

Curriculum vitae

Richard M. Myers, Ph.D.

Updated September 15, 2016

Title Faculty Investigator, Director and President, HudsonAlpha Institute for Biotechnology, Huntsville, Alabama

Adjunct Professor, Department of Genetics, University of Alabama at Birmingham School of Medicine

Contact Information

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Personal Information

Born: March 24, 1954

Education, Research and Professional Experience

2008-present	Faculty Investigator, Director and President, HudsonAlpha Institute for Biotechnology, Huntsville, Alabama
	Adjunct Faculty Member, Department of Genetics, University of Alabama at Birmingham Medical Center
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

Genomic and genetic analysis of human traits and diseases, including childhood genetic disorders, cancer, Huntington disease, Parkinson disease, psychiatric disorders, amyotrophic lateral sclerosis, autoimmune diseases; genome-scale analysis of *cis*-acting regulatory sequences, DNA binding proteins and epigenetic action involved in human gene regulation; genetics and genomics of differential responses to drugs and environmental agents.

Professional Activities

Current Activities

Member: Scientific Advisory Board, Canada Genomics Enterprise. 2016 – present.

Member and Chair: Search Committee for the Department of Energy Joint Genome Institute Director. 2016 - present.

Member: HeLa Genome Data Access Working Group, National Institutes of Health and the Henrietta Lacks family. 2013 - present.

Member: Scientific Advisory Board, Decheng Capital. 2015 - present.

Member: Review Committee for grant applications for the Salk-Stanford Center of Excellence in Stem Cell Genomics (CESCG). 2015 - present.

Member: Scientific Advisory Board, DNAnexus, Inc. 2009 - present.

Member: Scientific Advisory Board, Bay City Capital, San Francisco. 2008 - present.

Member: Research Advisory Board, Auburn University. 2010 - present.

Member: Biotechnology Association of Alabama. 2009 - present.

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

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

Past Activities

Member and Chair: Ad hoc Study Section, National Human Genome Research Institute, National Institutes of Health. 2016.

Member: Board of Directors, Leadership Alabama. 2010 - 2016.

Member: Scientific Advisory Committee, Department of Energy, Joint Genome Institute, Walnut Creek, CA, 2011 - 2015.

Member: Scientific Advisory Board, Biogen Idec, Inc. 2011 - 2015.

Member: Scientific Advisory Board, New York Genome Center, New York City, 2010 - 2015.

Member: External Advisory Panel, Pharmacogenomics Research Network. National Institutes of Health. 2011 - 2014.

Member and Chair: Ad hoc Study Section, National Human Genome Research Institute, National Institutes of Health. 2014 (two sessions) and 2015.

Member: Intramural Research Program Blue Ribbon Advisory Panel. National Human Genome Research Institute, National Institutes of Health. 2011 - 2013.

Member: Coordinating Committee for Prioritization of Sequencing Targets, National Human Genome Research Institute, National Institutes of Health. 2003 - 2013.

Founder: Kailos Genetics, Inc. Huntsville, AL. 2010.

Member: External Advisory Group, Wisconsin Center of Excellence in Genome Sciences. 2010 - 2013.

Member: NIH Intramural Sequencing Center Working Group, National Human Genome Research Institute, National Institutes of Health. 2006 - 2013.

Founder and Advisor: SwitchGear Genomics, Inc. Menlo Park, CA. 2005 - 2013.

Member: Advisory Council, National Human Genome Research Institute, National Institutes of Health. 2009 - 2012.

Member and Co-chair: ENCODE Data Analysis Working Group, National Human Genome Research Institute, National Institutes of Health. 2008 - 2012.

Chair: Genomics of Gene Expression Workshop, National Human Genome Research Institute, National Institutes of Health. October 2009.

Member: Scientific Director Search Committee, National Human Genome Research Institute, National Institutes of Health. 2009 - 2010.

Member and Chair: ENCODE Data Release Working Group, National Human Genome Research Institute, National Institutes of Health. 2007 - 2011.

