genome Research Institute
National Institutes of Health
31 Center Drive, MSC 2152
Building 31, Room 4B09
Bethesda, MD 20892-2152

Phone: 301-496-0844
FAX: 301-402-0837
E-Mail: egreen@nhgri.nih.gov
Web Site: http://www.genome.gov/Director

PRESENT POSITIONS:

Director, National Human Genome Research Institute
National Institutes of Health

Senior Investigator and Head, Physical Mapping Section
Genome Technology Branch
Division of Intramural Research
National Human Genome Research Institute
National Institutes of Health

EDUCATION:

1981	B.S., University of Wisconsin (Madison), Bacteriology
1987	M.D., Ph.D., Washington University, St. Louis, Missouri

Ph.D. Advisors: Dr. Jacques Baenziger and Dr. Irving Boime
Topic: "Structure and Biosynthesis of Asn-Linked Oligosaccharides on Pituitary Glycoprotein Hormones"

POST-GRADUATE TRAINING:

1987-1992	Resident in Laboratory Medicine Departments of Pathology and Internal Medicine Washington University School of Medicine
1990-1992	Chief Resident in Laboratory Medicine Departments of Pathology and Internal Medicine Washington University School of Medicine
1988-1992	Postdoctoral Research Fellow Laboratory of Dr. Maynard Olson Department of Genetics Washington University School of Medicine

MEDICAL LICENSURE:

National Boards (Parts I, II, and III)
Permanent Missouri Medical License (MD 100218)

APPOINTMENTS:

1992-1994	Assistant Professor, Departments of Pathology, Genetics, and Internal Medicine Washington University School of Medicine
1992-1994	Associate Director, Laboratory Medicine Residency Training Program Washington University School of Medicine
1992-1994	Associate Director, DNA Diagnostic Laboratory Washington University School of Medicine
1994-present	Head, Physical Mapping Section National Human Genome Research Institute National Institutes of Health
1994-1999	Adjunct Instructor, Department of Genetics Washington University School of Medicine
1995-1997	Director, DNA Sequencing Core National Human Genome Research Institute National Institutes of Health
1996-present	Tenured Senior Investigator, National Institutes of Health
1996-2009	Chief, Genome Technology Branch National Human Genome Research Institute National Institutes of Health
1997-2009	Director, NIH Intramural Sequencing Center (NISC) National Human Genome Research Institute National Institutes of Health
2002-2009	Scientific Director National Human Genome Research Institute National Institutes of Health

2009-present Acting Scientific Director
National Human Genome Research Institute
National Institutes of Health

2009-present Director
National Human Genome Research Institute
National Institutes of Health

EDITORIAL POSITIONS:

1991-1993 Associate Editor, *PCR Methods & Applications*
Cold Spring Harbor Laboratory Press

1993-1995 Editor, *PCR Methods & Applications*
Cold Spring Harbor Laboratory Press

1991-present Ad Hoc Reviewer for *Nature*, *Science*, *Proceedings of the National Academy of Sciences*, *Nature Genetics*, *Nature Review Genetics*, *Human Molecular Genetics*, *Nucleic Acid Research*, *Genomics*, *Human Genetics*, *American Journal of Human Genetics*, *PLoS Genetics*, and *PLoS Biology*

1994-2003 Board of Editors, *Clinical Chemistry*
American Association for Clinical Chemistry

1994-1998 Series Editor, *Genome Analysis: A Laboratory Manual*
Cold Spring Harbor Laboratory Press

Green ED, Birren B, Klapholz S, Myers RM, and
Hieter P, Series Editors

Volume 1: Analyzing DNA (1997)
Birren B, Green ED, Klapholz S, Myers RM, and
Roskams J, Volume Editors

Volume 2: Detecting Genes (1998)
Birren B, Green ED, Klapholz S, Myers RM, and
Roskams J, Volume Editors

Volume 3: Cloning Systems (1998)
Birren B, Green ED, Klapholz S, Myers RM, Riethman H,
and Roskams J, Volume Editors

Volume 4: Mapping Genomes (1998)
Birren B, Green ED, Hieter P, Klapholz S, Myers RM,
Riethman H, and Roskams J, Volume Editors

1995-present Editor, *Genome Research*
Cold Spring Harbor Laboratory Press

2001-present Section Head (Genomics)
Faculty of 1000

2002-present Editorial Board, *Mammalian Genome*, Springer-Verlag Press

2004-present Co-Editor, *Annual Reviews of Genomics and Human Genetics*

TEACHING EXPERIENCE:

1980-1981	Teaching Assistant, University of Wisconsin (Madison), Bacteriology
1983	Teaching Assistant, Washington University, Cell Biology
1991-1994	Course Organizer/Instructor, Cold Spring Harbor Laboratory Course: "Analysis and Genetic Manipulation of Yeast Artificial Chromosomes"
1996-2009	Preceptor, Predoctoral Training Program in Human Genetics Johns Hopkins University School of Medicine
1996-present	Co-Organizer and Lecturer, "Current Topics in Genome Analysis" Lecture Series National Institutes of Health

OTHER PROFESSIONAL EXPERIENCE:

1992-1993	Graduate School Admissions Committee Division of Biology and Biomedical Sciences Washington University
1992-2004	Ad Hoc Grant Reviewer, National Human Genome Research Institute National Institutes of Health
1992-1994	Investigator, Center for Genetics in Medicine Washington University Human Genome Mapping Center
1993	Organizer, Yeast Artificial Chromosome (YAC) Cloning Workshop Washington, D.C.
1993	Organizer, First International Workshop on Human Chromosome 7 Marburg, Germany
1995-1997	Organizer, Annual "Genome Mapping & Sequencing" Meeting Cold Spring Harbor Laboratory
1995-1997	Member, Quarterly Review Committee Genome Data Base (GDB)
1997-2001	Member, Genome Research Review Committee National Human Genome Research Institute National Institutes of Health
1998	Organizer, NIH Workshop "Genomic Alterations in Genetic Disease: Mechanisms of Structural Rearrangements"
1998	Organizer, ASHG Workshop "Human Genetics in the Sequence-Based Era" Annual American Society of Human Genetics Meeting
1998-2000	External Advisor, Cancer Chromosome Aberration Project National Cancer Institute National Institutes of Health
1999-2001	Member, Genome Resources Advisory Committee National Center for Biotechnology Information National Institutes of Health
1999	Member, Mammalian Gene Collection Implementation Working Group

	National Institutes of Health
2001-2005	Chair, NHGRI Bacterial Artificial Chromosome (BAC) Resource Steering Panel National Human Genome Research Institute, National Institutes of Health
2002	Member, Program Committee American Society of Human Genetics
2002-present	Co-Organizer, Annual "Advances in Genome Biology & Technology" Meeting Marco Island, Florida
2002-2009	Affiliate Member, McKusick-Nathans Institute of Genetic Medicine Johns Hopkins University School of Medicine
2002-2004	Advisor, Acute Myeloid Leukemia Genomics Program Washington University School of Medicine
2003	Co-Chairperson, Oncogenomics 2003 Meeting
2003-2005	Vice Chair (2003) & Chair (2005) "Human Genetics and Genomics" Gordon Research Conference
2003-2007	Chair, Scientific Advisory Board, Regulatory Genetics Project Montreal Genome Centre
2003-2004	Member, NSF Maize Genome Sequencing Advisory Committee
2004	Co-Organizer, 2004 NIH Research Festival
2004	Organizer, Genomics Workshop: "Identification of Functional Elements in Mammalian Genomes," Cold Spring Harbor Laboratory
2004	NHGRI ENCODE Project Resources Working Group
2004-2008	Annoting the Human Genome Working Group (Chair, 2006-2008)
2006-2007	Member, Sequencing Technology Evaluation Board, Wellcome Trust Sanger Institute
2006-2009	Chair, Scientific Advisory Board, Genome British Columbia Genomics Platforms, British Columbia Cancer Agency (BCCA) Genome Sciences Centre
2007-2008	Member, Scientific Review Board Starr Cancer Consortium

PROFESSIONAL HONORS:

1976	Elected to Membership in National Honor Society
1978	Elected to Membership in Phi Eta Sigma
1980	Elected to Membership in Gamma Sigma Delta
1981	Elected to Membership in Phi Kappa Phi
1981	Undergraduate Research Achievement Award University of Wisconsin (Madison)
1981-1985,	Predoctoral Trainee, National Institute of General Medical Sciences

1986-1987	Medical Scientist Training Award, Grant GM07200
1985-1986	Predoctoral Trainee, National Heart, Lung, and Blood Institute, Grant HL07275
1989	Young Investigator Award, Academy of Clinical Laboratory Physicians and Scientists
1989-1990	Helen Hay Whitney Postdoctoral Research Fellowship
1990	Young Investigator Award with Distinction Academy of Clinical Laboratory Physicians and Scientists
1990-1994	Lucille P. Markey Scholar Award in Biomedical Science
1994	Visiting Professor, Department of Pathology Emory University School of Medicine
1996	R. Lee West Lecturer, Department of Pathology and Laboratory Medicine East Carolina University School of Medicine
1998	SmithKline Beecham Lecturer, Department of Pathology State University of New York Health Science Center at Syracuse
2000	Gene Oliver Lecture, New York Pathological Society
2001	Keynote Speaker, Genetics Graduate Student Colloquium Case Western Reserve University
2001	Lillian M. Gilbreth Lectureship for Young Engineers National Academy of Engineering
2002	Elected to Membership in the American Society for Clinical Investigation
2004-present	Member, American Association of University Pathologists (Pluto Society)
2004	7th Annual Roy H. Behnke Distinguished Lectureship, University of South Florida College of Medicine, Health Sciences Center Research Day
2004	22nd Annual William B. Kinter Memorial Lectureship, Mount Desert Island Biological Laboratory
2004	NIH Merit Award
2005	Alumni Achievement Award, Washington University School of Medicine
2005	33rd Carl V. Moore Memorial Lecture, Washington University School of Medicine
2007	Elected to Membership in the Association of American Physicians
2008	Inaugural Maurice Green Lecture, St. Louis University School of Medicine

CONSULTING POSITIONS:

1993-1997	Member, Scientific Advisory Board, Mercator Genetics, Inc.
1997	Consultant, Mercator Genetics, Inc.
1998	Consultant, Progenitor, Inc.
1995-2002	Consultant, Life Technologies, Inc./Invitrogen, Inc.
1997-2005	Consultant, Monsanto Corporation
1998-2002	Member, Scientific Advisory Board, Cereon Genomics, LLC
1998-2004	Consultant, Exelixis Pharmaceuticals, Inc.

1999-2002	Consultant, Lexicon Genetics, Inc.
1999-2002	Consultant, Tularik, Inc.
2000-2002	Consultant, Specialty Laboratories
2002-2005	Member, Scientific Advisory Board, Aureon Biosciences Corporation
2003-2005	Member, Scientific Advisory Board, Geisinger Health System

SERVICE ON NIH COMMITTEES

2000	NIDCD Tenure-Track Investigator Search Committee (Chair)
2002	NCI Tenure-Track Investigator Search Committee
2002	NIH Central Tenure Committee
2003	ARAC Acquisitions Working Group
2003-2009	Technology Transfer Policy Board
2003-2008	NIH Office of Research Services Advisory Committee
2003-2004	NIH Ad Hoc Parking Advisory Committee
2004	Co-Organizer, NIH Research Festival
2004-2006	NIMH Scientific Director Search Committee
2005-2006	NIH Office of Research Services Director Search Committee
2005-2006	NIH Office of Human Resources Director Search Committee
2005	NIH Director's Lecture Series Selection Committee
2006	NIH Office of Intramural Training and Education Director Search Committee (Chair)
2006	Renovation/Space/Leasing Intramural Budget Stretching Committee
2006-2007	NIH Scientific Directors Shared Resources Subcommittee
2007	Co-Organizer, Genome-Wide Association Studies to Sequencing: NIH Think Tank and Multi-IC Training Workshop for the Genes and Environment Initiative (GEI)
2008	NIMH Scientific Director Search Committee
2008	NIH Ethics Office Senior Policy Advisor Search Committee
2008-2009	NIDCD Scientific Director Search Committee (Chair)
2002-present	Board of NIH Scientific Directors
2004-present	NIH Ethics Advisory Committee (NEAC)
2005-2009	NIH Office of Intramural Training and Education Steering Committee (Chair)
2007-2009	NIH Teleworking Task Force
2007-2009	NIH Scientific Directors Agenda-Setting Subcommittee
2008-present	Center for Inherited Disease Research Board of Governors (Co-Chair 2009-present)
2009-present	NIH Intramural Working Group
2009-present	NIDA Scientific Director Search Committee (Chair)
2009	NIEHS Scientific Director Search Committee

TALKS AT PROFESSIONAL MEETINGS, WORKSHOPS, AND COURSES:

1985	Gordon Conference: "Glycoproteins and Glycolipids"
1986	Federation of American Societies for Experimental Biology
1989	Cold Spring Harbor Laboratory Meeting: "Genome Mapping and Sequencing"
1989	Annual Meeting, Academy of Clinical Laboratory Physicians and Scientists
1989	Lake Tahoe Symposium: "Advances in Recombinant DNA Technology"

1990 Cold Spring Harbor Laboratory Meeting: "Genome Mapping and Sequencing"
1990 Annual Meeting, Academy of Clinical Laboratory Physicians and Scientists
1990 Cystic Fibrosis Foundation Conference: "The Gene— Nine Months Later"
1990 Annual Meeting, American Society of Human Genetics
1991 Cold Spring Harbor Laboratory Meeting: "Genome Mapping and Sequencing"
1991 Cold Spring Harbor Laboratory Course: "Molecular Genetic Analysis of Diseases of the Nervous System"
1991 Cold Spring Harbor Laboratory Course: "Genetic Approaches to Human Disease Using DNA Markers"
1991 U. of Pittsburgh Symposium: "Statistical Methods in Genome Analysis"
1991 International Congress of Human Genetics
1992 NIH-DOE Joint Working Group on the Mouse
1992 Conference on Bioinformatics, Supercomputers, and Complex Genome Analysis
1992 9th Wellcome Summer School: "DNA-Related Methods in Human Genetics"
1992 College of American Pathologist Conference XXIV: "Molecular Pathology"
1993 Cold Spring Harbor Laboratory Meeting: "Genome Mapping and Sequencing"
1993 First International Workshop on Human Chromosome 7
1994 American Society of Clinical Pathology/College of American Pathologists Annual Meeting
1995 Cold Spring Harbor Laboratory Course: "Cloning and Analysis of Large DNA Molecules"
1995 Annual Meeting, Electrophoresis Society
1995 College of American Pathologists House of Delegates' Annual Meeting
1995 Cold Spring Harbor Laboratory Course: "YACs in Structural and Biological Genome Analysis"
1995 American Society for Investigative Pathology Course: "Concepts in Molecular Biology"
1995 5th International Workshop on the Identification of Transcribed Sequences
1996 U.S. & Canadian Academy of Pathology: "Molecular Pathology"
1996 Annual Meeting, Academy of Clinical Laboratory Physicians and Scientists
1996 Annual Meeting of the Lucille P. Markey Scholars
1996 American Society for Investigative Pathology Course: "Concepts in Molecular Biology"
1996 Cold Spring Harbor Laboratory Course: "YACs in Structural and Biological Genome Analysis"
1997 Monbu-sho Symposium: "Human Genome Project" (Tokyo, Japan)
1997 Association of Biomolecular Resource Facilities Annual Meeting: "Techniques at the Genome/Proteome Interface"
1997 4th UNESCO South-North Human Genome Conference
1997 Cold Spring Harbor Laboratory Course: "Advanced Genome Sequence Analysis"
1997 Cold Spring Harbor Laboratory Course: "Positional Cloning— Contig to Candidate Gene"
1998 American Society for Investigative Pathology Course: "Concepts in Molecular Biology"
1998 Annual Meeting of the Teratology Society, NICHD Symposium: "Genomics in Birth Defect Research"
1998 NIH Workshop: "Genomic Alterations in Genetic Disease: Mechanisms of Structural Rearrangements"
1998 NICHD Workshop: "Structural Birth Defects"
1998 Centre for Cellular Biology at the University of Hong Kong Symposium: "Impacts of Genome Projects on Medicine and Biotechnology"

