

Curriculum vitae

Richard M. Myers, Ph.D.

TITLE Director and Faculty Investigator, HudsonAlpha Institute for Biotechnology, Huntsville, Alabama

BIRTHDATE March 24, 1954

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EDUCATION, RESEARCH AND PROFESSIONAL EXPERIENCE

- July 2008-present Director and Faculty Investigator, Hudson Alpha Institute for Biotechnology, Huntsville, AL
- 2002-2008 Stanford W. Ascherman Professor and Chairman, Department of Genetics and Director, Stanford Human Genome Center, Stanford University School of Medicine
- 1996-2002 Professor of Genetics and Director, Stanford Human Genome Center, Stanford University School of Medicine
- 1993 - 1996 Associate Professor of Genetics and Director, Stanford Human Genome Center, Stanford University School of Medicine
- 1990-1993 Associate Professor of Physiology and Biochemistry and Biophysics, and Director, Human Genome Center, University of California, San Francisco
- 1986-1990 Assistant Professor of Physiology and Biochemistry and Biophysics, University of California, San Francisco
- 1982-1985 Postdoctoral Fellow, Department of Biochemistry & Molecular Biology, Harvard University with Dr. Tom Maniatis
- 1977-1982 Graduate Student, Department of Biochemistry, University of California, Berkeley with Dr. Robert Tjian (awarded Ph.D. in Biochemistry, 1982)
- 1972-1977 Undergraduate Student, Department of Biology, University of Alabama, Tuscaloosa; research with Dr. Clifford Hand and Dr. John Hardman (awarded B.S. in Biochemistry, 1977)

RESEARCH INTERESTS

Molecular basis of human inherited diseases and traits, including Huntington disease, Parkinson disease, bipolar disease, atherosclerosis, insulin resistance and cancer; genome analysis, including genome-scale

analysis of *cis*-acting sequences, DNA binding proteins and epigenetic action involved in human gene regulation; genomic basis of vertebrate diversity; human population genetics; large-scale genomic and full-length cDNA sequencing and comparative sequence analysis.

TEACHING

Co-instructor (with Mike Cherry, Arend Sidow and Gavin Sherlock) of Genetics 211 ("Genomics", a course for graduate students), Stanford University School of Medicine, each Winter Quarter, 2002 - 2007.

Co-instructor (with Bob Simoni) of Genetics 106Q, a course in the logic of biological science for undergraduate sophomores at Stanford University, Winter Quarter, 1999 - 2007.

Co-instructor (with Jim Ford, Greg Barsh and other Stanford faculty) and Co-director of Genetics 202 ("Medical Genetics", a course for first year medical students), Stanford University School of Medicine, each Fall Quarter, 2003 - 2007.

Co-instructor (with Andy Fire) of "Stanford Graduate Summer Institute", a "boot-camp" to expose beginning Stanford Graduate Students to areas outside their chosen fields, Summer 2006.

Director: Stanford Genome Training Program, Stanford University School of Medicine, 1995 - present.

Co-director: Genetics and Developmental Biology Training Program, Stanford University School of Medicine, 2002 - present.

Co-instructor of Human Biology 2A (a year-long introductory biology course for undergraduates), Stanford University, 2005 - 2006.

Co-instructor (with Doug Vollrath) of Genetics 222 ("Method and Logic in Experimental Genetics", a course for graduate students), Stanford University School of Medicine, each Winter Quarter, 1995 - 2002; guest lecturer 2003, 2005.

Guest Lecturer: BMI 234 ("Medical Genomics", a course for graduate students and medical students), Stanford University School of Medicine, Winter Quarter, 2002.

Guest Lecturer: HRP (a course in genetic epidemiology), Stanford University, 2001 - 2005.

Guest Lecturer: Biology 2S (an undergraduate course in biology and bioethics), Stanford University, 2001 - 2007.

Guest Lecturer: Genetics 208 ("Human Genetics", a course for graduate and medical students), Stanford University School of Medicine, each Spring Quarter, 1999 - 2003.

Director: Genetics Graduate Program, Stanford University School of Medicine, 1993 - 2001.

Guest Lecturer: Course in Genetic Epidemiology, Cold Spring Harbor Laboratories, 2000, 2002.

Co-instructor (with Bob Simoni, David Siegmund, David Cox and David Botstein) of SME2A, B, C (Science, Mathematics and Engineering), a three-quarter course in the principles of science and mathematics for undergraduate non-science majors at Stanford University, 1996 - 1999.

Organizer of the Genome Seminar Series, a three-quarter series for graduate students and postdoctoral fellows in genome science, as part of the Genome Training Program, 1997 - 2000.