Member: Stanford Genetics/San Jose Tech Museum Science Education Partnership. 2001 - 2008.

Member: Biotech Advisory Board, Gunn High School, Palo Alto, 2005 - 2009.

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: Genome Centers Review Committee, Genome Canada. 2003, 2004.

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: Grant Review Committee, U.S. Department of Energy. 1999.

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, National Institutes of Health. 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 Center for Human Genome Research, National Institutes of Health. Four site visits, 1990 - present.

Member: Review Committee for Sanger Centre, Wellcome Trust, Cambridge, England. 1995.

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, Fellowships and Honors

AAAS Fellow, The American Association for the Advancement of Science. 2011.

Leadership Alabama Inductee, Class 20, 2009.

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 UC Berkeley).

Regents Fellowship, 1979 - 1980 (at UC Berkeley).

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

Phi Beta Kappa, 1975 (at University of Alabama).

Teaching

Lecturer in Genomics, a graduate course in genomics in the Department of Genetics, University of Alabama at Birmingham School of Medicine, 2010 - present.

Lecturer in Genomic Science, a 4-day short course funded by the NIH to provide training on next-generation DNA sequencing and analysis, with HudsonAlpha and University of Alabama at Birmingham School of Medicine faculty, 2011 - present.

Co-instructor (with Chris Gunter, Neil Lamb and Adam Hott) of BYS400/600, an undergraduate and masters-level graduate course in introductory neuroscience, University of Alabama in Huntsville, Winter/Spring semester, 2010.

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 - 2008.

Co-director: Genetics and Developmental Biology Training Program, Stanford University School of Medicine, 2002 - 2008.

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 - 2009.

Member of Dissertation Committees for 67 graduate students at UCSF and Stanford University, 1986 - 2009.

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.

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 Number 6,432,635, August 13, 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.

U.S. Patent Number 7,410,759, August 12, 2008, "Compositions and Methods for Diagnosing and Treating Mood Disorders", Akil, Huda; Bunney, Jr. William E.; Choudary, Prabhakara V.; Evans, Simon J.; Jones, Edward G.; Li, Jun; Lopez, Juan F.; Thompson, Robert C.; Myers, Richard; Tomita, Hiroaki; Vawter, Marquis P.; Watson, Stanley.

Education Outreach, Community Service and Other Activities

Lecturer: Biotech 101, a course for adult non-scientists led by Dr. Neil Lamb at HudsonAlpha Institute. Yearly, 2008 - present.

Lab mentor: High school and undergraduate students, HudsonAlpha BioTrain Program, two students each summer, 2008 - present.

Lecturer: High school and middle school classes, several per year, 1990 - 2010.

Member: Stanford Genetics/San Jose Tech Museum Science Education Partnership. 2001 - 2008 (see <http://genetics.stanford.edu/techmuseum/>).

Member: Biotech Advisory Board, Gunn High School Biotechnology Program, Palo Alto, 2005 - 2009.

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

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

Coach: Palo Alto YBAL Boys' Baseball, 1995 - 1996.

Coach and organizer: Palo Alto Boys' Baseball league, 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.

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. PMID: 332076.
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. PMID: 6255460. PMCID: PMC350138.
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. PMID: 6256739. PMCID: PMC350311.
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. PMID: 6269743.
6. Myers, R. M., Kligman, M. and Tjian, R. (1981). Does simian virus 40 T antigen unwind DNA? *J. Biol. Chem.* 256: 10156-10160. PMID: 6268627.
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. PMID: 6273580.
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 α -subunit. *Arch. Biochem. Biophys.* 220: 435-443. PMID: 6337554.
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. PMID: 6098305.
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. PMID: 6098470. PMCID: PMC557845.
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. PMID: 3969155.
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. PMID: 2987873. PMCID: PMC341224.
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. PMID: 4000972. PMCID: PMC341225.
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. PMID: 2990046.
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. PMID: 4071043.
16. Myers, R. M., Tilly, K. and Maniatis, T. (1986). Fine structure genetic analysis of a beta-globin promoter. *Science*. 232: 613-618. PMID: 3457470.
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. PMID: 3023357.