1998 Cold Spring Harbor Laboratory Course: "Positional Cloning— Contig to Candidate Gene"
1998 Hackensack University Medical Center Biomedical Ethics Symposium: "The Human Genome Project— The Science of Genetic Research and the Social Implications"
1998 NHGRI/Smithsonian Course "A User's Guide to Genetics— The Medicine of the Future"
1998 ASHG Workshop: "Human Genetics in the Sequence-Based Era"
1998 AACC's 8th Annual Clinical Chemistry Forum: "Issues in Genetic Testing"
1999 NIH Workshop: "Non-Mammalian Models"
1999 Cold Spring Harbor Laboratory Course: "Advanced Genome Sequence Analysis"
1999 Southeast Development Biology Meeting, St. Jude's Children's Research Hospital
1999 AACC's 31st Annual Oak Ridge Conference: "On the Road to Non-Invasive Testing"
1999 National Eye Institute Workshop: "Functional Genomics"
1999 St. Louis University: "Conference on Genetics and Ethics"
2000 Smithsonian Course "Biotechnology: The Future is Now"
2000 G2K: Back to Science Meeting: "Advances in Genome Biology and Technology"
2000 NAWJ Meeting: "Bioethics, Ethics, and the Law"
2000 NIH Workshop: "Setting Priorities for Phenotyping the Mouse Nervous System and Behavior"
2000 Teratology Society Satellite Symposium: "Genomics, Proteomics, Bioinformatics, and Developmental Toxicology in the 21st Century"
2000 Cold Spring Harbor Laboratory Meeting: "Mouse Molecular Genetics"
2000 National Academy of Engineering: Sixth Annual Symposium on Frontiers of Engineering
2000 2nd Meeting of Athena Pathology Society
2000 American Museum of Natural History Symposium: "Sequencing the Human Genome"
2000 NIH Research Festival Plenary Session: The Utility of Whole Genome Sequences— Early Glimpses of the Sequence-based Era"
2000 Pre-ICER Satellite Symposium 2000: "Ocular Genomics and Proteomics"
2001 Oncogenomics Conference 2001: "Dissecting Cancer Through Genome Research"
2001 Annual Meeting: "Advances in Genome Biology and Technology"
2001 AAAS Meeting: "2001 Genome Seminar— Beyond the Human Genome"
2001 Meeting of the Mid-Atlantic Chapter of the American Medical Writers Association
2001 Cold Spring Harbor Laboratory Meeting: "Genetic Basis of Neurological and BehavioralDisorders"
2001 1st International Workshop on the Genetics of Bone Disease
2001 Society of Toxicologic Pathology Meeting: "Toxicologic Pathology in the New Millennium"
2001 Jackson Laboratory Short Course in Medical and Experimental Genetics
2001 Gordon Research Conference: "Human Molecular Genetics"
2001 ASHG Workshop: "Comparing Genome Sequences of Vertebrates"
2001 NYU Medical School: "Advances in Dermatology"
2001 Delaware Medical Society Annual Meeting
2001 ASCB Minorities Affairs Committee Sponsored Symposium: "Log-on for Success"
2002 Plant, Animal, and Microbial Genomes X
2002 NRC Workshop: "Exploring Horizons for Domestic Animal Genomics"
2002 Cold Spring Harbor Laboratory Course: "Acquiring and Analyzing Genomic Sequence Data"
2002 St. Louis University Colloquium: "Genetic Engineering and the Question of Limits"
2002 Annual Meeting of the American Society for Clinical Investigation
2002 Oncogenomics Conference 2002: "Dissecting Cancer Through Genome Research"

2002 Cold Spring Harbor Meeting: "Genome Sequencing and Biology"
2002 University of Virginia Symposium: "Comparative Genomics— Biology from Genomes"
2002 3rd Annual Meeting, Great Plains States Society for Molecular Biology and Genetics
2002 42nd Annual Congress of the Federation of South African Societies of Pathology "Pathogenomics 2002"
2002 Jackson Laboratory Meeting: "Mouse Initiatives IV— Comparative Genomic Approaches to the Analysis of Gene Function and Human Disease"
2002 Genome Sequencing and Analysis Conference XIV
2002 Keck 2002 Bioinformatics Symposium (Keck Center for Computational and Structural Biology and the Gulf Coast Consortium for Bioinformatics)
2002 Annual Meeting of the American Society of Nephrology
2002 16th International Mouse Genome Conference
2003 Oncogenomics Conference 2003: "Dissecting Cancer Through Genome Research"
2003 NHGRI/NIH Symposium: "From Double Helix to Human Sequence— and Beyond"
2003 10th ASM Undergraduate Microbiology Education Conference: "Microbiology Education in the Next Decade: Focus on the Future"
2003 68th Cold Spring Harbor Symposium on Quantitative Biology: "The Genome of *Homo Sapiens*"
2003 Bovine Genomics Workshop (Montreal, Canada)
2003 International University of Ecuador: "Transcending Frontiers of Medicine"
2003 Gordon Research Conference: "Human Genetics and Genomics"
2003 Stem Cell Genome Anatomy Project Retreat
2003 18th Regional Cancer Research Symposium, Vermont Cancer Center
2003 13th Annual Irwin M. Arias, M.D. Symposium: "Bridging Basic Sciences and Liver Disease"
2003 Workshop on Wheat Genome Sequencing
2003 Smithsonian Institute Forum: Genetics and the Future of Our Health
2003 NHGRI Symposium: "From Base Pairs to Bedside"
2003 San Antonio Breast Cancer Satellite Symposium: "Molecular Markers in Breast Cancer"
2003 Cold Spring Harbor Laboratory Meeting: "Rat Genomics and Models"
2004 Annual Meeting of American Association of University Pathologists (Pluto Society)
2004 Strategic Research Institute Meeting: "Capturing the Full Potential of Biotechnology in Health Care Delivery"
2004 Cold Spring Harbor Laboratory Meeting (Banbury Center): "Finding the Functional Elements of the Genome"
2004 Experimental Biology 2004 Symposium: "A Bioinformatics How-To for the Wet-Lab Physiologist"
2004 Samuel Lunenfeld Research Institute International Symposium 2004: "Molecular Evolution"
2004 Genomes & Evolution 2004 (Joint Meeting of the Society for Molecular Biology and Evolution and American Genetic Association)
2004 AACR Workshop in Cancer Research: Molecular Biology in Clinical Oncology
2004 11th Mount Desert Island Biological Laboratory Environmental Health Sciences Symposium: "Insights from Comparative Genomic and Toxicogenomic Analyses"
2004 12th International Conference on Intelligent Systems for Molecular Biology/3rd European Conference on Computational Biology
2004 15th International Chromosome Conference (ICC XV)
2004 13th Annual Symposium of the Developmental Biology Center at the University of Minnesota: "From Egg to Organ: Development and Disease"

2004 Pseudoxanthoma Elasticum Research Meeting 2004
2005 Annual Meeting: "Advances in Genome Biology and Technology"
2005 Annual Meeting of the American Society for Biochemistry and Molecular Biology (Experimental Biology 2005)
2005 Washington University School of Medicine Alumni Reunion Scientific Program: "Medical Update 2005"
2005 Cold Spring Harbor Laboratory Meeting: "Genome Biology"
2005 15th International Congress of Comparative Endocrinology
2005 The Henry M. & Lillian Stratton Basic Research Single Topic Conference: "Exploring the Functional Genomics and Proteomics of Liver in Health and Disease"
2005 AACR Workshop on the Human Epigenome
2005 AACR Workshop in Cancer Research: Molecular Biology in Clinical Oncology
2005 Pennsylvania State University 24th Summer Symposium in Molecular Biology: "Comparative and Functional Genomics"
2005 Gordon Research Conference: "Human Genetics and Genomics"
2005 UCSD Project for Explaining the Origins of Humans Symposium: "Understanding Great Apes in the Genomic Era"
2005 Windber Research Institute Meeting: "4th Annual Showcase for Biotechnology"
2005 The Genomics Biotech Institute Meeting: "Genomics and Biologics— Their Impact on the Future of Patient Care"
2005 Iowa State University Growth Factor and Signal Transduction Symposium: "Integration of Structural and Functional Genomics"
2005 American Society of Clinical Pathologists Annual Meeting: "Pathology Today"
2005 17th Annual Meeting, Korean Society for Molecular and Cellular Biology
2005 Emory/Georgia Tech Predictive Health Initiative Symposium: "Seeking Ponce's Dream: The Promise of Predictive Health"
2006 Genetics Society of America Meeting: "Genetic Analysis: Model Organisms to Human Biology"
2006 Annual Meeting: "Advances in Genome Biology and Technology"
2006 Keystone Meeting: "Systems Biology: Integrating Biology, Technology, and Computation"
2006 31st Annual Meeting, Association of Genetic Technologists
2006 AACR Workshop in Cancer Research: Molecular Biology in Clinical Oncology
2006 Genetic Alliance Annual Conference
2006 2nd National Congress of Genomic Medicine, Mexico
2006 Keynote Speaker, University of Maryland Bioscience Research & Techology Review Day
2007 Genome British Columbia Genomics Forum: Biomarkers, New Sequencing Technologies, and Their Applications
2007 Capstone Speaker, 6th Annual BIO IT Coalition Conference: The State of Healthcare & Medical Technology in 2020
2007 Keynote Speaker, 2007 American Institute of Biological Sciences (AIBS) Annual Meeting
2007 Keynote Speaker, Institute of Genetic Medicine Annual Retreat, Johns Hopkins University School of Medicine
2007 AACR Workshop in Cancer Research: Molecular Biology in Clinical Oncology
2007 Gordon Research Conference: "Human Genetics and Genomics"
2007 International Conference on Genomics (Shenzhen, China)
2007 Cold Spring Harbor Laboratory Course: "Computational Genomics"

2008 Keynote Speaker, 4th International Conference "Advances in Canine and Feline Genomics and Inherited Diseases"
2008 AACR Workshop in Cancer Research: Molecular Biology in Clinical Oncology
2008 American Ceramic Society Annual Meeting
2009 AAAS Annual Meeting: "Studying Vertebrate Genomes: Reading Evolution's Notebooks"
2009 Cardiff University/The Wales Gene Park Meeting: "Clinical Medicine in the Genome Era"
2009 6th African Society of Human Genetics Meeting
2009 Wellcome Trust/NHGRI Frontiers Meeting: "Genetic Diversity in Health and Disease in African Populations"
2009 Oxford Workshop: "Identifying Loci Involved in the Susceptibility to Common Disease"
2009 Genome 10K Workshop
2009 Keynote Speaker, 4th Annual Sequencing, Finishing, and Analysis in the Future Meeting
2009 Keynote Speaker, American Genetic Association Conference: "Next Generation Genome Analysis in Non-model Organisms"
2009 AACR Workshop in Cancer Research: Molecular Biology in Clinical Oncology
2009 Gordon Research Conference: "Human Genetics and Genomics"
2009 Keynote Speaker, Montreal Bioinformatics Users Group (MonBUG) Bioinformatics Symposium 2009
2009 European Science Foundation (ESF)-COST Meeting: "Complex Systems and Changes—Darwin and Evolution: Nature-Culture Interfaces"
2009 NIH Symposium: "Finished Proofs? — A Symposium to Celebrate the 150th Anniversary of the Publication of *On the Origin of Species* (1859)"
2009 ACR/ARHP Annual Meeting: ACR Basic Research Conference

PUBLICATIONS:

1. Green ED, Gruenebaum J, Bielinska M, Baenziger JU, and Boime I: Sulfation of lutropin oligosaccharides with a cell-free system. *Proc Natl Acad Sci USA* 81:5320-5324, 1984. [PMCID: PMC391695]

2. Knecht DA, Green ED, Loomis WF, and Dimond RL: Developmental changes in the modification of lysosomal enzymes in *Dictyostelium discoideum*. *Devel Biol* 107:490-502, 1985.

3. Green ED, Morishima C, Boime I, and Baenziger JU: Structural requirements for sulfation of asparagine-linked oligosaccharides of lutropin. *Proc Natl Acad Sci USA* 82:7850-7854, 1985. [PMCID: PMC390867]

4. Green ED, Van Halbeek H, Boime I, and Baenziger JU: Structural elucidation of the disulfated oligosaccharide from bovine lutropin. *J Biol Chem* 260:15623-15630, 1985.

5. Green ED, Baenziger JU, and Boime I: Cell-free sulfation of human and bovine pituitary hormones: comparison of the sulfated oligosaccharides of lutropin, follitropin, and thyrotropin. *J Biol Chem* 260:15631-15638, 1985.

6. Hortin G, Green ED, Baenziger JU, and Strauss AW: Sulphation of proteins secreted by a human hepatoma-derived cell line: sulphation of *N*-linked oligosaccharides on alpha2-HS-glycoprotein. *Biochemical J* 235:407-414, 1986. [PMCID: PMC1146701]

7. Green ED, Knecht DA, and Dimond RL: Examination of isoelectric focusing and electrophoretic methods for resolving acidic proteins. *Electrophoresis* 7:407-413, 1986.

8. Green ED and Baenziger JU: Separation of anionic oligosaccharides by high-performance liquid chromatography. *Anal Biochem* 158:42-49, 1986.

9. Green ED, Boime I, and Baenziger JU: Biosynthesis of sulfated asparagine-linked oligosaccharides on bovine lutropin. *J Biol Chem* 261:16309-16316, 1986.

10. Green ED, Boime I, and Baenziger JU: Differential processing of Asn-linked oligosaccharides on pituitary glycoprotein hormones: implications for biologic function. *Molec Cell Biochem* 72:81-100, 1986.

11. Green ED and Baenziger JU: Oligosaccharide specificities of *Phaseolus vulgaris* leukoagglutinating and erythroagglutinating phytohemagglutinins: interactions with *N*-glycanase-released oligosaccharides. *J Biol Chem* 262:12018-12029, 1987.

12. Green ED, Brodbeck RM, and Baenziger JU: Lectin affinity high-performance liquid chromatography: interactions of *N*-glycanase-released oligosaccharides with *Ricinus communis* agglutinin I and *Ricinus communis* agglutinin II. *J Biol Chem* 262:12030-12039, 1987.

13. Green ED, Brodbeck RM, and Baenziger JU: Lectin affinity high-performance liquid chromatography: interactions of N-glycanase-released oligosaccharides with leukoagglutinating phytohemagglutinin, concanavalin A, *Datura stramonium* agglutinin, and *Vicia villosa* agglutinin. *Anal Biochem* 167:62-75, 1987.

14. Green ED and Baenziger JU: Asparagine-linked oligosaccharides on lutropin, follitropin, and thyrotropin: I. Structural elucidation of the sulfated and sialylated oligosaccharides on bovine, ovine, and human pituitary glycoprotein hormones. *J Biol Chem* 263:25-35, 1988.

15. Green ED and Baenziger JU: Asparagine-linked oligosaccharides on lutropin, follitropin, and thyrotropin: II. Distributions of sulfated and sialylated oligosaccharides on bovine, ovine, and human pituitary glycoprotein hormones. *J Biol Chem* 263:36-44, 1988.

16. Baenziger JU and Green ED: Pituitary glycoprotein hormone oligosaccharides: structure, synthesis, and function of the asparagine-linked oligosaccharides on lutropin, follitropin, and thyrotropin. *Biochim Biophys Acta* 947:287-306, 1988.

17. Green ED, Adelt G, Wilson S, Van Halbeek H, and Baenziger JU: The asparagine-linked oligosaccharides on bovine fetuin: structural analysis of *N*-glycanase-released oligosaccharides by 500-MHz 1H-NMR spectroscopy. *J Biol Chem* 263:18253-18268, 1988.

18. Green ED and Gast MJ: Hormonal evaluation of female infertility and reproductive disorders. *Clin Chem* 35:620-629, 1989.

19. Green ED and Baenziger JU: Characterization of oligosaccharides by lectin affinity high-performance liquid chromatography. *Trends Biochem Sci* 14:168-172, 1989.

20. Hardy RW, Green ED, Pikul FJ, Silva DP, Koenig JW, and Scott MG: The effects of hyperlipidaemia, hyperbilirubinaemia and haemolysis on tests performed by the Olympus AU 5000 multiple analyser. *J Automat Chem* 11:89-90, 1989. [PMCID: PMC2547791]

21. Green ED and Olson MV: Systematic screening of yeast artificial-chromosome libraries by use of the polymerase chain reaction. *Proc Natl Acad Sci USA* 87:1213-1217, 1990. [PMCID: PMC53441]

22. Green ED, Morrison LK, Love PE, DeSchryver-Kecskemeti K, Waltman SR, Smith ME, and Scott MG: A structurally aberrant immunoglobulin paraprotein in a patient with multiple myeloma and corneal crystal deposits. *Am J Med* 88:304-311, 1990.

23. Green ED, Curtis BR, Issitt PD, Gutgsell NS, Roelcke D, Farrar RP, and Chaplin H: Inhibition of an anti-Pr1d cold agglutinin by citrate present in red cell preservative solutions. *Transfusion* 30:267-270, 1990.

24. Huxley C, Green ED, and Dunham I: Rapid assessment of *S. cerevisiae* mating type by the PCR. *Trends Genet* 6:236, 1990.

25. Green ED and Olson MV: Chromosomal region of the cystic fibrosis gene in yeast artificial chromosomes: a model for human genome mapping. *Science* 250:94-98, 1990.