Guest Faculty Instructor, CAM Course for first year graduate students, Stanford University, School of Medicine, 1994 and 1995.

Examiner in Qualifying Exams for 59 graduate students at UCSF and Stanford, 1986 - present.

Member of Dissertation Committees for 67 graduate students at UCSF and Stanford University, 1986 - present.

Co-instructor of Biochemistry 210A and 210B (a course in regulation of biological systems for first year graduate students), Department of Biochemistry & Biophysics, UCSF, seven years (1986-1993).

Co-instructor of Physiology 101 (a course in endocrinology and GI physiology for medical students), Department of Physiology, UCSF, four years (1989-1992).

Co-instructor of Advanced Molecular Cloning Course (a three-week laboratory and lecture course), Cold Spring Harbor Laboratory, four years (1988-1991).

Tutor in the Biochemical Sciences, teaching biochemistry and molecular biology to undergraduates, Harvard University; 1982 - 1985.

Director of a six week laboratory course on DNA cloning techniques, Department of Biology, University of Alabama, 1982.

Teaching Assistant, Department of Biochemistry, University of California, Berkeley, 1979 and 1980.

PROFESSIONAL ACTIVITIES

Present Activities:

Associate Editor: Genome Research (Cold Spring Harbor Laboratory Press). 1995 - present.

Member and Chair: ENCODE Data Analysis Working Group, National Human Genome Research Institute, National Institutes of Health. 2008 - present.

Member and Chair: ENCODE Data Release Working Group, National Human Genome Research Institute, National Institutes of Health. 2007 - present.

Member: Human Genome Reference Consortium, National Human Genome Research Institute, National Institutes of Health. 2007 – present.

Member: Coordinating Committee for Prioritization of Sequencing Targets, National Human Genome Research Institute, National Institutes of Health. 2003 - present.

Member: Stanford Genetics/San Jose Tech Museum Science Education Partnership. 2001 - present.

Member: Biotech Advisory Board, Gunn High School, Palo Alto, 2005 - present.

Past Activities:

Member: Biology and Biotechnology Program Advisory Committee, U.S. Department of Energy. 2001 - 2008.

Member: Scientific Advisory Board, HudsonAlpha Institute for Biotechnology, 2005 – 2008.

Member: Board of Directors, Open Biosystems, Inc. 2007 – 2008.

Member: Scientific Advisory Board, Pharmacogenetics Knowledge Base, Stanford University School of Medicine. 2001- 2008.

Member: Diversity Committee, Stanford University School of Medicine, 2002 - 2008.

Member and Chair: Review Group, Large-scale DNA Sequencing Centers, National Human Genome Research Institute, National Institutes of Health. 2003 - 2006.

- Member and Chair: HapMap Advisory Committee, National Human Genome Research Institute, National Institutes of Health. 2002 - 2006.
- Member: Advisory Council, National Human Genome Research Institute, National Institutes of Health. 2003 - 2006.
- Member: ENCODE Advisory Committee, National Human Genome Research Institute, National Institutes of Health. 2002 - 2004.
- Member and Chair: Industry Liaison Committee, American Society of Human Genetics. 2002 - 2004.
- Member: GRASPP (Genome Resources and Sequencing Prioritization Panel), National Human Genome Research Institute, National Institutes of Health. 2001 - 2003.
- Member: Web Site Committee, American Society of Human Genetics. 2001 - 2003.
- Member: Committee on Functional Genomics, Genetics and Biocomputation, Stanford University School of Medicine, 1999 - 2002.
- Member (and Chair 1999 - 2002): Genome Research Review Committee, National Human Genome Research Institute, National Institutes of Health. 1998 - 2002.
- Member: Ad hoc Study Section, Sequencing of additional Drosophila Genomes, National Human Genome Research Institute, National Institutes of Health. 2001.
- Member: Board of Directors, American Society of Human Genetics. 1997 - 2001.
- Member: Safety Committee, Stanford University, 1996 - 2000.
- Member: Ad hoc Study Section, Sequencing of the Rat Genome, National Human Genome Research Institute, National Institutes of Health. 2000.
- Member: Intellectual Property Rights Committee, The Human Genome Organization. 1996 - 2000.
- Editorial Board Member: Human Molecular Genetics (Oxford University Press). 1992 - 2000.
- Member: Special Dean's Review Committee, Department of Genetics, Duke University School of Medicine. 2000.
- Member: Study Section, National Human Genome Research Institute, National Institutes of Health. 1994 - 1998.
- Member: Mouse Genomics and Genetics Subgroup, Preclinical Models for Cancer Working Group, National Cancer Institute. 1997 - 1998.
- Member: Committee on Stanford University School of Medicine/UCSF Academic Priorities and Strategies for Collaboration, Stanford University, 1996 - 1999.
- Member (and Chair, 1995-1996): Program Committee, American Society of Human Genetics, 1993 - 1996.
- Co-organizer (with Dr. C. Robertson): Biotechnology Training Grant Symposium, Stanford University, 1995.
- Member: Advisory Board, Program in Molecular and Genetic Medicine, Stanford University School of Medicine, 1995 - 1999.
- Member: Radioisotope Committee, Stanford University School of Medicine, 1994 - 1999.
- Co-organizer (with Dr. G. Barsh), Genetics Seminar Series, 1995.
- Member: Initial Review Group, National Institutes of Health. Four site visits, 1990 - present.