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. PMID: 3430628.
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. PMID: 3211138. PMCID: PMC363539.
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. PMID: 2523853.
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. PMID: 2643100. PMCID: PMC286438.
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. PMID: 2523854.
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. PMID: 1968226.
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. PMID: 2304472. PMCID: PMC360947.
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. PMID: 1970195.
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. PMID: 1691226.
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. PMID: 2144903. PMCID: PMC54733.
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. PMID: 2218528.
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. PMID: 2247475. PMCID: PMC55087.
30. Burmeister, M., Cox, D. R. and Myers, R. M. (1990). Dinucleotide repeat polymorphism located at D21S120. *Nucleic Acids Res.* 18: 4969. PMID: 2395674. PMCID: PMC332044.
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. PMID: 2300052. PMCID: PMC360828.
32. Burmeister, M., Cox, D. R. and Myers, R. M. (1991). TaqI RFLP at D21S137. *Nucleic Acids Res.* 19: 4020. PMID: 1677761. PMCID: PMC328526.
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. PMID: 1674130. PMCID: PMC333904.

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. PMID: 2004760.
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. PMID: 1916829.
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. PMID: 1718042.
37. Pritchard, C., Cox, D. R. and Myers, R. M. (1991). Dinucleotide repeat polymorphism located at D4S169. *Nucleic Acids Res.* 19: 6347. PMID: 1956808. PMCID: PMC329170.
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. PMID: 1684084. PMCID: PMC1686449.
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. PMID: 1475209. PMCID: PMC334544.
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. PMID: 1427886.
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. PMID: 1551659.
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. PMID: 1350884. PMCID: PMC1682573.
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. PMID: 1524828.
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. PMID: 1571147.
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.* 1 149-159. PMID: 1303170.
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. PMID: 8417342. PMCID: PMC358883.
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. PMID: 8493118. PMCID: PMC309454.
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. PMID: 8321233. PMCID: PMC359987.

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. PMID: 8364572.
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Biographical Information for Dr. Richard M. Myers

Dr. Richard M. Myers received his B.S. in Biochemistry from the University of Alabama in 1977, his Ph.D. in Biochemistry from the University of California, Berkeley in 1982, and did his post-doctoral training at Harvard University. He joined the faculty of the UCSF Medical Center in 1986 moved to Stanford University in 1993, where he served as Professor and Chair in the Department of Genetics. Since 2008, Dr. Myers has been President, Director and a Faculty Investigator of the HudsonAlpha Institute for Biotechnology, a non-profit research and teaching enterprise in Huntsville, Alabama. The Myers laboratory studies the human genome, with goals of understanding how allelic variation and gene expression changes contribute to human traits, including diseases, behaviors and other phenotypes. His group uses high-throughput genomic methods, including DNA sequencing, genotyping, chromatin immunoprecipitation, mRNA expression profiling, transcriptional promoter and DNA methylation measurements, as well as computational and statistical tools, to identify, characterize and understand the functional elements encoded in our genomes, and how they work together at the molecular level in normal and pathological conditions. His group also sequences whole genomes, whole exomes and targeted regions of the genome with ultrahigh-throughput DNA sequencing technologies to identify DNA sequence variants relevant to clinical and basic biological problems. The lab integrates these functional genomics, epigenetic and genetic data to understand how our genomes are involved in cancer, brain disorders, ALS, children born with developmental disorders, autoimmune diseases and other traits.

Detailed Biography

College and Graduate Education and Research

I obtained my undergraduate education at the University of Alabama in Tuscaloosa, graduating in 1977 with a B.S. in Biochemistry. There, I did research in physical chemistry and in enzymology. The work in physical chemistry was under the guidance of Dr. Clifford Hand, a remarkable teacher who helped me understand the scientific method and the excitement of doing research to answer basic questions about how the universe works. We studied the kinetics of gas phase reactions by using a flow reactor and mass spectrometry (all on homemade equipment!).