26. Silverman GA, Green ED, Young RL, Jockel JI, Domer PH, and Korsmeyer SJ: Meiotic recombination between yeast artificial chromosomes yields a single clone containing the entire *BCL-2* protooncogene. *Proc Natl Acad Sci USA* 87:9913-9917, 1990. [PMCID: PMC55284]

27. Baenziger JU and Green ED: Structure, synthesis, and function of the asparagine-linked oligosaccharides on pituitary glycoprotein hormones. In *Biology of Carbohydrates* (V Ginsburg and PW Robbins, eds; JAI Press, Ltd.), Vol. 3, pp. 1-46, 1991.

28. Green ED and Waterston RH: The Human Genome Project: prospects and implications for clinical medicine. *JAMA* 266:1966-1975, 1991.

29. Green ED, Mohr RM, Idol JR, Jones M, Buckingham JM, Deaven LL, Moyzis RK, and Olson MV: Systematic generation of sequence-tagged sites for physical mapping of human chromosomes: application to the mapping of human chromosome 7 using yeast artificial chromosomes. *Genomics* 11:548-564, 1991.

30. Green ED, Riethman HC, Dutchik JE, and Olson MV: Detection and characterization of chimeric yeast artificial-chromosome clones. *Genomics* 11:658-669, 1991.

31. Green ED and Green P: Sequence-tagged site (STS) content mapping of human chromosomes: theoretical considerations and early experiences. *PCR Methods & Applications* 1:77-90, 1991.

32. Coffey AJ, Roberts RG, Green ED, Cole CG, Butler R, Anand R, Giannelli F, and Bentley DR: Construction of a 2.6-Mb contig in yeast artificial chromosomes spanning the human dystrophin gene using an STS-based approach. *Genomics* 12:474-484, 1992.

33. Lengauer C, Riethman HC, Speicher MR, Taniwaki M, Konecki D, Green ED, Becher R, Olson MV, and Cremer T: Metaphase and interphase cytogenetics with Alu-PCR amplified yeast artificial chromosome clones containing the *BCR* gene and the protooncogenes c-*raf*-1, c-*fms*, c-*erbB*-2. *Cancer Res* 52:2590-2596, 1992.

34. Lengauer C, Green ED, and Cremer T: Fluorescence *in situ* hybridization of YAC clones after *Alu*-PCR amplification. *Genomics* 13:826-828, 1992.

35. Hockett Jr. RD and Green ED: Barnes Hospital Laboratory Reference Values. In *Manual of Medical Therapeutics* (AJ Whelan and MC Woodley, eds; Little, Brown, and Company), pp. 517-523, 1992.

36. Green ED: Physical mapping of human chromosomes: generation of chromosome-specific sequence-tagged sites. In *Methods in Molecular Genetics: Gene and Chromosome Analysis (Part A)* (KW Adolph, ed.; Academic Press, Inc.), Vol. 1, pp. 192-210, 1993.

37. Matsuda T, Sato S, Wada M, Kohno K, Green E, Schlessinger D, and Kuwano M: The isolation of human multidrug resistance 1 and 3 genes from a library of yeast artificial chromosome clones. In *The Mechanism and New Approach on Drug Resistance of Cancer Cells* (T Miyazaki, F Takaku, and K Sakurada, eds; Elsevier Publishing), pp. 29-32, 1993.

38. Grzeschik K-H, Tsui L-C, and Green ED: Report of the first international workshop on human chromosome 7 mapping 1993. *Cytogenet Cell Genet* 65:51-73, 1994.

39. Green ED, Idol JR, Mohr-Tidwell RM, Braden VV, Peluso DC, Fulton RS, Massa HF, Magness CL, Wilson AM, Kimura J, Weissenbach J, and Trask BJ: Integration of physical, genetic and cytogenetic maps of human chromosome 7: isolation and analysis of yeast artificial chromosome clones for 117 mapped genetic markers. *Hum Molec Genet* 3:489-501, 1994.

40. Umbricht CB, Griffen CA, Hawkins AL, Grzeschik KH, O'Connell P, Leach R, Green ED, and Kelly TJ: High-resolution genomic mapping of the three human replication protein A genes (RPA1, RPA2, RPA3). *Genomics* 20:249-257, 1994.

41. Maraia RJ, Sasaki-Tozawa N, Driscoll CT, Green ED, and Darlington GJ: The human Y4 small cytoplasmic RNA gene is controlled by upstream elements and resides on chromosome 7 with all other hY scRNA genes. *Nucl Acids Res* 22:3045-3052, 1994. [PMCID: PMC310274]

42. Cox DR, Green ED, Lander ES, Cohen D, and Myers RM: Assessing mapping progress in the Human Genome Project. *Science* 265:2031-2032, 1994.

43. Lewanda AF, Green ED, Weissenbach J, Jerald H, Taylor E, Summar ML, Phillips III JA, Cohen M, Feingold M, Mouradian W, Clarren S.K, and Jabs EW: Evidence that the Saethre-Chotzen syndrome locus lies between D7S664 and D7S507, by genetic analysis and detection of a microdeletion in a patient. *Am J Hum Genet*, 55:1195-1201, 1994. [PMCID: PMC1918444]

44. Wajnrajch MP, Chua SC, Green ED, and Leibel RL: Human growth hormone-releasing hormone receptor (GHRHR) maps to a YAC at chromosome 7p15. *Mamm Genome* 5:595, 1994.

45. Green ED, Cox DR, and Myers RM: The Human Genome Project and its impact on the study of human disease. In *The Metabolic and Molecular Bases of Inherited Disease, 7th Edition* (CR Scriver, AL Beaudet, WS Sly, and D Valle, eds; McGraw-Hill, Inc.), pp. 401-436, 1995.

46. Green ED, Braden VV, Fulton RS, Lim R, Ueltzen MS, Peluso DC, Mohr-Tidwell RM, Idol JR, Smith LM, Chumakov I, Le Paslier D, Cohen D, Featherstone T, and Green P: A human chromosome 7 yeast artificial chromosome (YAC) resource: construction, characterization, and screening. *Genomics* 25:170-183, 1995.

47. Keen TJ, Inglehearn CF, Patel RJ, Green ED, Peluso DC, and Bhattacharya SS: Localization of the Aquaporin 1 (AQP1) gene within a YAC contig containing the polymorphic markers D7S632 and D7S526. *Genomics* 25:599-600, 1995.

48. Curran ME, Splawski I, Timothy KW, Vincent GM, Green ED, and Keating MT: A molecular basis for cardiac arrhythmia: *HERG* mutations cause long QT syndrome. *Cell* 80:795-803, 1995.

49. Lee S, Zambas E, Green ED, and Redman C: Organization of the gene encoding the human Kell blood group protein. *Blood* 85:1364-1370, 1995.

50. Green ED: PCR-based screening of yeast artificial chromosome libraries. In *PCR Strategies* (MA Innis, DH Gelfand, and JJ Sninsky, eds; Academic Press, Inc.), pp. 277-288, 1995.

51. Krizman DB, Hofmann TA, DeSilva U, Green ED, Meltzer PS, and Trent JM: Identification of 3'-terminal exons from yeast artificial chromosomes. *PCR Methods & Applications* 4:322-326, 1995.

52. Green ED, Maffei M, Braden VV, Proenca R, DeSilva U, Zhang Y, Chua Jr. SC, Leibel RL, Weissenbach J, and Friedman JM: The human Obese (OB) gene: RNA expression pattern and mapping on the physical, cytogenetic, and genetic maps of chromosome 7. *Genome Res* 5:5-12, 1995.

53. Keen TJ, Inglehearn CF, Green ED, Cunningham AF, Patel RJ, Peacock RE, Gerken S, White R, Weissenbach J, and Bhattacharya SS: A YAC contig spanning the dominant retinitis pigmentosa locus (RP9) on chromosome 7p. *Genomics* 28:383-388, 1995.

54. Torigoe K, Sato S, Kusaba H, Kohno K, Kuwano M, Okumura K, Green ED, Tsui L-C, Scherer SW, Schlessinger D, and Wada M: A YAC-based contig of 1.5 Mb spanning the human multidrug resistance gene region and delineating the amplification unit in three human multidrug-resistant cell lines. *Genome Res* 5:233-244, 1995.

55. Kusaba H, Kohno K, Asakuno K, Kuwano M, Okumura K, Green ED, Schlessinger D, and Wada M: Functional expression of yeast artificial chromosome-human multidrug resistance genes in mouse cells. *Genome Res* 5:245-258, 1995.

56. Johnson EW, Iyer LM, Rich SS, Orr HT, Gil-Nagel A, Kurth JH, Zabramski JM, Marchuk DA, Weissenbach J, Clericuzio CL, Davis LE, Hart BL, Gusella JF, Kosofsky BE, Louis DN, Morrison LA, Green ED, and Weber JL: Refined localization of the cerebral cavernous malformation gene (*CCM1*) to a 4-cM interval of chromosome 7q contained in a well-defined YAC contig. *Genome Res* 5:368-380, 1995.

57. Hamer L, Johnston M, and Green ED: Isolation of yeast artificial chromosomes free of endogenous yeast chromosomes: construction of alternate hosts with defined karyotypic alterations. *Proc Natl Acad Sci USA* 92:11706-11710, 1995. [PMCID: PMC40471]

58. Hoglund P, Haila S, Scherer SW, Tsui L-C, Green ED, Weissenbach J, Holmberg C, de la Chapelle A, and Kere J: Positional candidate genes for congenital chloride diarrhea suggested by high-resolution physical mapping in chromosome region 7q31. *Genome Res* 6:202-120, 1996.

59. McGuire RE, Jordan SA, Braden VV, Bouffard GG, Humphries P, Green ED, and Daiger SP: Mapping the RP10 locus for autosomal dominant retinitis pigmentosa on 7q: refined genetic positioning and localization within a well-defined YAC contig. *Genome Res* 6:255-266, 1996.

60. Reed DR, DingY, Xu W, Cather C, Green ED, and Price RA: Extreme obesity may be linked to markers flanking the human *OB* gene. *Diabetes* 45:691-694, 1996.

61. Frangiskakis JM, Ewart AK, Morris CA, Mervis CB, Bertrand J, Robinson BF, Klein BP, Ensing GJ, Everett LA, Green ED, Proschel C, Gutowski NJ, Noble M, Atkinson DL, Odelberg SJ, and Keating MT: *LIM-kinase1* hemizygosity implicated in impaired visuospatial constructive cognition. *Cell* 86:59-69, 1996.

62. Clendenning JB, Humbert R, Green ED, Wood C, Traver D, and Furlong CE: Structural organization of the human *PON1* gene. *Genomics* 35:586-589, 1996.

63. Le Beau MM, Espinosa III R, Davis EM, Eisenbart JD, Larson RA, and Green ED: Cytogenetic and molecular delineation of the region of chromosome 7 commonly deleted in malignant myeloid diseases. *Blood* 88:1930-1935, 1996.

64. Maraia R, Sakulich AL, Brinkmann E, and Green ED: Gene for human Ro-associated autoantigen Y5 RNA. *Nucl Acids Res* 24:3552-3559, 1996. [PMCID: PMC146121]

65. Tazawa R, Green ED, Ohashi K, Wu KK, and Wang L-H: Characterization of the complete genomic structure of human thromboxane synthase gene and functional analysis of its promoter. *Arch Biochem Biophys* 334:349-359, 1996.

66. Zhan S, Vazquez N, Zhan S, Wientjes FB, Budarf ML, Schrock E, Ried T, Green ED, and Chanock SJ: Genomic structure, chromosomal localization, start of transcription, and tissue expression of the human p40-phox, a new component of the nicotinamide adenine dinucleotide phosphate-oxidase complex. *Blood* 88:2714-2721, 1996.

67. Reynolds PA, Powlesland RM, Keen TJ, Inglehearn CF, Cunningham AF, Green ED, and Brown KW: Localization of a novel t(1;7) translocation associated with Wilms' tumor predisposition and skeletal abnormalities. *Genes Chromosomes Cancer* 17:151-155, 1996.

68. Howard TD, Paznekas WA, Green ED, Chiang LC, Ma N, De Luna RIO, Delgado CG, Gonzalez-Ramos M, Kline AD, and Jabs EW: Mutations in *TWIST*, a basic helix-loop-helix transcription factor, in Saethre-Chotzen syndrome. *Nat Genet* 15:36-41, 1997.

69. Bouffard GG, Iyer LM, Idol JR, Braden VV, Cunningham AF, Weintraub LA, Mohr-Tidwell RM, Peluso DC, Fulton RS, Leckie MP, and Green ED: A collection of 1814 human chromosome 7-specific STSs. *Genome Res* 7:59-64, 1997.

70. DeSilva U, D'Arcangelo G, Braden VV, Chen J, Miao GG, Curran T, and Green ED: The human reelin gene: isolation, sequencing, and mapping on chromosome 7. *Genome Res* 7:157-164, 1997.

71. Touchman JW, Bouffard GG, Weintraub LA, Idol JR, Wang L, Robbins CM, Nussbaum JC, Lovett M, and Green ED: 2006 expressed-sequence tags derived from human chromosome 7-enriched cDNA libraries. *Genome Res* 7:281-292, 1997.

72. McGuire RE, Daiger SP, and Green ED: Localization and characterization of the human ADP-ribosylation factor 5 (ARF5) gene. *Genomics* 41:481-484, 1997.

73. Van Laer L, Van Camp G, Green ED, Huizing EH, and Willems PJ: Physical mapping of the HOXA1 gene and the hnRPA2B1 gene in a YAC contig from human chromosome 7p14-p15. *Human Genetics* 99:831-833, 1997.

74. Kang S, Allen J, Graham Jr. JM, Grebe T, Clericuzio C, Patronas N, Ondrey F, Green E, Schaffer A, Abbott M, and Biesecker LG: Linkage mapping and phenotypic analysis of autosomal dominant Pallister-Hall syndrome. *J Med Genet* 34:441-446, 1997.

75. Behrens F, Claussen U, Iyer LM, Green ED, Horsthemke B, Williamson R, Huxley C, and Coutelle C: Isolation of DNA from the centromere of human chromosome 7 by microdissection. *Chromosome Res* 5:215-220, 1997.

76. Gorlach A, Lee PL, Roesler J, Hopkins PJ, Christensen B, Green ED, Chanock SJ, and Curnutte JT: A p47-*phox* pseudogene carries the most common mutation causing p47-*phox*-deficient chronic granulomatous disease. *J Clin Invest* 100:1907-1918, 1997. [PMCID: PMC508379]

77. Bouffard GG, Idol JI, Braden VV, Iyer LM, Cunningham AF, Weintraub LA, Touchman JW, Mohr-Tidwell RM, Peluso DC, Fulton RS, Ueltzen MS, Weissenbach J, Magness CL, and Green ED: A physical map of human chromosome 7: an integrated YAC contig map with average STS spacing of 79 kb. *Genome Res* 7:673-692, 1997.

78. Chen M, Compton ST, Coviello VF, Green ED, and Ashlock MA: Transient gene expression from yeast artificial chromosome DNA in mammalian cells is enhanced by adenovirus. *Nucl Acids Res* 25:4416-4418, 1997. [PMCID: PMC147053]

79. Everett LA, Glaser B, Beck JC, Idol JR, Buchs A, Heyman M, Adawi F, Hazani E, Nassir E, Baxevanis AD, Sheffield VC, and Green ED: Pendred syndrome is caused by mutations in a putative sulphate transporter gene (*PDS*). *Nat Genet* 17:411-422, 1997.

80. Marra MA, Kucaba TA, Dietrich NL, Green ED, Brownstein B, Wilson RK, McDonald KM, Hillier LW, McPherson JD, and Waterston RW: High throughput fingerprint analysis of large-insert clones. *Genome Res* 7:1072-1084, 1997. [PMCID: PMC310686]

81. Van Laer L, Van Camp G, van Zuijlen D, Green ED, Verstreken M, Schatteman I, Van de Heyning P, Balesmans W, Coucke P, Greinwald JH, Smith RJH, Huizing E, and Willems P: Refined mapping of a gene for autosomal dominant progressive sensorineural hearing loss (DFNA5) to a 2-cM region, and exclusion of a candidate gene that is expressed in the cochlea. *Eur J Hum Genet* 5:397-405, 1997.

82. Green ED, Cox DR, and Myers RM: The Human Genome Project and its impact on the study of human disease. In *The Genetic Basis of Human Cancer, 1st Edition* (B Vogelstein and KW Kinzler, eds; McGraw-Hill, Inc.), pp. 33-63, 1998.

83. Li XC, Everett LA, Lalwani AK, Desmukh D, Friedman TB, Green ED, and Wilcox ER: A mutation in *PDS* causes non-syndromic deafness. *Nat Genet* 18:215-217, 1998.

84. Liang H, Fairman J, Claxton DF, Nowell PC, Green ED, and Nagarajan L: Molecular anatomy of chromosome 7q deletions in myeloid neoplasms: evidence for multiple critical loci. *Proc Natl Acad Sci USA* 95:3781-3785, 1998. [PMCID: PMC19914]

85. Kusaba H, Nakayama M, Harada T, Torigoe K, Green ED, Scherer S, Kohno K, Kuwano M, and Wada M: Maintenance of hypomethylation status and preferential expression of exogenous human *MDR1/PGY1* gene in mouse L cells by YAC mediated transfer. *Somat Cell Molec Genetics* 23:259-274, 1998.