Member: GESTEC Review Committees, National Center for Human Genome Research (Washington University GESTEC; Whitehead Institute GESTEC): 1994 - 1996.

Member: Board of Scientific Counselors, National Center for Human Genome Research Intramural Research Program. 1994 - 1996.

Member: Scientific Advisory Board, Neurogenetics Center, Duke University School of Medicine, Research Triangle Park, NC, 1994 - 1995.

Ad hoc Council member, National Center for Human Genome Research, National Institutes of Health, 1993 and 1995.

Associate Editor: PCR: Methods and Applications (Cold Spring Harbor Laboratory Press). 1991 - 1995.

Meeting Co-Organizer: Genome Mapping and Sequencing Meeting, Cold Spring Harbor Laboratory, three years (1992 - 1994).

Meeting Organizer: Human Chromosome 4 Workshop, Stanford University, 1993.

Member of 38 University committees, UCSF. 1986 - 1993.

Co-organizer and Session Chair, "Winding Your Way Through DNA", a joint UCSF-Exploratorium Symposium for the public on understanding the scientific and societal impact of the recombinant DNA revolution. 1992.

AWARDS AND FELLOWSHIPS

Honorary Doctorate in Humane Letters, December 2005 (University of Alabama).

Blount Initiative Award, October 2003 (University of Alabama).

Pritzker Foundation Award, April 2002 (University of Michigan).

Darden Lecture Award, March 2002 (University of Alabama).

Wills Foundation Award, 1986 - 2003 (at UCSF/Stanford).

Searle Scholar, 1987 - 1990 (at UCSF).

Basil O'Connor Starter Scholar Research Award, 1988 (at UCSF).

Leukemia Society of America Senior Postdoctoral Fellowship, 1984 - 1985 (at Harvard).

Damon Runyon-Walter Winchell Cancer Fund Fellowship, 1982 - 1984 (at Harvard).

Honor Students' Society, 1980 - 1981 (at UCB).

Regents Fellowship, 1979 - 1980 (at UCB).

Abraham Rosenberg and Kaiser Fellowships, 1977 - 1978 (at UCB).

Phi Beta Kappa, 1975 (at UA).

PATENTS

U. S. Patent Number 4,946,773, August 7, 1990, "Detection of base pair mismatches using RNAase A", Thomas P. Maniatis and Richard M. Myers.

U. S. Patent, allowed March 2002, "Mutations in the cystatin B gene in Progressive Myoclonus Epilepsy", Richard M. Myers, David R. Cox, Len A. Pennacchio, Anna-Elina Lehesjoki and Albert de la Chapelle.

EDUCATIONAL, COMMUNITY SERVICE AND OTHER ACTIVITIES

Coach: Palo Alto YMCA Boys' Basketball team, 1996 - 2001.

Coach: Palo Alto YMCA Girls' Basketball team, 2000 - 2003.

Coach: Palo Alto YBAL Boys' Baseball team, kindergarten through grade 1, 1995 - 1996.

Coach and organizer: Palo Alto Boys' Baseball league, grade 2 through grade 8, 1997 - 2003.

Presented science lessons and laboratory tours for Bay Area primary, middle and high schools, each year 1995 – 2008.

Volunteer: L. M. Nixon Elementary School, Palo Alto, 1995 - 2005.

Volunteer: Terman Middle School, Palo Alto, 2005 – 2008.

Workshop Presenter: Sally Ride Science Festivals, Stanford University, October, 2003 - 2006.

Member: Biotech Advisory Board, Gunn High School Biotechnology Program, Palo Alto, 2005 – 2008.

Member: Stanford Genetics/San Jose Tech Museum Science Education Partnership. 2001 – present (see <http://genetics.stanford.edu/techmuseum/>).