I began to get exposure to biology, particularly biochemistry and molecular biology, so I changed into a different lab, and did research my last two years in college in Dr. John Hardman's lab, a biochemist who studied how enzymes work. My project was to study of the mechanisms of enzyme action and allostery, using *E. coli* tryptophan synthase as a model system. I synthesized an affinity substrate to label the enzyme and used it to probe the reaction kinetics in the last step of tryptophan biosynthesis.

In 1977, I moved to Berkeley, California to do my graduate work in the Department of Biochemistry at the University of California at Berkeley. I obtained my Ph.D. in 1982 in the laboratory of Dr. Robert Tjian ("Tij"), who arrived there in my second year as a beginning faculty member. I studied SV40 T antigen, including its DNA binding properties, its role in DNA replication, and the mechanisms of transcriptional regulation imparted by its binding to the viral genome. My projects involved purifying and studying proteins, similar to my undergraduate work, but also introduced me to molecular biology (DNA cloning, which had just been invented), and studying protein:DNA interactions, an interest that continues to the present.

Postdoctoral Work

In 1982, after graduate school, I joined Dr. Tom Maniatis's lab at Harvard University in the Department of Biochemistry and Molecular Biology to do my postdoctoral work. When I began my project, I studied mammalian gene expression, using the β -globin locus to probe elements that control transcription of the gene cluster in erythroid cells. We developed a new method for generating single base mutations in cloned segments of DNA, and used it to saturate the β -globin gene promoter with more than 150 mutations. I tested these mutations for their effect on transcription by transferring plasmid constructs

carrying them into cultured human and mouse cells, which gave a detailed picture of the *cis*-acting elements that contribute to levels of mRNA of the gene.

The mutagenesis method involved treating naked DNA fragments with various mutagens, cloning the fragments as a pool into a plasmid vector, and then purifying the mutant promoters from the wild type (which was the vast majority) by using an unusual gel system that had just been developed by Dr. Leonard Lerman, a biophysicist with whom Tom Maniatis had done his graduate work, then at SUNY Albany. This electrophoretic method was called denaturing gradient gel electrophoresis (DGGE), and it has the remarkable property of separating DNA fragments differing by only a single base pair in a polyacrylamide gel, based on the melting behavior of the DNA.

It occurred to us that the separation could be used not only to purify mutant fragments, but also as a way to detect mutations, so I spent much of my postdoc work (and some of the first few years of my first faculty appointment) developing this and another method involving cleavage of mismatched RNA:DNA hybrids (called RNase cleavage) for mutation detection. I began to learn about human genetics for the first time, and applied the two detection methods we developed to identifying people who carried mutations as well as neutral polymorphisms in their genomes. Such methods were sorely needed, because, at the time, the only ways to detect mutations or polymorphisms were to clone and sequence the fragments from each person or to use restriction enzymes, or to use expensive (at the time) oligonucleotides and gel electrophoresis followed by Southern blotting.

Because we began to talk about these methods in seminars and at scientific meetings, Tom was invited to attend a small conference in Alta, Utah concerned with human genetics, and sponsored by the U.S. Department of Energy and the International Commission for Protection Against Environmental Mutagens and Carcinogens. His interest was more in gene expression, and, being a very generous postdoctoral advisor, he sent me instead. In December 1984, I, along with a group of 18 other researchers met at a ski resort (I don't ski, so I mostly just tried to stay warm in the hotel) to discuss a difficult problem that had basic science as well as tremendous social significance. The question was, is it possible to determine whether the Hiroshima and Nagasaki atomic bomb blasts at the end of World War II increased the rate of mutations in the sperm or eggs of survivors of the bombings, in other words, did the exposure to high doses of irradiation increase the germline mutation rate? The question was whether any methods were available to measure mutations in the offspring of survivors, and to determine whether the number of mutations was higher than in unexposed people. A variety of cell-based mutation assays and other approaches by the folks who had been working in this field for a long time were discussed, and I presented the methods we had developed for mutation detection. It was clear that the problem was huge; the baseline rate of mutation in people was so low that we did not have a clear number based on data. So how could we determine whether there was an increase in offspring of exposed individuals if we didn't know the rate of mutation in people not exposed to radiation? The problem was so vexing that someone at the meeting (not me, I'm sad to say!) commented that "the rate is so low that we would have to sequence the entire human genome to know the answer". After the laughter died down, it is clear that the D.O.E. folks, and probably others at the meeting, took this concept clearly, as not long after, that very entity proposed the basis for the Human Genome Project, which began in earnest in 1990. I take no credit for this vision, but was very excited to be part of the meeting and to rub elbows with a new (to me) community of scientists who eventually became my colleagues. I especially owe a debt to Drs. Maynard Olson and Jim Neel, two gentlemen who were experts in genetics and who encouraged me to move into the field of human genetics and provided early and continuing mentorship that helped me find my way in this new field.