86. Torigoe K, Harada T, Kusaba H, Uchiumi T, Kohno K, Green ED, Scherer SW, Tsui L-C, Schlessinger D, Kuwano M, and Wada M: Localization of 67 exons on a YAC contig spanning 1.5 Mb around the multidrug resistance gene region of human chromosome 7q21.1. *Genomics* 49:14-22, 1998.

87. Cremers CWRJ, Bolder C, Admiraal RJC, Everett LA, Joosten FBM, van Hauwe P, Green ED, and Otten BJ: Progressive sensorineural hearing loss and a widened vestibular aquaduct in Pendred syndrome. *Arch Otolaryngol Head Neck Surg* 124:501-505, 1998.

88. Van Hauwe P, Everett LA, Coucke P, Scott DA, Kraft ML, Ris-Stalpers C, Bolder C, Otten B, de Vijlder JJM, Dietrich NL, Ramesh A, Srisailapathy SCR, Parving A, Cremers CWRJ, Willems PJ, Smith RJH, Green ED, and Van Camp G: Two frequent missense mutations in Pendred syndrome. *Hum Molec Genet* 7:1099-1104, 1998.

89. Knutsen T, Mickley LA, Ried T, Green ED, du Manoir S, Schrock E, Macville M, Ning Y, Robey R, Polymeropoulos M, Torres R, and Fojo T: Cytogenetic and molecular characterization of random chromosomal rearrangements activating the drug resistance gene, *MDR1/P-Glycoprotein*, in drug-selected cell lines and patients with drug refractory ALL. *Genes Chromosomes Cancer* 23:44-54, 1998.

90. Green ED, Hieter P, and Spencer FA: Yeast artificial chromosomes. In Genome Analysis: *A Laboratory Manual, Vol. 3, Cloning Systems* (B Birren, ED Green, S Klapholz, RM Myers, H Riethman, and J Roskams, eds; Cold Spring Harbor Laboratory Press), pp. 297–565, 1998.

91. Cremers CWRJ, Admiraal RJC, Huygen PLM, Bolder C, Everett LA, Joosten FBM, Green ED, van Camp G, and Otten BJ: Progressive hearing loss, hypoplasia of the cochlea and widened vestibular aqueducts are very common features in Pendred's syndrome. *Int J Ped Otorhinolaryngol* 45:113-123, 1998.

92. Meng X, Lu X, Li Z, Green ED, Massa H, Trask BJ, Morris CA, and Keating MT: Complete physical map of the common deletion region in Williams syndrome and identification and characterization of three novel genes. *Hum Genet* 103:590-599, 1998.

93. Kuehl PM, Weisemann JM, Touchman JW, Green ED, and Boguski MS: An effective approach for analyzing 'prefinished' genomic sequence data. *Genome Res* 9:189-194, 1999. [PMCID: PMC310715]

94. Jin D-Y, Kozak CA, Pangilinan F, Spencer F, Green ED, and Jeang K-T: Mitotic checkpoint locus *MAD1L1* maps to human chromosome 7q22 and mouse chromosome 5. *Genomics* 55:563-564, 1999.

95. Anikster Y, Lucero C, Touchman JW, Huizing M, McDowell G, Shotelersuk V, Green ED, and Gahl WA: Identification and detection of the common 65-kb deletion breakpoint in the nephropathic cystinosis gene (*CTNS*). *Mol Genet Metab* 66:111-116, 1999.

96. Zenklusen JC, Weintraub LA, and Green ED: Construction of a high-resolution physical map of the ~1-Mb region of human chromosome 7q31.1-q31.2 harboring a putative tumor suppressor gene. *Neoplasia* 1:16-22, 1999. [PMCID: PMC1764836]

97. DeSilva U, Massa H, Trask BJ, and Green ED: Comparative mapping of the region of human chromosome 7 deleted in Williams syndrome. *Genome Res* 9:428-436, 1999. [PMCID: PMC310780]

98. Ellsworth RE, Ionasescu V, Searby C, Sheffield VC, Braden VV, Kucaba TA, McPherson JD, Marra MA, and Green ED: The *CMT2D* locus: refined genetic position and construction of a bacterial clone-based physical map. *Genome Res* 9:568-574, 1999. [PMCID: PMC310773]

99. Southard-Smith EM, Collins JE, Ellison JS, Smith KJ, Baxevanis AD, Touchman JW, Green ED, Dunham I, and Pavan WJ: Comparative analyses of the *Dominant megacolon-SOX10* genomic interval in mouse and human. *Mamm Genome* 10:744-749, 1999.

100. Thomas JW, Lee-Lin S-Q, and Green ED: Human-mouse comparative mapping of the genomic region containing CDK6: localization of an evolutionary breakpoint. *Mamm Genome* 10:764-767, 1999.

101. Coucke PJ, Van Hauwe P, Everett LA, Demirhan O, Kabakkaya Y, Dietrich NL, Smith RJH, Coyle E, Reardon W, Trembath R, Wilhems PJ, Green ED, and Van Camp G: Identification of two different mutations in the PDS gene in an inbred family with Pendred syndrome. *J Med Genet* 36:475-477, 1999.

102. Everett LA, Morsli H, Wu DK, and Green ED: Expression pattern of the mouse ortholog of the Pendred's syndrome gene (*Pds*) suggests a key role for pendrin in the inner ear. *Proc Natl Acad Sci USA* 96:9272-9732, 1999. [PMCID: PMC22278]

103. Everett LA and Green ED: A family of mammalian anion transporters and their involvement in human genetic diseases. *Hum Molec Genet* 8:1883-1891, 1999.

104. Sahoo T, Johnson EW, Thomas JW, Kuehl PM, Jones TL, Dokken CG, Touchman JW, Gallione CJ, Lee-Lin S-Q, Kosofsky B, Kurth JH, Louis DN, Mettler G, Morrison L, Gil-Nagel A, Rich SS, Zabramski JM, Boguski MS, Green ED, and Marchuk DA: Mutations in the gene encoding KRIT1, a Krev-1/rap1a binding protein, cause cerebral cavernous malformations (*CCM1*). *Hum Molec Genet* 8:2325-2333, 1999.

105. Royaux IE, Suzuki K, Mori A, Katoh R, Everett LA, Kohn LD, and Green ED: Pendrin, the protein encoded by the Pendred syndrome gene (*PDS*), is an apical porter of iodide in the thyroid and is regulated by thyroglobulin in FRTL-5 cells. *Endocrinology* 141:839-845, 2000. [PMCID: PMC31206]

106. Ellsworth RE, Jamison DC, Touchman JW, Chissoe SL, Braden Maduro VV, Bouffard GG, Dietrich NL, Beckstrom-Sternberg SM, Iyer LM, Weintraub LA, Cotton M, Courtney L, Edwards J, Maupin R, Ozersky P, Rohlfing T, Wohldmann P, Miner T, Kemp K, Kramer J, Korf I, Pepin K, Antonacci-Fulton L, Fulton RS, Minx P, Hillier LW, Wilson RK, Waterston RH, Miller W, and Green ED: Comparative genomic sequence analysis of the human and mouse cystic fibrosis transmembrane conductance regulator genes. *Proc Natl Acad Sci USA* 97:1172-1177, 2000. [PMCID: PMC15558]

107. Touchman JW, Anikster Y, Dietrich NL, Braden Maduro VV, McDowell G, Shotelersuk V, Bouffard GG, Beckstrom-Sternberg SM, Gahl WA, and Green ED: The genomic region encompassing the nephropathic cystinosis gene (*CTNS*): complete sequencing of a 200-kb segment and discovery of a novel gene within the common cystinosis-causing deletion. *Genome Res* 10:165-173, 2000. [PMCID: PMC310836]

108. Kirsch IR, Green ED, Yonescu R, Strausberg R, Carter N, Bentley D, Leversha MA, Dunham I, Braden VV, Hilgenfeld E, Schuler G, Lash AE, Shen GL, Martelli M, Kuehl WM, Klausner RD, and Ried T: A systematic, high-resolution linkage of the cytogenetic and physical maps of the human genome. *Nat Genet* 24:339-340, 2000.

109. Zenklusen JC, Hodges LC, LaCava M, Green ED, and Conti CJ: Definitive functional evidence for a tumor suppressor gene on human chromosome 7q31.1 neighboring the Fra7G site. *Oncogene* 19:1729-1733, 2000.

110. Thomas JW, Summers TJ, Lee-Lin S-Q, Braden Maduro VV, Idol JR, Mastrian SD, Ryan JF, Jamison DC, and Green ED: Comparative genome mapping in the sequence-based era: early experience with human chromosome 7. *Genome Res* 10:624-633, 2000. [PMCID: PMC310865]

111. Wilcox ER, Everett LA, Li XC, Lalwani AK, and Green ED: The *PDS* gene, Pendred syndrome, and non-syndromic deafness DFNB4. *Adv Otorhinolaryngol* 56:145-151, 2000.

112. Lai CSL, Fisher SE, Hurst JA, Levy ER, Hodgson S, Fox M, Jeremiah S, Povey S, Jamison DC, Green ED, Vargha-Khadem F, and Monaco AP: The *SPCH1* region on human 7q31: genomic characterization of the critical interval and localization of translocations associated with speech and language disorder. *Am J Hum Genet* 67:357-368, 2000. [PMCID: PMC1287211]

113. DeSilva U, Miller E, Gorlach A, Foster CB, Green ED, and Chanock SJ: Molecular characterization of the mouse p47-*phox* (*Ncf1*) gene and comparative analysis of the mouse p47-*phox* (*Ncf1*) gene to the human *NCF1* gene. *Molec Cell Biol Res Commun* 3:224-230, 2000.

114. Jamison DC, Thomas JW, and Green ED: ComboScreen facilitates the multiplex hybridization-based screening of high-density clone arrays. *Bioinformatics* 16:678-684, 2000.

115. Yan W, Guan X-Y, Green ED, Nicolson R, Yap TK, Zhang J, Jacobsen LK, Krasnewich DM, Kumra S, Lenane MC, Gochman P, Damschroder-Williams PJ, Esterling LE, Long, RT, Martin BM, Sidransky E, Rapoport JL, and Ginns EI: Childhood-onset schizophrenia/autistic disorder and t(1;7) reciprocal translocation: identification of a BAC contig spanning the translocation breakpoint at 7q21. *Am J Med Genet* 96:749-753, 2000.

116. Doyle JL, DeSilva U, Miller W, and Green ED: Divergent human and mouse orthologs of a novel gene (WBSCR15/*Wbscr15*) reside within the genomic interval commonly deleted in Williams syndrome. *Cytogenet Cell Genet* 90:285-290, 2000.

117. Green ED: The Human Genome Project and its impact on the study of human disease. In *The Metabolic and Molecular Bases of Inherited Disease, 8th Edition* (CR Scriver, AL Beaudet, WS Sly, D Valle, B Childs, KW Kinzler, and B Vogelstein, eds; McGraw-Hill, Inc.), pp. 259-298, 2001.

118. Everett LA, Belyantseva IA, Noben-Trauth K, Cantos R, Chen A, Thakkar SI, Hoogstraten-Miller SL, Kachar B, Wu DK, and Green ED: Targeted disruption of mouse *Pds* provides insight about the inner-ear defects encountered in Pendred syndrome. *Hum Molec Genet* 10:153-161, 2001.

119. Kohn LD, Suzuki K, Nakazato M, Royaux I, and Green ED: Effects of thyroglobulin and pendrin on iodide flux through the thyrocyte. *Trends Endocrinol Metab* 12:10-16, 2001.

120. Sahoo T, Goenaga-Dias E, Serebriiskii IG, Thomas JW, Kotova E, Cuellar JG, Peloquin JM, Golemis E, Beitinjaneh F, Green ED, Johnson EW, and Marchuk DA: Computational and experimental analyses reveal previously undetected coding exons of the *KRIT1* (*CCM1*) gene. *Genomics* 71:123-126, 2001.

121. Green ED: The Human Genome Project: elucidating our genetic blueprint. Frontiers of Engineering: Reports on Leading-Edge Engineering from the 2000 NAE Symposium on Frontiers of Engineering (*National Academy of Engineering*), pp. 47-53, 2001.

122. The International Human Genome Mapping Consortium (McPherson JD, Marra M, Hillier L, Waterston RH, Chinwalla A, Wallis J, Sekhon M, Wylie K, Mardis ER, Wilson RK, Fulton R, Kucaba TA, Wagner-McPherson C, Barbazuk WB, Gregory SG, Humphray SJ, French L, Evans RS, Bethel G, Whittaker A, Holden JL, McCann OT, Dunham A, Soderlund C, Scott CE, Bentley DR, Schuler G. Chen H-C, Jang W, Green ED, Idol JR, Braden Maduro VV, Montgomery KT, Lee E, Miller A, Emerling S, Kucherlapati R, Gibbs R, Scherer S, Gorrell JH, Sodergren E, Clerc-Blankenburg K, Tabor P, Naylor S, Garcia D, de Jong PJ, Catanese JJ, Nowak N, Osoegawa K, Qin S, Rowen L, Madan A, Dors M, Hood L, Trask B, Friedman C, Massa H, Cheung VG, Kirsch IR, Reid T, Yonescu R, Weissenbach J, Bruls T, Heilig R, Branscomb E, Olsen A, Doggett N, Cheung J-F, Hawkins T, Myers RM, Shang J, Ramirex L, Schmutz J, Velasquez O, Dixon K, Stone NE, Cox DR, Haussler D, Kent WJ, Furey T, Rogic S, Kennedy S, Jones S, Rosenthal A, Wen G, Schilhabel M, Gloeckner G, Nyakatura G, Siebert R, Schlegelberger B, Korenberg J, Chen X-N, Fujiyama A, Hattori M, Toyoda A, Yada T, Park H-S, Sakaki Y, Shimizu N, Asakawa S, Kawasaki K, Sasaki T, Shintani A, Shimizu A, Shibuya K, Kudoh J, Minoshima S, Ramser J, Seranski P, Hoff C, Poustka A, Reinhardt R, and Lehrach H): A physical map of the human genome. *Nature* 409:934-941, 2001.

123. Royaux IE, Wall SM, Karniski LP, Everett LA, Suzuki K, Knepper MA, and Green ED: Pendrin, encoded by the Pendred syndrome gene, resides in the apical region of renal intercalated cells and mediates biocarbonate secretion. *Proc Natl Acad Sci USA* 98:4221-4226, 2001.

124. Zenklusen JC, Conti CJ, and Green ED: Mutational and functional analyses reveal that *ST7* is a highly conserved tumor-suppressor gene on human chromosome 7q31. *Nat Genet* 27:392-398, 2001.

125. Perotti D, Adele Testi M, Mondini P, Pilotti S, Green ED, Pession A, Sozzi G, Pierotti MA, Fossati-Bellani F, and Radice P: Refinement within single yeast artificial chromosome clones of a minimal region commonly deleted on the short arm of chromosome 7 in Wilms tumours. *Genes Chromosomes Cancer* 31:42-47, 2001.

126. Summers TJ, Thomas JW, Lee-Lin S-Q, Maduro VVB, Idol JR, and Green ED: Comparative physical mapping of targeted regions of the rat genome. *Mamm Genome* 12:508-512, 2001.

127. Green ED. and Chakravarti A: The human genome sequence expedition: views from the "base camp." *Genome Res* 11:645-651, 2001.

128. Green ED: Strategies for the systematic sequencing of complex genomes. *Nat Rev Genet* 2:573-583, 2001.

129. Kratz CP, Emerling BM, Donovan S, Laig-Webster M, Taylor BR, Thompson P, Jensen S, Banerjee A, Bonifas J, Makalowski W, Green ED, Le Beau MM, and Shannon KM: Candidate gene isolation and comparative analysis of a commonly deleted segment of 7q22 implicated in myeloid malignancies. *Genomics* 77:171-180, 2001.

130. Zhang J, Kuehl P, Green ED, Touchman JW, Watkins P, Daly A, Hall SD, Maurel P, Relling M, Brimer C, Yasuda K, Wrighton SA, Hancock M, Kim R, Strom S, Thummel K, Russell CG, Hudson Jr. JR, Schuetz EG, and Boguski MS: The human pregnane X receptor: genomic structure and identification and functional characterization of natural allelic variants. *Pharmacogenetics* 11:1-18, 2001.

131. Tentler D, Brandberg G, Betancu C, Gillberg C, Anneren G, Orsmark C, Green ED, Carlsson B, and Dahl N: A balanced reciprocal translocation t(5;7)(q14;q32) associated with autistic disorder: molecular analysis of the chromosome 7 breakpoint. *Am J Med Genet* 105:729-736, 2001.