REFEREED PUBLICATIONS

1. Hand, C. W. and Myers, R. M. (1976). Arrhenius parameters for the reaction of oxygen atoms with dicyanoacetylene. *J. Physical Chemistry* **80**: 557-558.
2. Hodo, H. G., Murphy, J., Hardman, J. K. and Myers, R. M. (1977). Substrate interactions with the alpha-subunit of the *Escherichia coli* tryptophan synthase. *Arch. Biochem. Biophys.* **181**: 419-427.
3. Rio, D., Robbins, A., Myers, R. and Tjian, R. (1980). Regulation of simian virus 40 early transcription *in vitro* by a purified tumor antigen. *Proc. Natl. Acad. Sci. USA* **77**: 5706-5710.
4. Myers, R. M. and Tjian, R. (1980). Construction and analysis of simian virus 40 origins defective in tumor antigen binding and DNA replication. *Proc. Natl. Acad. Sci. USA* **77**: 6491-6495.
5. Myers, R. M., Rio, D. C., Robbins, A. K., and Tjian, R. (1981). SV40 gene expression is modulated by the cooperative binding of T antigen to DNA. *Cell* **25**: 373-384.
6. Myers, R. M., Kligman, M. and Tjian, R. (1981). Does simian virus 40 T antigen unwind DNA? *J. Biol. Chem.* **256**: 10156-10160.
7. Myers, R. M., Williams, R. C. and Tjian, R. (1981). Oligomeric structure of a simian virus 40 T antigen in free form and bound to DNA. *J. Mol. Biol.* **148**: 347-353.
8. Brock, P. W., Myers, R., Baker, D. C. and Hardman, J. K. (1983). Photoaffinity labeling of the indole sites on the *Escherichia coli* tryptophan synthase a-subunit. *Arch. Biochem. Biophys.* **220**: 435-443.

9. Fisher, E. F., Feist, P. L., Beaucage, S. L., Myers, R. M., Tjian, R. and Caruthers, M. H. (1984). Interaction of AD2+D2 protein and simian virus 40 large T antigen with the large tumor antigen binding site I. *Biochemistry* **23**: 5938-5944.
10. Jones, K. A., Myers, R. M., and Tjian, R. (1984). Mutational analysis of simian virus 40 large T antigen binding sites. *EMBO J.* **3**: 3247-3255.
11. Myers, R. M., Lumelsky, N., Lerman, L. S. and Maniatis, T. (1985). Detection of single base substitutions in total genomic DNA. *Nature* **313**: 495-498.
12. Myers, R. M., Fischer, S. G., Maniatis, T. and Lerman, L.S. (1985). Modification of the melting properties of duplex DNA by attachment of a GC-rich DNA sequence as determined by denaturing gradient gel electrophoresis. *Nucleic Acids Res.* **13**: 3111-3130.
13. Myers, R. M., Fischer, S. G., Lerman, L. S. and Maniatis, T. (1985). Nearly all single base substitutions in DNA fragments joined to a GC-clamp can be detected by denaturing gradient gel electrophoresis. *Nucleic Acids Res.* **13**: 3131-3146.
14. Myers, R. M., Lerman, L. S. and Maniatis, T. (1985). A general method for saturation mutagenesis of cloned DNA fragments. *Science* **229**: 242-247.
15. Myers, R. M., Larin, Z. and Maniatis, T. (1985). Detection of single base substitutions by ribonuclease cleavage of mismatches in RNA:DNA duplexes. *Science* **230**: 1242-1246.
16. Myers, R. M., Tilly, K. and Maniatis, T. (1986). Fine structure genetic analysis of a beta-globin promoter. *Science* **232**: 613-618.
17. Milton, D. L., Napier, M. L., Myers, R. M. and Hardman, J. K. (1986). *In vitro* mutagenesis and overexpression of the *E. coli trpA* gene and the partial characterization of the resultant tryptophan synthase mutant alpha-subunits. *J. Biol. Chem.* **261**: 16604-16615.
18. Collins, M. and Myers, R. M. (1987). Alterations in DNA helix stability due to base modifications can be evaluated using denaturing gradient gel electrophoresis. *J. Mol. Biol.* **198**: 737-744.
19. Cowie, A. and Myers, R. M. (1988). DNA sequences involved in transcriptional regulation of the mouse beta-globin promoter in murine erythroleukemia cells. *Molec. Cell. Biol.* **8**: 3122-3128.
20. Cox, D. R., Pritchard, C. A., Uglum, E., Casher, D., Kobori, J., and Myers, R. M. (1989). Segregation of the Huntington disease region of human chromosome 4 in a somatic cell hybrid. *Genomics* **4**: 397-407.
21. Sheffield, V. C., Cox, D. R., Lerman, L. S. and Myers, R. M. (1989). Attachment of a 40-base-pair G+C-rich sequence (GC-clamp) to genomic DNA fragments by the polymerase chain reaction results in improved detection of single-base changes. *Proc. Natl. Acad. Sci. USA* **86**: 232-236.
22. Pritchard, C. A., Casher, D., Uglum, E., Cox, D. R., and Myers, R. M. (1989). Isolation and field-inversion gel electrophoresis analysis of DNA markers located close to the Huntington disease gene. *Genomics* **4**: 408-418.
23. Yost, C. S., Lopez, C. D., Prusiner, S. B., Myers, R. M. and Lingappa, V. R. (1990). Non-hydrophobic extracytoplasmic determinant of stop transfer in the prion protein. *Nature* **343**: 669-672.
24. Stuvé, L. L. and Myers, R. M. (1990). A directly repeated sequence in the beta-globin promoter regulates transcription in murine erythroleukemia cells. *Molec. Cell Biol.* **10**: 972-981.
25. Lopez, C. D., Yost, C. S., Prusiner, S. B., Myers, R. M. and Lingappa, V. R. (1990). Unusual topogenic sequence directs prion protein biogenesis. *Science* **248**: 226-229.

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26. Brodsky, M. H., Warton, M., Myers, R. M. and Littman, D. R. (1990). Analysis of the site in CD4 that binds to the HIV envelope glycoprotein. *J. Immunol.* **144**: 3078-3086.
 27. Pritchard, C. A., Casher, D., Bull, L., Cox, D. R. and Myers, R. M. (1990). A cloned DNA segment from the telomeric region of human chromosome 4p is not detectably rearranged in Huntington disease patients. *Proc. Natl. Acad. Sci. USA.* **87**: 7309-7313.
 28. Cox, D. R., Burmeister, M., Price, E. R., Kim, S. and Myers, R. M. (1990). Radiation hybrid mapping: A somatic cell genetic method for constructing high-resolution maps of mammalian chromosomes. *Science* **250**: 245-250.
 29. Duyk, G. M., Kim, S., Myers, R. M. and Cox, D. R. (1990). Exon trapping: A genetic screen to identify transcribed sequences in cloned mammalian genomic DNA. *Proc. Natl. Acad. Sci. USA.* **87**: 8995-8999.
 30. Burmeister, M., Cox, D. R. and Myers, R. M. (1990). Dinucleotide repeat polymorphism located at D21S120. *Nucleic Acids Res.* **18**: 4969.
 31. deLange, T., Shiue, L., Myers, R. M., Cox, D. R., Naylor, S. L., Killery, A. M. and Varmus, H. E. (1990). Structure and variability of human chromosome ends. *Molec. Cell Biol.* **10**: 518-527.
 32. Burmeister, M., Cox, D. R. and Myers, R. M. (1991). TaqI RFLP at D21S137. *Nucleic Acids Res.* **19**: 4020.
 33. Burmeister, M., diSibio, G., Cox, D. R. and Myers, R. M. (1991). Identification of polymorphisms by genomic denaturing gradient gel electrophoresis: application to the proximal region of human chromosome 21. *Nucleic Acids Res.* **19**: 1475-1481.
 34. Burmeister, M., Kim, S., Price, E. P., de Lange, T., Tantravahi, U., Myers, R. M. and Cox, D. R. (1991). A map of the distal region of the long arm of human chromosome 21 constructed by radiation hybrid mapping and pulsed-field gel electrophoresis. *Genomics* **9**: 19-30.
 35. Gaensler, K. M. L., Burmeister, M., Brownstein, B. H., Taillon-Miller, P. and Myers, R. M. (1991). Physical mapping of yeast artificial chromosomes containing sequences from the human beta-globin gene region. *Genomics* **10**: 976-984.
 36. Maricq, A. V., Peterson, A. S., Brake, A. J., Myers, R. M. and Julius, D. (1991). Primary structure and functional expression of a serotonin-gated ion channel. *Science* **254**: 432-437.
 37. Pritchard, C., Cox, D. R. and Myers, R. M. (1991). Dinucleotide repeat polymorphism located at D4S169. *Nucleic Acids Res.* **19**: 6347.
 38. Richard, C. W., Withers, D. A., Meeker, T. C., Maurer, S., Evans, G., Myers, R. M. and Cox, D. R. (1991). A radiation hybrid map of the proximal long arm of human chromosome 11 containing the MEN-1 and bcl-1 disease gene loci. *Amer. J. Hum. Genet.* **49**: 1189-1196.
 39. Dugaiczky, A., Goold, R., diSibio, G., and Myers, R. M. (1992). Improved sequencing of cosmids using new primers and linearized DNA. *Nucleic Acids Res.* **20**: 6421-6422.
 40. Frazer, K. A., Boehnke, M., Budarf, M. L., Wolff, R. K., Emanuel, B. S., Myers, R. M., and Cox, D. R. (1992). A radiation hybrid map of the region on human chromosome 22 containing the neurofibromatosis type 2 locus. *Genomics* **14**: 574-584.