132. DeSilva U, Elnitski L, Idol JR, Doyle JL, Gan W, Thomas JW, Schwartz S, Dietrich NL, Beckstrom-Sternberg SM, McDowell JC, Blakesley RW, Bouffard GG, Thomas PJ, Touchman JW, Miller W, and Green ED: Generation and comparative analysis of ~3.3 Mb of mouse genomic sequence orthologous to the region of human chromosome 7q11.23 implicated in Williams syndrome. *Genome Res* 12:3-15, 2002. [PMCID: PMC155257]

133. Kratz CP, Emerling BM, Bonifas J, Wang W, Green ED, Le Beau MM, and Shannon KM: Genomic structure of the *PIK3CG* gene on chromosome 7 band 7q22 and evaluation as a candidate myeloid tumor suppressor. *Blood* 99:372-374, 2002.

134. Suzuki K, Royaux IE, Everett LA, Mori-Aoki A, Suzuki S, Nakamura K, Sakai T, Katoh R, Toda S, Green ED, and Kohn LD: Expression of *PDS*/*Pds*, the Pendred syndrome gene, in endometrium. *J Clin Endocrin Metab* 87:938-941, 2002.

135. Shevchenko Y, Bouffard GG, Butterfield YSN, Blakesley RW, Hartley JL, Young AC, Marra MA, Jones SJM, Touchman JW, and Green ED: Systematic sequencing of cDNA clones using the transposon Tn5. *Nucl Acids Res* 30:2469-2477, 2002. [PMCID: PMC117195]

136. Yoshida A, Taniguchi S, Hisatome I, Royaux IE, Green ED, Kohn LD, and Suzuki K: Pendrin is an iodide-specific apical porter responsible for iodide efflux from thyroid cells. *J Clin Endocrin Metab* 87:3356-3361, 2002.

137. Emerling BM, Bonifas J, Kratz CP, Donovan S, Taylor BR, Green ED, Le Beau MM, and Shannon KM: *MLL5*, a homolog of *Drosophila trithorax* located within a segment of chromosome band 7q22 implicated in myeloid leukemia. *Oncogene* 21:4849-4854, 2002.

138. Etzioni A, Sturla L, Antonellis A, Green ED, Gershoni-Baruch R, Berninsone PM, Hirschberg CB, and Tonetti M: Leukocyte adhesion deficiency (LAD) type II/carbohydrate deficient glycoprotein (CDG) IIc founder effect and genotype/phenotype correlation. *Am J Med Genet* 110:131-135, 2002.

139. Lipkin SM, Moens PB, Wang V, Lenzi M, Shanmugarajah D, Gilgeous A, Thomas J, Cheng J, Touchman JW, Green ED, Schwartzberg P. Collins FS, and Cohen PE: Meiotic arrest and aneuploidy in MLH3-deficient mice. *Nat Genet* 31:385-390, 2002.

140. Thomas JW, Prasad AB, Summers TJ, Lee-Lin S-Q, Maduro VVB, Idol JR, Ryan JF, Thomas PJ, McDowell JC, and Green ED: Parallel construction of orthologous sequence-ready clone contig maps in multiple species. *Genome Res* 12:1277-1285, 2002. [PMCID: PMC186643]

141. Sultana R, Yu C-E, Yu J, Munson J, Chen D, Hua W, Estes A, Cortes F, de la Barra F, Yu D, Haider ST, Trask BJ, Green ED, Raskind WH, Disteche CM, Wijsman E, Dawson G, Storm DR, Schellenberg GD, and Villacres EC: Identification of a novel gene on chromosome 7q11.2 interrupted by a translocation breakpoint in a pair of autistic twins. *Genomics* 80:129-134, 2002.

142. Karniski LP, Wang T, Everett LA, Green ED, Giebisch G, and Aronson PS: Formate-stimulated NaCl absorption in the proximal tubule is independent of the pendrin protein. *Am J Physiol Renal Physiol* 283:F952-F956, 2002.

143. Rotman-Pikielny P, Hirschberg K, Maruvada P, Suzuki K, Royaux IE, Green ED, Kohn LD, Lippincott-Schwartz J, and Yen PM: Retention of pendrin in the endoplasmic reticulum is a major mechanism for Pendred syndrome. *Hum Molec Genet* 11:2625-2633, 2002.

144. Green ED: Sequencing the human genome— elucidating our genetic blueprint. In *The Genomic Revolution: Unveiling the Unity of Life* (M Yudell and R DeSalle, eds; Joseph Henry Press), pp. 35-47, 2002.

145. Jackson T, Thomas J, Green ED, and Noben-Trauth K: Genetic and physical maps of *jerker* (*Espn*^{je}) on mouse chromosome 4. *Biochem Biophys Res Commun* 296:1143-1147, 2002.

146. Mouse Genome Sequencing Consortium (Waterston RH, Lindblad-Toh K, Birney E, Rogers J, Abril JF, Agarwal P, Agarwala R, Ainscough R, Alexandersson M, An P, Antonarakis SE Attwood J, Baertsch R, Bailey J, Barlow K, Beck S, Berry E, Birren B, Bloom T, Bork P, Botcherby M, Bray N, Brent MR, Brown DG, Brown SD, Bult C, Burton J, Butler J, Campbell RD, Carninci P, Cawley S, Chiaromonte F, Chinwalla AT, Church DM, Clamp M, Clee C, Collins FS, Cook LL, Copley RR, Coulson A, Couronne O, Cuff J, Curwen V, Cutts T, Daly M, David R, Davies J, Delehaunty KD, Deri J, Dermitzakis ET, Dewey C, Dickens NJ, Diekhans M, Dodge S, Dubchak I, Dunn DM, Eddy SR, Elnitski L, Emes RD, Eswara P, Eyras E, Felsenfeld A, Fewell GA, Flicek P, Foley K, Frankel WN, Fulton LA, Fulton RS, Furey TS, Gage D, Gibbs RA, Glusman G, Gnerre S, Goldman N, Goodstadt L, Grafham D, Graves TA, Green ED, Gregory S, Guigó R, Guyer M, Hardison RC, Haussler D, Hayashizaki Y, Hillier LW, Hinrichs A, Hlavina W, Holzer T, Hsu F, Hua A, Hubbard T, Hunt A, Jackson I, Jaffe DB, Johnson LS, Jones M, Jones TA, Joy A, Kamal M, Karlsson EK, Karolchik D, Kasprzyk A, Kawai J, Keibler E, Kells C, Kent WJ, Kirby A, Kolbe DL, Korf I, Kucherlapati RS, Kulbokas III EJ, Kulp D, Landers T, Leger JP, Leonard S, Letunic I, Levine R, Li J, Li M, Lloyd C, Lucas S, Ma B, Maglott DR, Mardis ER, Matthews L, Mauceli E, Mayer JH, McCarthy M, McCombie WR, McLaren S, McLay K, McPherson JD, Meldrim J, Meredith B, Mesirov JP, Miller W, Miner TL, Mongin E, Montgomery KT, Morgan M, Mott R, Mullikin JC, Muzny DM, Nash WE, Nelson JO, Nhan MN, Nicol R, Ning Z, Nusbaum C, O'Connor MJ, Okazaki Y, Oliver K, Overton-Larty E, Pachter L, Parra G, Pepin KH, Peterson J, Pevzner P, Plumb R, Pohl CS, Poliakov A, Ponce TC, Ponting CP, Potter S, quail M, Reymond A, Roe BA, Roskin KM, Rubin EM, Rust AG, Santos R, Sapojnikov V, Schultz B, Schultz J, Schwartz MS, Schwartz S, Scott C, Seaman S, Searle S, Sharpe T, Sheridan A, Shownkeen R, Sims S, Singer JB, Slater G, Smit A, Smith DR, Spencer B, Stabenau A, Stange-Thomann N, Sugnet C, Suyama M, Tesler G, Thompson J, Torrents D, Trevaskis E, Tromp J, Ucla C, Ureta-Vidal A, Vinson JP, von Niederhausern AC, Wade CM, Wall M, Weber RJ, Weiss RB, Wendl MC, West AP, Wetterstrand K, Wheeler R, Whelan S, Wierzbowski J, Willey D, Williams S, Wilson RK, Winter E, Worley KC, Wyman D, Yang S, Yang S-P, Zdobnov EM, Zody MC, and Lander ES): Initial sequencing and comparative analysis of the mouse genome. *Nature* 420:520-562, 2002.

147. Mammalian Gene Collection (MGC) Program Team (Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD, Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T, Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL, Scheetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P, Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH, Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW, Villalon DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J, Helton E, Ketteman M, Madan A, Rodrigues S, Sanchez A, Whiting M,

Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW, Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J, Schmutz J, Myers RM, Butterfield YSN, Krzywinski MI, Skalska U, Smailus DE, Schnerch A, Schein JE, Jones SJM, and Marra MA): Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences. *Proc Natl Acad Sci USA* 99:16899-16903, 2002.

148. Thomas JW, Schueler MG, Summers TJ, Blakesley RW, McDowell JC, Thomas PJ, Idol JR, Maduro VVB, Lee-Lin S-Q, Touchman JW, Bouffard GG, Beckstrom-Sternberg SM, NISC Comparative Sequencing Program, and Green ED: Pericentromeric duplications in the laboratory mouse. *Genome Res* 13:55-63, 2003. [PMCID: PMC430956]

149. Wall SM, Hassell KA, Royaux IE, Green ED, Chang JY, Shipley GL, and Verlander JW: Localization of pendrin in mouse kidney. *Am J Physiol Renal Physiol* 284:F229-F241, 2003.

150. Vernon EG, Malik K, Reynolds P, Powlesland R, Dallosso AR, Jackson S, Henthorn K, Green ED, and Brown KW: The parathyroid hormone-responsive B1 gene is interrupted by a t(1;7)(q42;p15) breakpoint associated with Wilms' tumour. *Oncogene* 22:1371-1380, 2003.

151. Liu G, NISC Comparative Sequencing Program, Zhao S, Bailey JA, Sahinalp SC, Alkan C, Tuzun E, Green ED, and Eichler EE: Analysis of primate genomic variation reveals a repeat-driven expansion of the human genome. *Genome Res* 13:358-368, 2003. [PMCID: PMC430288]

152. Green P, Ewing B, Miller W, Thomas PJ, NISC Comparative Sequencing Program, and Green ED: Transcription-associated mutational asymmetry in mammalian evolution. *Nat Genet* 3:514-517, 2003.

153. Brudno M, Do, CB, Cooper GM, Kim MF, Davydov, E, NISC Comparative Sequencing Program, Green ED, Sidow A, and Batzoglou S: LAGAN and multi-LAGAN: efficient tools for large-scale multiple alignment of genomic DNA. *Genome Res* 13:721-731, 2003. [PMCID: PMC430158]

154. Collins FS, Green ED, Guttmacher AE, and Guyer MS: A vision for the future of genomics research: a blueprint for the genomic era. *Nature* 422:835-847, 2003.

155. Antonellis A, Ellsworth RE, Sambuughin N, Puls I, Abel A, Lee-Lin S-Q, Jordanova A, Kremensky I, Christodoulou K, Middleton LT, Sivakumar K, Ionasescu V, Funalot B, Vance JM, Goldfarb LG, Fischbeck KH, and Green ED: Glycyl tRNA synthetase mutations in Charcot-Marie-Tooth disease type 2D and distal spinal muscular atrophy type V. *Am J Hum Genet* 72:1293-1299, 2003. [PMCID: PMC1180282]

156. Cooper GM, Brudno M, NISC Comparative Sequencing Program, Green ED, Batzoglou S, and Sidow A: Quantitative estimates of sequence divergence for comparative analyses of mammalian genomes. *Genome Res* 13:813-820, 2003. [PMCID: PMC430923]

157. Schwartz S, Elnitski L, Li M, Weirauch M, Riemer C, Smit A, NISC Comparative Sequencing Program, Green ED, Hardison RC, and Miller W: MultiPipMaker and supporting tools: alignments and analysis of multiple genomic DNA sequences. *Nucl Acids Res* 31:3518-3524, 2003. [PMCID: PMC168985]

158. Hillier LW, Fulton RS, Fulton LA, Graves TA, Pepin KH, Wagner-McPherson C, Layman D, Maas J, Jaeger S, Walker R, Wylie K, Sekhon M, Becker MC, O'Laughlin MD, Schaller ME, Fewell GA, Delehaunty KD, Miner TL, Nash WE, Cordes M, Du H, Sun H, Edwards J, Bradshaw-Cordum H, Ali J, Andrews S, Isak A, VanBrunt A, Nguyen C, Du F, Lamar B, Courtney L, Kalicki J, Ozersky P, Bielicki L, Scott K, Holmes A, Harkins R, Harris A,

Strong CM, Hou S, Tomlinson C, Dauphin-Kohlberg S, Kozlowicz-Reilly A, Leonard S, Rohlfing T, Rock SM, Tin-Wollam A-M, Abbott A, Minx P, Maupin R, Strowmatt C, Latreille P, Miller N, Johnson D, Murray J, Woessner JP, Wendl MC, Yang S-P, Schultz BR, Wallis JW, Spieth J, Bieri TA, Nelson JO, Berkowicz N, Wohldmann PE, Cook LL, Hickenbotham MT, Eldred J, Williams D, Bedell JA, Mardis ER, Clifton SW, Chissoe SL, Marra MA, Raymond C, Haugen E, Gillett W, Zhou Y, James R, Phelps K, Iadanoto S, Bubb K, Simms E, Levy R, Clendenning J, Kaul R, Kent WJ, Furey TS, Baertsch RA, Brent MR, Keibler E, Flicek P, Bork P, Suyama M, Bailey JA, Portnoy ME, Torrents D, Chinwalla AT, Gish WR, Eddy SR, McPherson JD, Olson MV, Eichler EE, Green ED, Waterston RH, and Wilson RK: The DNA sequence of human chromosome 7. *Nature* 424:157-164, 2003.

159. Thomas JW, Touchman JW, Blakesley RW, Bouffard GG, Beckstrom-Sternberg SM, Margulies EH, Blanchette M, Siepel AC, Thomas PJ, McDowell JC, Maskeri B, Hansen NF, Schwartz MS, Weber RJ, Kent WJ, Karolchik D, Bruen TC, Bevan R, Cutler DJ, Schwartz S, Elnitski L, Idol JR, Prasad AB, Lee-Lin S-Q, Maduro VVB, Summers TJ, Portnoy ME, Dietrich NL, Akhter N, Ayele K, Benjamin B, Cariaga K, Brinkley CP, Brooks SY, Granite S, Guan X, Gupta J, Haghighi P, Ho S-L, Huang MC, Karlins E, Laric PL, Legaspi R, Lim MJ, Maduro QL, Masiello CA, Mastrian SD, McCloskey JC, Pearson R, Stantripop S, Tiongson EE, Tran JT, Tsurgeon C, Vogt JL, Walker MA, Wetherby KD, Wiggins LS, Young AC, Zhang L-H, Osoegawa K, Zhu B, Zhao B, Shu CL, De Jong PJ, Lawrence CE, Smit AF, Chakravarti A, Haussler D, Green P, Miller W, and Green ED: Comparative analyses of multi-species sequences from targeted genomic regions. *Nature* 424:788-793, 2003.

160. Verlander JW, Hassell KA, Royaux IE, Glapion DM, Wang M-E, Everett LA, Green ED, and Wall SM: Deoxycorticosterone upregulates *PDS* (*Slc26a4*) in mouse kidney: role of pendrin in mineralocorticoid-induced hypertension. *Hypertension* 42:356-362, 2003.

161. Royaux IE, Belyantseva IA, Wu T, Kachar B, Everett LA, Marcus DC, and Green ED: Localization and functional studies of pendrin in the mouse inner ear provide insight about the etiology of deafness in Pendred syndrome. *J Assoc Res Otolaryngol* 4:394-404, 2003.

162. Thomas JW, NISC Comparative Sequencing Program, and Green ED: Comparative sequence analysis of a single-gene conserved segment in mouse and human. *Mamm Genome* 14:673-678, 2003.

163. Margulies EH, Blanchette M, NISC Comparative Sequencing Program, Haussler D, and Green ED: Identification and characterization of multi-species conserved sequences. *Genome Res* 13:2507-2518, 2003. [PMCID: PMC403793]

164. Margulies EH, NISC Comparative Sequencing Program, and Green ED: Detecting highly conserved regions of the human genome by multispecies sequence comparisons. *Cold Spring Harbor Symposia on Quantitative Biology (Volume 68): The Genome of Homo Sapiens*, pp. 255-263, 2003.

165. McCallion AS, Emison ES, Kashuk CS, Bush RT, Kenton M, Carrasquillo MM, Jones KW, Kennedy GC, Portnoy ME, Green ED, and Chakravarti A: Genomic variation in multigenic traits: Hirschsprung disease. *Cold Spring Harbor Symposia on Quantitative Biology (Volume 68): The Genome of Homo Sapiens*, pp. 373-381, 2003.

166. Shugart YY, Mundorff J, Kilshaw J, Doheny K, Doan B, Wanyee J, Green ED, and Drayna D: Results of a genome-wide linkage scan for stuttering. *Am J Med Genet* 124A:133-135, 2004.

167. Crawford GE, Holt IE, Mullikin JC, Tai D, National Institutes of Health Intramural Sequencing Center, Green ED, Wolfsberg TG, and Collins FS: Identifying gene regulatory elements by genome-wide recovery of DNase hypersensitive sites. *Proc Natl Acad Sci USA* 101:992-997, 2004. [PMCID: PMC327130]

168. Blanchette M, Kent WJ, Riemer C, Elnitski L, Smit AFA, Roskin KM, Baertsch R, Rosenbloom K, Clawson H, Green ED, Haussler D, and Miller W: Aligning multiple genomic sequences with the threaded blockset aligner. *Genome Res* 14:708-715, 2004. [PMCID: PMC383317]

169. Rat Genome Sequencing Project Consortium (Gibbs RA, Weinstock GM, Metzker ML, Muzny DM, Sodergren EJ, Scherer S, Scott G, Steffen D, Worley KC, Burch PE, Okwuonu G, Hines S, Lewis L, DeRamo C, Delgado O, Dugan-Rocha S, Miner G, Morgan M, Hawes A, Gill R, Holt RA, Adams MD, Amanatides PG, Baden-Tillson H, Barnstead M, Chin S, Evans CA, Ferriera S, Fosler C, Glodek A, Gu Z, Jennings D, Kraft CL, Nguyen T, Pfannkoch CM, Sitter C, Sutton GG, Venter JC, Woodage T, Smith D, Lee HM, Gustafson E, Cahill P, Kana A, Doucette-Stamm L, Weinstock K, Fechtel K, Weiss RB, Dunn DM, Green ED, Blakesley RW, Bouffard GG, De Jong PJ, Osoegawa K, Zhu B, Marra M, Schein J, Bosdet I, Fjell C, Jones S, Krzywinski M, Mathewson C, Siddiqui A, Wye N, McPherson J, Zhao S, Fraser CM, Shetty J, Shatsman S, Geer K, Chen Y, Abramzon S, Nierman WC, Havlak PH, Chen R, James Durbin K, Egan A, Ren Y, Song XZ, Li B, Liu Y, Qin X, Cawley S, Worley KC, Cooney AJ, D'Souza LM, Martin K, Qian Wu J, Gonzalez-Garay ML, Jackson AR, Kalafus KJ, McLeod MP, Milosavljevic A, Virk D, Volkov A, Wheeler DA, Zhang Z, Bailey JA, Eichler EE, Tuzun E, Birney E, Mongin E, Ureta-Vidal A, Woodwark C, Zdobnov E, Bork P, Suyama M, Torrents D, Alexandersson M, Trask BJ, Young JM, Huang H, Wang H, Xing H, Weinstock K, Daniels S, Gietzen D, Schmidt J, Stevens K, Vitt U, Wingrove J, Camara F, Mar Alba M, Abril JF, Guigo R, Smit A, Dubchak I, Rubin EM, Couronne O, Poliakov A, Hubner N, Ganten D, Goesele C, Hummel O, Kreitler T, Lee YA, Monti J, Schulz H, Zimdahl H, Himmelbauer H, Lehrach H, Jacob HJ, Bromberg S, Gullings-Handley J, Jensen-Seaman MI, Kwitek AE, Lazar J, Pasko D, Tonellato PJ, Twigger S, Ponting CP, Duarte JM, Rice S, Goodstadt L, Beatson SA, Emes RD, Winter EE, Webber C, Brandt P, Nyakatura G, Adetobi M, Chiaromonte F, Elnitski L, Eswara P, Hardison RC, Hou M, Kolbe D, Makova K, Miller W, Nekrutenko A, Riemer C, Schwartz S, Taylor J, Yang S, Zhang Y, Lindpaintner K, Andrews TD, Caccamo M, Clamp M, Clarke L, Curwen V, Durbin R, Eyras E, Searle SM, Cooper GM, Batzoglou S, Brudno M, Sidow A, Stone EA, Venter JC, Payseur BA, Bourque G, Lopez-Otin C, Puente XS, Chakrabarti K, Chatterji S, Dewey C, Pachter L, Bray N, Yap VB, Caspi A, Tesler G, Pevzner PA, Haussler D, Roskin KM, Baertsch R, Clawson H, Furey TS, Hinrichs AS, Karolchik D, Kent WJ, Rosenbloom KR, Trumbower H, Weirauch M, Cooper DN, Stenson PD, Ma B, Brent M, Arumugam M, Shteynberg D, Copley RR, Taylor MS, Riethman H, Mudunuri U, Peterson J, Guyer M, Felsenfeld A, Old S, Mockrin S, and Collins F): Genome sequence of the Brown Norway rat yields insights into mammalian evolution. *Nature* 428:493-521, 2004.

170. Piontkivska H, Zhang Y, Green ED, NISC Comparative Sequencing Program, and Elnitski L: Multi-species sequence comparison reveals dynamic evolution of the elastin gene that has involved purifying selection and lineage-specific insertions/deletions. *BMC Genomics* 5:31, 2004. [PMCID: PMC436053]

171. Jiao Z, Mollaaghababa R, Pavan WJ, Antonellis A, Green ED, and Hornyak TJ: Direct interaction of Sox10 with the promoter of murine *dopachrome tautomerase* (Dct) and synergistic activation of *Dct* expression with Mitf. *Pigment Cell Res* 17:352-362, 2004.

172. Angata T, Margulies EH, Green ED, and Varki A: Large-scale sequencing of the CD33-related Siglec gene cluster in five mammalian species reveals rapid evolution by multiple mechanisms. *Proc Natl Acad Sci USA* 101:13251-13256, 2004. [PMCID: PMC516556]

173. Yoshida A, Hisatome I, Taniguchi S, Sasaki N, Yamamoto Y, Miake J, Fukui H, Shimizu H, Okamura T, Okura T, Igawa O, Shigemasa C, Green ED, Kohn LD, and Suzuki K: Mechanism of iodide/chloride exchange by Pendrin. *Endocrinology* 145:4301-4308, 2004.

174. Wangemann P, Itza EM, Albrecht B, Wu T, Jabba SV, Maganti RJ, Lee JH, Everett LA, Wall SM, Royaux IE, Green ED, and Marcus DC: Loss of KCNJ10 protein expression abolishes endocochlear potential and causes deafness in Pendred syndrome mouse model. *BMC Med* 2:30, 2004. [PMCID: PMC516044]

175. Scherer SW and Green ED: Human chromosome 7 circa 2004: a model for structural and functional studies of the human genome. *Hum Molec Genet* 13:R303-R313, 2004.

176. Mortlock DP, Portnoy ME, Chandler RL, Green ED, and NISC Comparative Sequencing Program: Comparative sequence analysis of the *Gdf6* locus reveals a duplicon-mediated chromosomal rearrangement in rodents and rapidly diverging coding and regulatory sequences. *Genomics* 84:814-823, 2004.

177. The ENCODE Project Consortium: The ENCODE (ENCyclopedia Of DNA Elements) Project. *Science* 306:636-640, 2004.

178. The MGC Project Team (Gerhard DS, Wagner L, Feingold EA, Shenmen CM, Grouse LH, Schuler G, Klein SL, Old S, Rasooly R, Good P, Guyer M, Peck AM, Derge JG, Lipman D, Collins FS, Jang W, Sherry S, Feolo M, Misquitta L, Lee E, Rotmistrovsky K, Greenhut SF, Schaefer CF, Buetow K, Bonner TI, Haussler D, Kent J, Kiekhaus M, Furey T, Brent M, Prange C, Schreiber K, Shapiro N, Bhat NK, Hopkins RF, Hsie F, Driscoll T, Soares MB, Casavant TL, Scheetz TE, Brown-stein MJ, Usdin TB, Toshiyuki S, Carninci P, Piao Y, Dudekula DB, Ko MS, Kawakami K, Suzuki Y, Sugano S, Gruber CE, Smith MR, Simmons B, Moore T, Waterman R, Johnson SL, Ruan Y, Wei CL, Mathavan S, Gunaratne PH, Wu J, Garcia AM, Hulyk SW, Fuh E, Yuan Y, Sneed A, Kowis C, Hodgson A, Muzny DM, McPherson J, Gibbs RA, Fahey J, Helton E, Ketteman M, Madan A, Rodrigues S, Sanchez A, Whiting M, Madari A, Young AC, Wetherby KD, Granite SJ, Kwong PN, Brinkley CP, Pearson RL, Bouffard GG, Blakesly RW, Green ED, Dickson MC, Rodriguez AC, Grimwood J, Schmutz J, Myers RM, Butterfield YS, Griffith M, Griffith OL, Krzywinski MI, Liao N, Morrin R, Palmquist D, Petrescu AS, Skalska U, Smailus DE, Stott JM, Schnerch A, Schein JE, Jones SJ, Holt RA, Baross A, Marra MA, Clifton S, Makowski KA, Bosak S, and Malek J): The status, quality, and expansion of the NIH full-length cDNA project: The Mammalian Gene Collection (MGC). *Genome Res* 14:2121-2127, 2004.

179. Blakesley RW, Hansen NF, Mullikin JC, Thomas PJ, McDowell JC, Maskeri B, Young AC, Benjamin B, Brooks SY, Coleman BI, Gupta J, Ho S-L, Karlins EM, Maduro QL, Stantripop S, Tsurgeon C, Vogt JL, Walker MA, Masiello CA, Guan X, NISC Comparative Sequencing Program, Bouffard GG, and Green ED: An intermediate grade of finished genomic sequence suitable for comparative analyses. *Genome Res* 14:2235-2244, 2004. [PMCID: PMC525681]

180. Wall SM, Kim YH, Stanley L, Glapion DM, Everett LA, Green ED, and Verlander JW: NaCl restriction upregulates renal *Slc26a4* through subcellular redistribution: role in Cl^- conservation. *Hypertension* 44:982-987, 2004.

181. Blanchette M, Green ED, Miller W, and Haussler D: Reconstructing large regions of an ancestral mammalian genome in silico. *Genome Res* 14:2412-2423, 2004. [PMCID: PMC534665]

182. Kellner WA, Sullivan RT, Carlson BH, NISC Comparative Sequencing Program (Green ED, Director), and Thomas JW: Uprobe: a genome-wide universal probe resource for comparative physical mapping in vertebrates. *Genome Res* 15:166-173, 2005.

183. Margulies EH, NISC Comparative Sequencing Program, Maduro VVB, Thomas PJ, Tomkins JP, Amemiya CT, Luo M, and Green ED: Comparative sequencing provides insights about the structure and conservation of marsupial and monotreme genomes. *Proc Natl Acad Sci USA* 102:3354-3359, 2005. [PMCID: PMC549084]

184. Margulies EH, Vinson JP, NISC Comparative Sequencing Program, Miller W, Jaffe DB, Lindblad-Toh K, Chang JL, Green ED, Lander ES, Mullikin JC, and Clamp M: An initial strategy for the systematic identification of functional elements in the human genome by low-redundancy comparative sequencing. *Proc Natl Acad Sci USA* 102:4795-4800, 2005. [PMCID: PMC555705]

185. Lei B, Morris DP, Smith MP, Svetkey LP, Newman MF, Rotter JI, Buchanan TA, Beckstrom-Sternberg SM, Green ED, and Schwinn DA: Novel human α_{1a}-adrenoceptor single nucleotide polymorphisms alter receptor pharmacology and biological function. *Naunyn Schmiedeberg's Arch Pharmacol* 371:229-239, 2005. [PMCID: PMC2367253]

186. Emison ES, McCallion AS, Kashuk CS, Bush RT, Grice E, Lin S, Portnoy ME, Cutler DJ, Green ED, and Chakravarti A: A common sex-dependent mutation in a *RET* enhancer underlies Hirschsprung disease risk. *Nature* 434:857-863, 2005.

187. Curtiss NP, Bonifas JM, Lauchle JO, Balkman JD, Kratz CP, Emerling BM, Green ED, Le Beau MM, and Shannon KM: Isolation and analysis of candidate myeloid tumor suppressor genes from a commonly deleted segment of 7q22. *Genomics* 85:600-607, 2005.

188. Kashuk CS, Stone EA, Grice EA, Portnoy ME, Green ED, Sidow A, Chakravarti A, and McCallion AS: Phenotype-genotype correlation in Hirschsprung disease is illuminated by comparative analysis of the RET protein sequence. *Proc Natl Acad Sci USA* 102:8949-8954, 2005. [PMCID: PMC1157046]

189. Cooper GM, Stone EA, Asimenos G, NISC Comparative Sequencing Program, Green ED, Batzoglou S, and Sidow A: Distribution and intensity of constraint in mammalian genomic sequence. *Genome Res* 15:901-913, 2005. [PMCID: PMC1172034]

190. Schueler MG, Dunn JM, Bird CP, Ross MT, Viggiano L, NISC Comparative Sequencing Program, Rocchi M, Willard HF, and Green ED: Progressive proximal expansion of the primate X chromosome centromere. *Proc Natl Acad Sci USA* 102:10563-10568, 2005. [PMCID: PMC1180780]

191. Portnoy ME, McDermott KJ, Antonellis A, Margulies EH, Prasad AB, NISC Comparative Sequencing Program, Kingsley DM, Green ED, and Mortlock DP: Detection of potential *GDF6* regulatory elements by multispecies sequence comparisons and identification of a skeletal joint enhancer. *Genomics* 86:295-305, 2005.

192. Sivakumar K, Kyriakides T, Puls I, Nicholson GA, Funalot B, Antonellis A, Sambuughin N, Christodoulou K, Beggs JL, Zamba-Papanicolaou E, Ionasescu V, Dalakas MC, Green ED, Fischbeck KH, and Goldfarb LG: Phenotypic spectrum of disorders associated with glycyl-

tRNA synthetase mutations. *Brain* 128:2304-2314, 2005.

193. Portnoy ME and Green ED: Comparative sequencing of vertebrate genomes. In *Encyclopedia of Genetics, Genomics, Proteomics, and Bioinformatics* (LB Jorde, PFR Little, KJ Dunn, and S Subramaniam, eds; John Wiley & Sons Ltd), pp. 1239-1248, 2005.

194. Kim Y-H, Verlander JW, Matthews SW, Kurtz I, Shin W, Weiner ID, Everett LA, Green ED, Nielsen S, and Wall SM: Intercalated cell H^+/OH^- transporter expression is reduced in *Slc26a4* null mice. *Am J Physiol Renal Physiol* 289:F1262-F1272, 2005.

195. Grice EA, Rochelle ES, Green ED, Chakravarti A, and McCallion AS: Evaluation of the *RET* regulatory landscape reveals the biological relevance of a HSCR-implicated enhancer. *Hum Mol Genet* 14:3837-3845, 2005.

196. Riazuddin S, Khan SN, Ahmed ZM, Ghosh M, Caution K, Nazli S, Kabra M, Zafar AU, Chen K, Naz S, Antonellis A, Pavan WJ, Green ED, Wilcox ER, Friedman PL, Morell, RJ, Riazuddin S, and Friedman TB: Mutations in *TRIOBP*, which encodes a putative cytoskeletal-organizing protein, are associated with nonsyndromic recessive deafness. *Am J Hum Genet* 78:137-143, 2006. [PMCID: PMC1380211]

197. Antonellis A, Bennett WR, Menheniott TR, Prasad AB, Lee-Lin S-Q, NISC Comparative Sequencing Program, Green ED, Paisley D, Kelsh RN, Pavan WJ, and Ward A: Deletion of long-range sequences at *Sox10* compromises developmental expression in a mouse model of Waardenburg-Shah (WS4) syndrome. *Hum Molec Genet* 15:259-271, 2006.

198. Lee S, Chen J, Zhou G, Shi RZ, Bouffard GG, Kocherginsky M, Ge X, Sun M, Jayathilaka N, Kim YC, Emmanuel N, Bohlander SK, Minden M, Kline J, Ozer O, Larson RA, LeBeau MM, Green ED, Trent J, Karrison R, Liu PP, Wang SM, and Rowley JD: Gene expression profiles in acute myeloid leukemia with common translocations using SAGE. *Proc Natl Acad Sci USA* 103:1030-1035, 2006. [PMCID: PMC1347995]

199. Elango N, Thomas JW, NISC Comparative Sequencing Program (Green ED, Director), and Yi SV: Variable molecular clocks in hominoids. *Proc Natl Acad Sci USA* 103:1370-1375, 2006.

200. Margulies EH, Chen CW, and Green ED: Differences between pair-wise and multi-sequence alignment methods affect vertebrate genome comparisons. *Trends Genet* 22:187-193, 2006.

201. Caceres M, NISC Comparative Sequencing Program (Green ED, Director), and Thomas JW: The gene of retroviral origin syncytin 1 is specific to hominoids and is inactive in Old World monkeys. *J Hered* 97:100-106, 2006.