 41. Law, A., Richard, C. W., Cottingham, R. W., Lathrop, G. M., Cox, D. R. and Myers, R. M. (1992). Genetic linkage analysis of bipolar affective disorder in an Old Order Amish pedigree. *Hum. Genet.* **88**: 562-568.
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42. Pritchard, C., Zhu, N., Zuo, J., Bull, L., Pericak-Vance, M. A., Vance, J. M., Roses, A. D., Milatovich, A., Francke, U., Cox, D. R. and Myers, R. M. (1992). Recombination of 4p16 DNA markers in an unusual family with Huntington disease. *Amer. J. Hum. Genet.* **50**: 1218-1230.
43. Rajpara, S. M., Garcia, P. D., Roberts, R., Eliassen, J. C., Owens, D. F., Maltby, D., Myers, R. M. and Mayeri, E. (1992). Identification and molecular cloning of a neuropeptide Y homolog that produces prolonged inhibition in *Aplysia* neurons. *Neuron* **9**: 505-513.
44. Sheffield, V. C., Beck, J. S., Stone, E. M. and Myers, R. M. (1992). A simple and efficient method for attachment of a 40-base pair, GC-rich sequence to PCR-amplified DNA. *BioTechniques* **12**: 386-387.
45. Zuo, J., Robbins, C., Taillon-Miller, P., Cox, D. R. and Myers, R. M. (1992). Cloning of the Huntington disease region in yeast artificial chromosomes. *Hum. Molec. Genet.* **1** (3): 149-159.
46. Hartzog, G. and Myers, R. M. (1993). Discrimination among potential activators of the beta-globin CACCC element by correlation of binding and transcriptional properties. *Molec. Cell. Biol.* **13**: 44-56.
47. Bull, L. N., Hewitt, J. E., Cox, D. R. and Myers, R. M. (1993). Sensitivity of *HincII* to CpG methylation. *Nucleic Acids Res.* **21**: 2021.
48. Stuvé, L. L. and Myers, R. M. (1993). Identification and characterization of a beta-globin promoter-binding factor from murine erythroleukemia cells. *Molec. Cell. Biol.* **13**: 4311-4322.
49. Zuo, J., Robbins, C., Baharloo, S., Cox, D. R., and Myers, R. M. (1993). Construction of cosmid contigs and high-resolution restriction mapping of the Huntington disease region of chromosome 4. *Hum. Molec. Genet.* **2**: 889-899.
50. Goold, R. D., diSibio, G. L., Xu, H., Lang, D. B., Dadgar, J., Magrane, G. G., Dugaiczyk, A., Smith, K. A., Cox, D. R., Masters, S.B. and Myers, R. M. (1993). The development of sequence-tagged sites for human chromosome 4. *Hum. Molec. Genet.* **2**: 1271-1288.
51. Richard III, C. W., Boehnke, M. Berg, D. J. Lichy, J. J., Meeker, T. C., Hauser, E., Myers, R. M. and Cox, D. R. (1993). A radiation hybrid map of the distal short arm of human chromosome 11, containing the Beckwith-Weidemann and associated embryonal tumor disease loci. *Am. J. Hum. Genet.* **52**: 915-921.
52. Garcia, P. D. and Myers, R. M. (1994). Pituitary cell line GH3 expresses two somatostatin receptor subtypes that inhibit adenylyl cyclase: Molecular cloning and functional expression in HEK 293 cells of rat somatostatin receptor subtypes SSTR1 and SSTR2. *Molec. Pharmacol.* **45**: 402-409.
53. Fan, J.-B., DeYoung, J., Lagacé, R., Lina, R. A., Xu, Z., Murray, J. C., Buetow, K. H., Weissenbach, J., Goold, R. D., Cox, D. R. and Myers, R. M. (1994). Isolation of yeast artificial chromosome clones from 54 polymorphic loci mapped with high odds on human chromosome 4. *Hum. Molec. Genet.* **3**: 243-246.