202. She X, Liu G, Ventura M, Zhao S, Misceo D, Roberto R, Cardone MF, Rocchi M, NISC Comparative Sequencing Program, Green ED, Archidiacano N, and Eichler EE: A preliminary comparative analysis of primate segmental duplications shows elevated substitution rates and a great-ape expansion of intrachromosomal duplications. *Genome Res* 16:576-583, 2006. [PMCID: PMC1457043]

203. Morin RD, Chang E, Petrescu A, Liao N, Griffith M, Kirkpatrick R, Butterfield YS, Young AC, Stott J, Barber S, Babakaiff R, Dickson MC, Matsuo C, Wong D, Yang GS, Smailus DE, Wetherby KD, Kwong PN, Grimwood J, Brinkley III CP, Brown-John M, Reddix-Dugue ND, Mayo M, Schmutz J, Beland J, Park M, Gibson S, Olson T, Bouffard GG, Tsai M, Featherstone R, Chand S, Siddiqui AS, Jang W, Lee E, Klein SL, Blakesley RW, Zeeberg BR, Narasimhan S, Weinstein JN, Pennacchio CP, Myers RM, Green ED, Wagner L, Gerhard DS, Marra MA, Jones SJM, and Holt RA: Sequencing and analysis of 10,967 full-length cDNA clones from *Xenopus laevis* and *Xenopus tropicalis* reveals post-

tetraploidization transcriptome remodeling. *Genome Res* 16:796-803, 2006. [PMCID: PMC1479861]

204. Verlander JW, Kim YH, Shin W, Pham TD, Hassell KA, Beierwaltes WH, Green ED, Everett L, Matthews SW, and Wall SM: Dietary Cl^- restriction upregulates pendrin expression within the apical plasma membrane of type B intercalated cells. *Am J Physiol Renal Physiol* 291:F833-839, 2006.

205. Antonellis A, Lee-Lin S-Q, Wasterlain A, Leo P, Quezado M, Goldfarb LG, Myung K, Burgess S, Fischbeck KH, and Green ED: Functional analyses of glycyl-tRNA synthetase mutations suggest a key role for tRNA-charging enzymes in peripheral axons. *J Neurosci* 26:10397-10406, 2006.

206. Johnson ME, NISC Comparative Sequencing Program, Cheng Z, Morrison VA, Scherer S, Ventura M, Gibbs RA, Green ED, and Eichler EE: Recurrent duplication-driven transposition of DNA during hominoid evolution. *Proc Natl Acad Sci USA* 103:17626-17631, 2006. [PMCID: PMC1693797]

207. Harold D, Paracchini S, Scerri T, Dennis M, Cope N, Hill G, Moskvina V, Walter J, Richardson AJ, Owen MJ, Stein JF, Green ED, O'Donovan MC, Williams J, and Monaco AP: Further evidence that the *KIAA0319* gene confers susceptibility to developmental dyslexia. *Mol Psychiatry* 11:1086-1091, 2006.

208. Jabba SV, Oelke A, Singh R, Maganti RJ, Fleming S, Wall SM, Everett LA, Green ED, and Wangemann P: Macrophage invasion contributes to degeneration of stria vascularis in Pendred syndrome mouse model. *BMC Med* 4:37, 2006. [PMCID: PMC1796619]

209. Keebaugh AC, Sullivan RT, NISC Comparative Sequencing Program (Green ED, Director), and Thomas JW: Gene duplication and inactivation in the HPRT gene family. *Genomics* 89:134-142, 2007.

210. Nikolaev S, Montoya-Burgos JI, Margulies EH, NISC Comparative Sequencing Program (Green ED, Director), Rougemont J, Nyffeler B, and Antonarakis SE: Early history of mammals is elucidated with the ENCODE multiple species sequencing data. *PLoS Genet* 3:e2, 2007. [PMCID: PMC1761045]

211. Hurle B, Swanson W, NISC Comparative Sequencing Program, and Green ED: Comparative sequence analyses reveal rapid and divergent evolutionary changes of the *WFDC* locus in the primate lineage. *Genome Res* 17:276-286, 2007. [PMCID: PMC1800918]

212. Nakaya K, Harbidge DG, Wangemann P, Schultz BD, Green ED, Wall SM, and Marcus DC: Lack of pendrin HCO_3^- transport elevates vestibular endolymphatic $[Ca^{2+}]$ by inhibition of acid-sensitive TRPV5 and TRPV6 channels. *Am J Physiol Renal Physiol* 292:F1314-1321, 2007. [PMCID: PMC2515270]

213. The ENCODE Project Consortium: Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. *Nature* 447:799-816, 2007. [PMCID: PMC2212820]

214. Margulies EH, Cooper GM, Asimenos G, Thomas DJ, Dewey CN, Siepel A, Birney E, Keefe D, Schwartz AS, Hou M, Taylor J, Nikolaev S, Montoya-Burgos JI, Loytynoja A, Whelen S, Pardi F, Massingham T, Brown JB, Bickel P, Holmes I, Mullikin JC, Ureta-Vidal A, Paten B, Stone EA, Rosenbloom KR, Kent WJ, NISC Comparative Sequencing Program, Bayor College of Medicine Human Genome Sequencing Center, Washington University Genome Sequencing Center, Broad Institute, UCSC Genome Brower Team, British Columbia Cancer Agency

Genome Sciences Center, Antonarakis SE, Batzoglou S, Goldman N, Hardison R, Haussler D, Miller W, Pachter L, Green ED, and Sidow A: Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. *Genome Res* 17:760-774, 2007. [PMCID: PMC1891336]

215. Cretekos CJ, Deng J-M, Green ED, NISC Comparative Sequencing Program, Rasweiler JJ, and Behringer RR: Isolation, genomic structure, and developmental expression of *Fgf8* in the short-tailed fruit bat, *Carollia perspicillata*. *Int J Del Biol* 51:333-338, 2007.

216. Caceres M, NISC Comparative Sequencing Program (Green ED, Director), Sullivan RT, and Thomas JW: A recurrent inversion on the eutherian X chromosome. *Proc Natl Acad Sci USA* 104:18571-18576, 2007. [PMCID: PMC2141818]

217. Kim YH, Pech V, Spencer KB, Beierwaltes WH, Everett LA, Green ED, Shin W, Verlander JW, Sutliff RL, and Wall SM: Reduced ENaC protein abundance contributes to the lower blood pressure observed in pendrin-null mice. *Am J Physiol Renal Physiol* 293: F1314-F1324, 2007.

218. Pontius JU, Mullikin JC, Smith DR,Agencourt Sequencing Team, Lindblad-Toh K, Gnerre S, Clamp M, Chang J, Stephens R, Neelam B, Volfovsky N, Schaffer AA, Agarwala R, Narfstrom K, Murphy WJ, Giger U, Roca AL, Antunes A, Menotti-Raymond M, Yuhki N, Pecon-Slattery J, Johnson WE, Bourque G, Tesler G, NISC Comparative Sequencing Program (Green ED, Director), and O'Brien SJ: Initial sequence and comparative analysis of the cat genome. *Genome Res* 17:1675-1689, 2007. [PMCID: PMC2045150]

219. Zhang W, Bouffard GG, Wallace SS, Bond JP, and NISC Comparative Sequencing Program (Green ED, Director): Estimation of DNA sequence context-dependent mutation rates using primate genomic sequences. *J Mol Evol* 65:207-214, 2007.

220. Nikolaev SI, Montoya-Burgos JI, Popadin K, Parand L, Margulies EH; NISC Comparative Sequencing Program (Green ED, Director), and Antonarakis SE: Life-history traits drive the evolutionary rates of mammalian coding and noncoding genomic elements. *Proc Natl Acad Sci USA* 104:20443-20448, 2007. [PMCID: PMC2154450]

221. Idol JR, Addington AM, Long RT, Rapoport JL, and Green ED: Sequencing and analyzing the *t*(1;7) reciprocal translocation breakpoints associated with a case of childhood-onset schizophrenia/autistic disorder. *J Autism Dev Disord* 38:668-677, 2008.

222. Blanchette M, Banire Diallo A, Green ED, Miller W, and Haussler D: Computational reconstruction of ancestral DNA sequences. In *Methods in Molecular Biology: Phylogenomics* (W Murphy, ed; Humana Press, Inc.), pp. 171-184, 2008.

223. Cretekos CJ, Wang Y, Green ED, NISC Comparative Sequencing Program, Martin JF, Rasweiler IV JJ, and Behringer RR: Regulatory divergence modifies limb length between mammals. *Genes Dev* 22:141-151, 2008. [PMCID: PMC2192750]

224. Hughes I, Binkley J, Hurle B, Green ED, NISC Comparative Sequencing Program, Sidow A, and Ornitz DM: Identification of the Otopetrin Domain, a conserved domain in vertebrate otopetrins and invertebrate otopetrin-like family members. *BMC Evol Biol* 8:41, 2008. [PMCID: PMC2268672]

225. Nakao I, Kanaji S, Ohta S, Matsushita H, Arima K, Yuyama N, Yamaya M, Nakayama K, Kubo H, Watanabe M, Sagara H, Sugiyama K, Tanaka H, Toda S, Hayashi H, Inoue H, Hoshino T, Shiraki A, Inoue M, Suzuki K, Aizawa H, Okinami S, Nagai H, Hasegawa M, Fukuda T, Green ED, and Izuhara K: Identification of pendrin as a common mediator for mucus production in bronchial asthma and chronic obstructive pulmonary disease. *J Immunol* 180:6262-6269, 2008.

226. Elango N, Kim S-H, NISC Comparative Sequencing Program (Green ED, Director), Vigoda E, and Yi SV: Mutations of different molecular origins exhibit contrasting patterns of regional substitution rate variation. *PLoS Comp Biol* 4:e1000015, 2008. [PMCID: PMC2265638]

227. Sullivan RT, Morehouse CB, NISC Comparative Sequencing Program (Green ED, Director), and Thomas JW: Uprobe 2008: an online resource for universal overgo hybridization-based probe retrieval and design. *Nucl Acids Res* 36:W149-W153, 2008. [PMCID: PMC2447791]

228. Grice EA, Kong HH, Renaud G, Young AC, NISC Comparative Sequencing Program (Green ED, Director), Bouffard GG, Blakesley RW, Wolfsberg TG, Turner ML, and Segre JA: A diversity profile of the human skin microbiota. *Genome Res* 18:1043-1050, 2008. [PMCID: PMC2493393]

229. Prasad AB, Allard MW, NISC Comparative Sequencing Program, and Green ED: Confirming the phylogeny of mammals by use of large comparative sequence data sets. *Mol Biol Evol* 25:1795-1808, 2008. [PMCID: PMC2515873]

230. Antonellis A and Green ED: The role of aminoacyl-tRNA synthetases in genetic diseases. *Annu Rev Genomics Hum Genet* 9:87-107, 2009.

231. Antonellis A and Green ED: Inter-species comparative sequence analysis: a tool for genomic medicine. In *Genomic and Personalized Medicine* (HF Willard and GS Ginsburg, eds; Elsevier, Inc.), pp. 120-130, 2008.

232. Antonellis A, Huynh JL, Lee-Lin S-Q, Vinton RM, Renaud G, Loftus SK, Elliot G, Wolfsberg TG, Green ED, McCallion AS, and Pavan WJ: Identification of neural crest and glial enhancers at the mouse *Sox10* locus through transgenesis in zebrafish. *PLoS Genet* 4:e1000174, 2008. [PMCID: PMC2518861]

233. Rahimov F, Marazita ML, Visel A, Cooper ME, Hitchler MJ, Rubini M, Domann FE, Govil M, Christensen K, Bille C, Melbye M, Jugessur A, Lie RT, Wilcox AJ, Fitzpatrick DR, Green ED, NISC Comparative Sequencing Program, Mossey PA, Little J, Steegers-Theunissen RP, Pennacchio LA, Schutte BC, and Murray JC: Disruption of an AP-2α binding site in an *IRF6* enhancer is associated with cleft lip. *Nat Genet* 40:1341-1347, 2008.

234. Tsipouri V, Schueler MG, Hu S , NISC Comparative Sequencing Program, Dutra A, Pak E, Riethman H, and Green ED: Comparative sequence analyses reveal sites of ancestral chromosomal fusions in the Indian muntjac genome. *Genome Biol* 9:R155, 2008.

235. Rudd MK, Endicott RM, Friedman C, Walker M, Young JM, Osoegawa K, NISC Comparative Sequencing Program, de Jong PJ, Green ED, and Trask BJ: Comparative sequence analysis of primate subtelomeres originating from a chromosome fission event. *Genome Res* 19:33-41, 2009. [PMCID: PMC2612970]

236. Loftus SK, Antonellis A, Matera I, Renaud G, Baxter LL, Reid D, Wolfsberg TG, Chen Y, Wang C, NISC Comparative Sequencing Program, Prasad MK, Bessling SL, McCallion AS, Green ED, Bennett DC, and Pavan WJ: *Gpnmb* is a melanoblast-expressed, MITF-dependent gene. *Pigment Cell Melanoma Res* 22:99-110, 2009. [PMCID: PMC2714741]

237. Kurzweil VC, Getman M, NISC Comparative Sequencing Program, Green ED, and Lane RP: Dynamic evolution of V1R putative pheromone receptors between Mus musculus and Mus spretus. *BMC Genomics* 10:74, 2009. [PMCID: PMC2644715]

238. Dennis MY, Paracchini S, Scerri TS, Prokunina-Olsson L, Knight JC, Wade-Martins R, Coggill P, Beck S, Green ED, and Monaco AP: A common variant associated with dyslexia reduces expression of the *KIAA0319* gene. *PLoS Genet* 5:e1000436, 2009. [PMCID: PMC2653637]

239. Church DM, Goodstadt L, Hillier LW, Zody MC, Goldstein S, She X, Bult CJ, Agarwala R, Cherry JL, DiCuccio M, Hlavina W, Kapustin Y, Meric P, Maglott D, Birtle Z, Marques AC, Graves T, Zhou S, Teague B, Potamousis K, Churas C, Place M, Herschleb J, Runnheim R, Forrest D, Amos-Landgraf J, Schwartz DC, Cheng Z, Lindblad-Toh K, Eichler EE, Ponting CP, and The Mouse Genome Sequencing Consortium: Lineage-specific biology revealed by a finished genome assembly of the mouse. *PLoS Biol* 7:e1000112, 2009. [PMCID: PMC2680341]

240. Grice EA, Kong HH, Conlan S, Deming CB, Davis J, Young AC, NISC Comparative Sequencing Program, Bouffard GG, Blakesley RW, Murray PR, Green ED, Turner ML, and Segre JA: Topographical and temporal diversity of the human skin microbiome. *Science* 324:1190-1192, 2009.

241. Scharschmidt TC, List K, Grice EA, Szabo R, NISC Comparative Sequencing Program (Green ED, Director), Renaud G, Lee C-CR, Wolfsberg TG, Bugge TH, and Segre JA: Matriptase-deficient mice exhibit ichthyotic skin with a selective shift of skin microbiota. *J Invest Derm* 129:2435-2442, 2009.

242. Biesecker LG, Mullikin JC, Facio FM, Turner C, Cherukuri PF, Blakesley RW, Bouffard GG, Chines PS, Cruz P, Hansen NF, Teer JK, Maskeri B, Young AC, NISC Comparative Sequencing Program, Manolio TA, Wilson AF, Finkel T, Hwang P, Arai A, Remaley AT, Sachdev V, Shamburek R, Cannon RO, and Green ED: The ClinSeq Project: piloting large-scale genome sequencing for research in genomic medicine. *Genome Res* 19:1665-1674, 2009.

243. Romanov MN, Tuttle EM, Houck ML, Modi WS, Chemnick LG, Korody ML, Stremel Mork EM, Otten CA, Renner T, Jones KC, Dandekar S, Papp JC, Da Y, NISC Comparative Sequencing Program, Green ED, Magrini V, Hickenbotham MT, Glasscock J, McGrath S, Mardis ER, and Ryder OA: The value of avian genomics to the conservation of wildlife. *BMC Genomics* 10:S10, 2009. [PMCID: PMC2709253]

244. Longo MS, Carone DM, NISC Comparative Sequencing Program, Green ED, O'Neill MJ, and O'Neill RJ: Distinct retroelement classes define evolutionary breakpoints demarcating sites of evolutionary novelty. *BMC Genomics* 10:334, 2009. [PMCID: PMC2736999]

245. Zhang Y, Song G, Vinar T, Green ED, Siepel A, and Miller W: Evolutionary history reconstruction for mammalian complex gene clusters. *J Comp Biol* 16:1051-1070, 2009.

246. 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, Kyrpides 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, and Yu J: Prepublication data sharing. *Nature* 461:168-170, 2009.

247. Andres AM, Hubisz MJ, Indap A, Torgerson DG, Degenhardt JD, Boyko AR, Gutenkunst RN, White TJ, Green ED, Bustamante CD, Clark AG, and Nielsen R: Targets of balancing selection in the human genome. *Mol Biol Evol* 26:2755-2764, 2009.

248. MGC Project Team: Temple G, Gerhard DS, Rasooly R, Feingold EA, Good PJ, Robinson C, Mandich A, Derge JG, Lewis J, Shoaf D, Collins FS, Jang W, Wagner L, Shenmen CM, Misquitta L, Schaefer CF, Buetow KH, Bonner TI, Yankie L, Ward M, Phan L, Astashyn A, Brown G, Farrell C, Hart J, Landrum M, Maidak BL, Murphy M, Murphy T, Rajput B, Riddick L, Webb D, Weber J, Wu W, Pruitt KD, Maglott D, Siepel A, Brejova B, Diekhans M, Harte R, Baertsch R, Kent J, Haussler D, Brent M, Langton L, Comstock CL, Stevens M, Wei C, van Baren MJ, Salehi-Ashtiani K, Murray RR, Ghamsari L, Mello E, Lin C, Pennacchio C, Schreiber K, Shapiro N, Marsh A, Pardes E, Moore T, Lebeau A, Muratet M, Simmons B, Kloske D, Sieja S, Hudson J, Sethupathy P, Brownstein M, Bhat N, Lazar J, Jacob H, Gruber CE, Smith MR, McPherson J, Garcia AM, Gunaratne PH, Wu J, Muzny D, Gibbs RA, Young AC, Bouffard GG, Blakesley RW, Mullikin J, Green ED, Dickson MC, Rodriguez AC, Grimwood J, Schmutz J, Myers RM, Hirst M, Zeng T, Tse K, Moksa M, Deng M, Ma K, Mah D, Pang J, Taylor G, Chuah E, Deng A, Fichter K, Go A, Lee S, Wang J, Griffith M, Morin R, Moore RA, Mayo M, Munro S, Wagner S, Jones SJ, Holt RA, Marra MA, Lu S, Yang S, Hartigan J, Graf M, Wagner R, Letovksy S, Pulido JC, Robison K, Esposito D, Hartley J, Wall VE, Hopkins RF, Ohara O, and Wiemann S: The completion of the Mammalian Gene Collection (MGC). *Genome Res* 19:2324-2333, 2009.

249. Genome 10K Community of Scientists: Genome 10K: a proposal to obtain whole-genome sequence for 10,000 vertebrate species. *J Hered* 100:659-674, 2009.

250. Blech-Hermoni YN, Ziegler SG, Hruska KS, Stubblefield BK, Lamarca ME, Portnoy ME, NISC Comparative Sequencing Program, Green ED, and Sidransky E: In silico and functional studies of the regulation of the glucocerebrosidase gene. *Mol Genet Metab*, in press, 2010.

251. Modi WS, Romanov M, Green ED, Ryder O: Molecular cytogenetics of the California Condor: evolutionary and conservation implications. *Cytogenet Genome Res*, in press, 2010.

252. Blakesley RW, Hansen NF, Gupta J, McDowell JC, Maskeri B, Barnabas BB, Brooks SY, Coleman H, Haghighi P, Ho SL, Schandler K, Stantripop S, Vogt JL, Thomas PJ, Comparative Sequencing Program N, Bouffard GG, and Green ED: Effort required to finish shotgun-generated genome sequences differs significantly among vertebrates. *BMC Genomics*, in press, 2010.

253. Prickett TD, Agrawal NS, Wei X, Yates KE, Lin JC, Wunderlich JR, Cronin JC, Cruz P, NISC Comparative Sequencing Program (Green ED, Director), Rosenberg SA, and Samuels Y: Analysis of the tyrosine kinome in melanoma reveals recurrent mutations in *ERBB4*. *Nat Genet*, in press, 2010.

ABSTRACTS:

1. Cooper MH, Green ED, and Massopust LC: The hypoglossal nucleus of the rat: an HRP study. *Anat Record* 196:265, 1980.

2. Green ED, Gruenebaum J, Bielinska M, Baenziger JU, and Boime I: Sulfation of lutropin oligosaccharides using a novel cell-free system. *Fed Proc* 43:2022, 1984.

3. Green ED, Morishima C, Boime I, and Baenziger JU: Structural requirements for sulfation of bovine lutropin (LH) Asn-linked oligosaccharides. *Glycoconjugates: Proceedings of the VIIIth International Symposium*, 38-39, 1985.

4. Green ED, Baenziger JU, and Boime I: Oligosaccharide sulfation: comparative studies of bovine and human pituitary glycoprotein hormones. *Glycoconjugates: Proceedings of the VIIIth International Symposium*, 209-210, 1985.

5. Green ED, Boime I, and Baenziger JU: Differences in the Asn-linked oligosaccharide structures on pituitary LH and FSH: implications for biological function. *Fed Proc* 45:280, 1986.

6. Baenziger JU and Green ED: Structure, synthesis, and function of glycoprotein hormone oligosaccharides. *Glycoconjugates: Proceedings of the IXth International Symposium*, L-2, 1987.

7. Green ED, Brodbeck RM, and Baenziger JU: Structural characterization of oligosaccharides by lectin affinity high-performance liquid chromatography. *FASEB J* 2:A1031, 1988.

8. Adelt G, Green ED, Van Halbeek H, and Baenziger JU: Structural elucidation of the Asn-linked oligosaccharides on bovine fetuin. *FASEB J* 2:A1031, 1988.

9. Green ED, Curtis BR, Issitt PD, Farrar RP, and Chaplin H: Inhibition of an anti-Pr cold agglutinin by citrate. *Blood* 72:264A, 1988.

10. Green ED, Brodbeck RM, and Baenziger JU: Structural characterization of oligosaccharides by lectin affinity high-performance liquid chromatography. *J Cell Biochem* 13A:128, 1989.

11. Coffey AJ, Green ED, Roberts R, Cole CG, Bobrow M, Giannelli FB, and Bentley DR: Attainment of long-range continuity of overlapping YAC clones which span the dystrophin gene. *Am J Hum Genet* 47:A248, 1990.

12. Green ED and Olson MV: Isolation of the intact cystic fibrosis transmembrane conductance regulator (CFTR) gene in yeast artificial-chromosome (YAC) clones. *Am J Hum Genet* 47:A253, 1990.

13. Green ED and Olson MV: Isolation and analysis of large contiguous regions of mammalian chromosomes in yeast artificial chromosomes (YACs). *Am J Hum Genet* 49:10, 1991.

14. Lengauer C, Riethman H, Konecki D, Speicher M, Taniwaki M, Green ED, Olson MV, and Cremer T: Rapid physical mapping of IRS-PCR amplified YAC-clones from human oncogenes by chromosomal in situ suppression (CISS-) hybridization. *Am J Hum Genet* 49:383, 1991.

15. Humbert R, Richter RJ, Sundstrom JA, Wood C, Green E, and Furlong CE: Structure of the human paraoxonase gene. *Am J Hum Genet* 51:A396, 1992.

16. Green ED, Idol JR, Tidwell RM, Braden VV, Ueltzen MS, Wilson AM, Fulton RS, Peluso DC, Leckie MP, and Featherstone T: Towards a complete YAC-based STS-content map of human chromosome 7. *Cytogenet Cell Genet* 65:64-65, 1994.

17. Umbricht CB, Green ED, Griffin CA, Hawkins AL, Grzeschik L-C, O'Connel P, Leach R, Wang-Jabs E, and Kelly TJ: High resolution genomic mapping of the three human Replication Protein A genes. *Cytogenet Cell Genet* 65:67-68, 1994.

18. Kroisel PM, Wagner K, Green ED, Guan X-Y, Meltzer PS, de Jong P, and Rosenkranz W: Analysis of the 7p11→14 region using microdissection libraries. *Cytogenet Cell Genet* 65:69-70, 1994.

19. Lewanda AF, Green ED, Weissenbach J, Taylor EW, Summar M, Phillips III JA, Cohen M, Feingold M, Mouradian W, Clarren SK, and Jabs EW: Refinement of the Saethre-Chotzen syndrome locus between D7S664 and D7S507 which flank a translocation breakpoint in an affected individual. *Am J Hum Genet* 55:A193, 1994.

20. Inglehearn CF, Keen TJ, Green ED, Patel R, Peacock R, Peluso DC, and Bhattacharya SS: A YAC contig encompassing the chromosome 7p locus for autosomal dominant retinitis pigmentosa. *Am J Hum Genet* 55:A260, 1994.

21. Kere J, Hoglund P, Green ED, Haila S, de la Chapelle A, and Holmberg C: Physical mapping of the congenital chloride diarrhea gene region in human chromosome 7. *Am J Hum Genet* 55:A261, 1994.

22. Behrens F, Claussen U, Green ED, Coutelle C, Williamson R, and Huxley C: Analysis of the centromeric region of human chromosome 7. *Am J Hum Genet* 57:A108, 1995.

23. Goodman BK, Green ED, Lewanda AF, Rosengren S, Jabs EW: Molecular cytogenetic analysis of chromosome 7p anomalies and clinical correlations with Saethre-Chotzen syndrome. *Am J Hum Genet* 57:A114, 1995.

24. Johnson EW, Green ED, Rich SS, Orr HT, Gil-Nagel A, Kurth JH, Sabramski JM, Glusker P, Spiegel R, Marchuk DA, Otero E, and Weber JL: A gene for familial cerebral cavernous malformation maps to a 4 cM region of chromosome 7q in several affected families. *Am J Hum Genet* 57:A194, 1995.

25. Frangiskakis JM, Ewart AK, Morris CA, Ensing G, Mervis CB, Bertrand J, Green ED, and Keating MT: WS2 hemizygosity may contribute to the Williams syndrome cognitive profile. *Am J Hum Genet* 57:A239, 1995.

26. Henthorn KS, Keen TJ, Inglehearn CF, Bhattacharya SS, and Green ED: High-resolution physical mapping of the candidate region for an autosomal dominant form of retinitis pigmentosa (RP9) on chromosome 7p14-15. *Am J Hum Genet* 57:A260, 1995.

27. Keen TJ, Patel RJ, Green ED, Peacock RE, Bhattacharya SS, Inglehearn CF: Progress towards the identification of the RP9 autosomal dominant retinitis pigmentosa gene. *Am J Hum Genet* 57:A261, 1995.

28. McGuire RE, Jordan SA, Humphries P, Green ED, and Daiger SP: Genetic and physical mapping of the RP10 region. *Am J Hum Genet* 57:A264, 1995.

29. Kang S, Graham Jr. JM, Abbott M, Schaffer A, Green ED, Rosenberg M, Allen J, Clericuzio C, Grebe T, Haskins-Olney A, and Biesecker LG: Autosomal dominant Pallister-Hall syndrome maps to 7p13. *Am J Hum Genet* 59:A17, 1996.

30. McGuire RE, Green ED, Daiger SP: Possible role for an ADP-ribosylation factor in retinitis pigmentosa: Is ARF5 RP10?. *Am J Hum Genet* 59:A399, 1996.

31. Van Laer L, Van Camp G, Green ED, and Willems PJ: The HOXA cluster and the hnRPA2B1 gene map in a YAC contig from human chromosome 7p14-p15, between D7S1838 and D7S2496. *Am J Hum Genet* 59:A408, 1996.

32. McDowell GA, Touchman J, Anikster Y, Chen D, Isogai T, Green E, and Gahl WA: A high resolution STS and EST map within the cystinosis critical region on human 17p13. *Am J Hum Genet* 61:A239, 1997.

33. McGuire RE, Searby C, Braden VV, Jegathesan A, Marra M, McPherson JD, Ionasescu V, and Green ED: The CMT2D locus on chromosome 7p: refined genetic localization and high-resolution physical mapping. *Am J Hum Genet* 61:A298, 1997.

34. Van Laer L, Van Camp G, van Zuijlen D, Green ED, Verstreken M, Schatteman I, Van den Heyning P, Balemans W, Coucke P, Greinwald JH, Smith RJH, Huizing E, and Willems P: Refinement of the DFNA5 candidate region, construction of a YAC contig, and exclusion of a fetal-cochlear expressed candidate gene. *Am J Hum Genet* 61:A298, 1997.

34. Green ED: Overview of the Human Genome Project. *Teratology* 57:210, 1998.

35. McGuire Ellsworth RE, Washington University Genome Sequencing Center, NIH Intramural Sequencing Center, Braden VV, Jamison DC, and Green ED: Complete genomic sequence of the human and mouse CFTR genes. *Am J Hum Genet* 63:A187, 1998.

36. Meng X, Lu XJ, Li ZH, Green ED, Massa H, Trask BJ, Morris CA, and Keating MT: Molecular characterization of Williams syndrome deletion: an integrated physical, deletion and transcript map. *Am J Hum Genet* 63:A335, 1998.

37. Everett LA, Morsli H, Dietrich NL, Touchman JW, Wu DK, and Green ED: Characterization of the Pendred syndrome gene. *Am J Hum Genet* 63:A360, 1998.

38. Anikster Y, Touchman JW, Orvisky E, Krasnewich D, Green ED, and Gahl WA: A novel carbohydrate-kinase gene on chromosome 17p13, contiguous with *CTNS*, is homozygously deleted in approximately half the patients with nephropathic cystinosis (NC). *Am J Hum Genet* 65:A46, 1999.

39. Basu S, Ashley-Koch A, Wolpert CM, Menold MM, Matsumoto N, Powell CM, Qumsiyeh MB, Cuccaro ML, Ledbetter DH, Green ED, Vance JM, Pericak-Vance MA, and Gilbert JR: Autistic Disorder and chromosome 7: Analysis of an inversion breakpoint in a multiplex family. *Am J Hum Genet* 65:A264, 1999.

40. Sahoo T, Thomas JW, Lee-Lin S-Q, Kuehl PM, Dokken C, Johnson EW, Green ED, and Marchuk DA: Physical and transcript map of CCM1 candidate interval on chromosome 7q. *Am J Hum Genet* 65:A418, 1999.

41. Everett LA, Belyantseva IA, Noben-Trauth K, Cantos R, Chen A, Thakkar SI, Hoogstraten-Miller SL, Kachar B, Wu DK, and Green ED: Targeted disruption of mouse *Pds* provide key insight about the inner-ear defects encountered in Pendred syndrome. *Am J Hum Genet* 67:A19, 2000.

42. Agbuya P, Ashley-Koch A, Wolpert CM, Menold MM, Matsumoto N, Basu S, Greenblatt DM, Powell CM, Cuccaro ML, Ledbetter DH, Green ED, Vance JM, Pericak-Vance MA, and Gilbert JR: Isolation and analysis of Autism candidate genes on 7q. *Am J Hum Genet* 67:A2025, 2000.

43. Lipkin SM, Wang V, Shanmugarajah D, Cheng J, Pam E, Thomas J, Green E, Touchman J, Collins F, and Cohen P: A targeted ablation of the Mlh3 locus. *Am J Hum Genet* 69:A804, 2001.

44. Margulies EH, NISC Comparative Sequencing Program, and Green ED: Computational approaches for performing multi-species comparative sequence analysis: a platform for targeted studies of genome architecture, function, and evolution. *Am J Hum Genet* 71:A203, 2002.

45. Liu G, NISC Comparative Sequencing Program, Green ED, and Eichler EE: Nature and pattern of primate genomic variation. *Am J Hum Genet* 71:A397, 2002.

46. McCallion AS, Portnoy ME, Grice E, Cashuk C, Emison E, Green ED and Chakravarti A: A common mutation in the *RET* gene in all forms of Hirschsprung disease (HSCR). *Am J Hum Genet* 73:195, 2003.

47. Crawford G, Holt I, Tai D, NIH Intramural Sequencing Center, Green E, Wolfsberg T, and Collins F: Generation of a genome-wide library of regulatory sequences through the use of a novel DNAse hypersensitive site cloning procedure. *Am J Hum Genet* 73:208, 2003.

48. Antonellis A, Lee-Lin SQ, Baxter LL, Wolfsberg TG, N.C.S Program, Pavan WJ, and Green ED: Multi-species comparative sequence analysis of the *WS4/CMT1/Sox10* locus. *Am J Hum Genet* 73:350, 2003.

49. Mortlock DP, Chandler RL, McDermott KJ, Portnoy ME, NIH Intramural Sequencing Center, and Green ED: A mammalian chromosomal rearrangement involving a cis-regulatory element of the *Gdf6* gene: implications for duplication-mediated gene evolution and for gene regulatory boundaries. *Am J Hum Genet* 73:430, 2003.

50. Green E and NISC Comparative Sequencing Program: Deciphering human genome function by multi-species sequence comparisons. *Chrom Res* 12:L180, 2004.

51. Zaremba CM, Wiszniewski W, Lewis RA, Margulies EH, Green ED, and Lupski JR: Identification of *ABCA4* regulatory mutations in recessive Stargart families. A*m Soc Hum Genet Annual Meeting*, Abstract 1070, 2005.

52. Hruska KS, LaMarca ME, Ziegler SG, Portnoy ME, NISC Comparative Sequencing Program, Green ED, and Sidransky E: Analysis of conserved regulatory elements in the glucocerebrosidase gene locus. A*m Soc Hum Genet Annual Meeting*, Abstract 1115, 2005.