54. John, R. M., Robbins, C. A. and Myers, R. M. (1994). Identification of genes within CpG-enriched DNA from human chromosome 4p16.3. *Hum. Molec. Genet.* **3**: 1611-1616.
55. Patil, N., Peterson, A., Rothman, A., de Jong, P. J., Myers, R. M. and Cox, D. R. (1994). A high resolution physical map of 2.5 Mbp of the Down Syndrome region on human chromosome 21. *Hum. Molec. Genet.* **3**: 1811-1817.
56. Peterson, A., Patil, N., Robbins, C., Wang, L., Cox, D. R. and Myers, R. M. (1994). A transcript map of the Down Syndrome critical region on human chromosome 21. *Hum. Molec. Genet.* **3**: 1735-1742.
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57. Jou, Y.-S., Goold, R. D. and Myers, R. M. (1994). Localization of the beta-2-macroglobulin receptor-associated protein 1 gene (LRPAP1) and other gene fragments to human chromosome 4p16.3 by direct cDNA selection. *Genomics* **24**: 410-413.
58. Jou, Y.-S. and Myers, R. M. (1995). Evidence from antibody studies that the CAG-repeat in the Huntington disease gene is expressed in the protein. *Hum. Mol. Genet.* **4**: 465-469.
59. Patil, N., Cox, D. R., Bhat, D., Faham, M., Myers, R. M. and Peterson, A. S. (1995). A potassium channel mutation in weaver mice implicates membrane excitability in granule cell differentiation. *Nature Genet.* **11**: 126-129.
60. Stone, N.E., Fan, J.B., Willour, V., Pennacchio, L.A., Warrington, J., Hu, A., de la Chapelle, A., Lehesjoki, A.E., Cox, D.R. and Myers, R.M. (1996). Construction of a 750 kb bacterial clone contig and restriction map in the region of human chromosome 21 containing the Progressive Myoclonus Epilepsy (EPM1) gene. *Genome Res.* **6**: 218-225.
61. Burke, J., R., Enghild, J. J., Martin, M. E., Jou, Y.-S., Myers, R. M., Roses, A. D., Vance, J. M. and Strittmatter, W. J. (1996). Huntingtin and DRPLA proteins selectively interact with the enzyme GAPDH. *Nature Med.* **2**: 347-350.
62. Pennacchio, L. A., Lehesjoki, A-E., Stone, N. E., Willour, V. L., Virtaneva, K., Miao, J., D'Amato, E., Ramirez, L., Faham, M., Koskiniemi, M., Warrington, J., Norio, R., de la Chapelle, A., Cox, D.R. and Myers, R. M. (1996). Mutations in the gene encoding cystatin B in Progressive Myoclonus Epilepsy (EPM1). *Science* **271**: 1731-1734.
63. Johnson, R. L., Rothman, A. L., Xie, J., Goodrich, L. V., Bare, J. W., Bonifas, J. M., Quinn, A. G., Myers, R. M., Cox, D. R., Epstein, E. H. and Scott, M. P. (1996). Human homolog of *patched*, a candidate gene for the basal cell nevus syndrome. *Science* **272**: 1668-1671.
64. Mastrianni, J. A., Iannicola, C., Myers, R. M., DeArmond, S. and Prusiner, S. B. (1996). Mutation of the prion protein gene at codon 208 in familial Creutzfeldt-Jakob disease. *Neurology.* **47**: 1305-1312.
65. Virtaneva, K., Miao, J., Traskelin, A.-L., Stone, N., Warrington, J., Weissenbach, J., Myers, R. M., Cox, D.R., Sistonen, P., de la Chapelle and Lehesjoki, A-E. (1996). Progressive myoclonus epilepsy EPM1 locus maps to a 175 kb interval in distal 21q. *Am. J. Hum. Genet.* **58**: 1247-1253.
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Biographical Description (Dr. Richard Myers):

My laboratory studies the human genome, with interests in understanding how allelic variation and gene expression changes contribute to understanding a wide range of human traits, including diseases, behaviors and other phenotypes. We use high-throughput genomic methods, including DNA sequencing, genotyping, chromatin immunoprecipitation, mRNA expression profiling, transcriptional promoter and methylation measurements, and computational and statistical tools to identify, characterize and understand the functional elements encoded in our genomes. We recently started projects to sequence individual genomes with next generation sequencing technologies.

Detailed Description:

In July 2008, I moved my laboratory and Genome Center from Stanford University to Huntsville Alabama to become the Director of a new enterprise called the HudsonAlpha Institute for

Biotechnology. This non-profit research institute, located in Cummings Research Park next to NASA headquarters and home to several hundred engineering, computer and biotechnology companies, is dedicated to using genomics and genetics to make and apply discoveries for solving important problems in human health, energy and environmental science. At HudsonAlpha Institute, we are continuing work that my laboratory started at Stanford, while recruiting new Faculty Investigators to work collaboratively on a wide range of problems.

In the human genetics work in my laboratory, we have mostly studied brain and cardiovascular phenotypes, including Huntington disease, Parkinson disease, bipolar disease, insulin resistance and atherosclerosis, as well as cancer and population genetics. These studies involve identifying DNA sequence differences between affected and unaffected individuals in an effort to understand the genetic basis of the disease. We are part of the Pritzker Consortium, a collaboration between six laboratories around the U.S., where we study mood disorders not only with genetic approaches, but also by assessing gene expression patterns in brains of people with the disease compared to individuals who are not affected. Recently, we expanded our interests in genetics to study cancer, autoimmune disease, and human population variation. We are part of The Cancer Genome Atlas (TCGA) Project, where we are using genome-wide SNP genotyping to measure structural genomic variation associated with a variety of tumors. We used similar genotyping approaches to measure genetic diversity in human populations, including 51 populations from around that world that were collected by the Human Genome Diversity Project, and are applying these methods to additional populations. At HudsonAlpha, we are expanding our cancer projects to provide a comprehensive genomic comparison of tumors compared to non-tumor tissues in a variety of cancers. These experiments not only include copy number variation, but genome-wide DNA methylation, mRNA and microRNA profiling, DNA sequencing for mutations, and epigenetic modifications. We have also begun to apply this type of comprehensive genomic analysis to autoimmune disease, including lupus (with Dr. Robert Kimberly and colleagues at the University of Alabama in Birmingham) and rheumatoid arthritis (with Dr. Sara Marsal at Vall d'Hebron Hospital in Barcelona, Spain).

Our sequencing group at the Stanford Human Genome Center was established in 1990 as one of the first genome centers of the Human Genome Project. We collaborated with the Joint Genome Institute in Walnut Creek, California during the International Human Genome Sequencing Consortium's effort to sequence the human genome. Our groups, funded by the U.S. Department of Energy, contributed 11% of the sequence (human chromosomes 5, 16 and 19). We have continued to work with the JGI and have sequenced the genomes of more than 40 organisms, mostly concerned with bioenergy, agricultural and environmental problems. We are also engaged in other sequencing projects, including sequencing full-length cDNAs for the Mammalian Gene Collection, projects with David Kingsley's lab at Stanford to use stickleback fish to study vertebrate diversity, and a variety of positional cloning projects. DNA sequencing with new "next generation" technologies is a major focus of our group's efforts at HudsonAlpha, where we are applying it to a large number of genetic and functional genomic problems.

Another major interest of our group is functional genomics. We use high-throughput methods, including chromatin immunoprecipitation (ChIP), mRNA expression profiling, transcriptional promoter and methylation measurements, and computational and statistical tools to study human biology. We are part of the ENCODE Consortium, which has the goal of identifying and understanding all the functional elements in the human genome. With Dr. Barbara Wold and her lab at Caltech, we developed ChIP-seq, a method that uses ultra-high throughput sequencing to identify comprehensively sites in the genome bound by transcription factors in living cells. We also developed a similar approach, called Methyl-seq, to measure the methylation status at almost every CpG island in the human genome. We continue to collaborate with Dr. Wold's lab not only to participate in the ENCODE Project, but also to use these methods, including a new sequencing-based approach to measure mRNA and microRNA levels, to study transcription control in humans. Among our interests are particular transcription factors and networks of

factors involved in interesting human biological problems, including responses to hormones such as glucocorticoids, the stress response, neuronal development, and human language.

In addition to my research, I participate in a wide variety of teaching, educational outreach, and institutional and national service activities. At UCSF and Stanford, I taught in several courses in genetics and genomics to undergraduate, medical and graduate students. I also have a special interest in teaching science to non-science majors. I helped established a partnership between the Department of Genetics and the San Jose Tech Museum (“Stanford at the Tech”, see <http://genetics.stanford.edu/techmuseum/>), which helps to develop scientific exhibits as well as providing a venue for training graduate students in the art of teaching to the public. In addition, I am involved in a variety of teaching activities for local schools, from the primary level through the junior college level, as well as for a number of laygroups; these include lectures, organized tours of our laboratory, laboratory exercises, and curriculum development. I am particularly interested in increasing and nurturing diversity in the scientific community, and I am active in several programs involved with under-represented groups at the graduate school level and earlier. I am continuing these activities at the HudsonAlpha Institute, where we have a dedicated effort to teaching, education outreach and service to the community (see <http://www.hudsonalpha.org/pages/edu-goals.html>).

I serve on a variety of advisory panels and editorial boards, including several panels for the National Human Genome Research Institute and the U.S. Department of Energy. I am an Associate Editor of Genome Research and participate in grant reviews for the NIH, DOE and other agencies.