Faculty Positions at UCSF and Stanford University

I began my first faculty position at the University of California in San Francisco in late 1985, with my primary appointment in the Department of Physiology and my secondary appointment in the Department of Biochemistry and Biophysics. I set up my lab to continue studying globin gene expression, and some of my graduate students and postdocs worked on both *cis*- and *trans*-acting components that regulate transcription of the gene for the next six years. I also wanted to learn more about human genetics, and

was interested in identifying the gene that is mutated in people with Huntington disease (gene hunting by positional cloning had just been developed, and the disease was compelling to me). During my first months, I had the very good fortune to meet Dr. David Cox, a brilliant physician-scientist who was a medical geneticist and also had a Ph.D. in yeast genetics. We immediately joined forces, and for 15 years our laboratories were essentially a joint lab. I learned a tremendous amount about inheritance and quantitative biology from David, and we not only worked on Huntington disease, but also other diseases of the nervous system. We developed and improved several technologies for gene hunting, including radiation hybrid mapping, a method that used high-energy x-rays to fragment human chromosomes that were recovered in somatic cell hybrids and then used to determine the locations of DNA markers in our genome. This led us to apply for and have awarded one of the first NIH grants to establish a human genome center in 1990, as one of the inaugural labs participating in the public Human Genome Project (HGP).

In early 1993, David and I moved our laboratories and the Human Genome Center to the Department of Genetics at Stanford University School of Medicine. Our labs continued to work on inherited human diseases, including not only brain diseases and phenotypes, but also others. We identified the genes for an inherited form of childhood progressive epilepsy (called “EPM1”), for a key step in development of the cerebellum (the “weaver” gene), and with others, genes involved in inherited skin cancer, hemochromatosis, and an autoimmune disease. My lab generated and studied mouse models of Huntington disease and EPM1 during those years.

At the Stanford Human Genome Center, we applied radiation hybrid and other mapping technologies to human chromosomes as part of the HGP, but also began collaborating with the Joint Genome Institute (JGI) in Walnut Creek to sequence human genomic DNA with funding from the U.S. Department of Energy. Ultimately, this led to maps of the entire genome that were instrumental in piecing the entire sequence together, as well as to a substantial amount of finished, contiguous DNA sequence. By the time we reached the finish line in 2003, our group was responsible for genome-wide maps, and with the JGI, for 11% of the finished human genome sequence, including the entirety of chromosomes 5, 16 and 19. We also contributed to the final sequence of human chromosome 4 with Washington University’s Genome Center.

In 2000, David left Stanford for industry (Perlegen and then Pfizer), and, sadly, died unexpectedly in 2012. I continued to run the Stanford Human Genome Center, as well as a lab of about 15 graduate students and postdocs working on human genetics and genomics. In addition, I was Vice Chair and then Chair of the Department of Genetics during my last 11 years at Stanford. During that time, I began to combine genome-wide approaches with my old interest in transcriptional regulation, which led to a close and still-active collaboration with Dr. Barbara Wold and her lab at Caltech. Our groups have worked together to develop and apply methods for measuring gene expression, protein:DNA interactions and epigenetic events on a genome-wide scale, including chromatin immunoprecipitation (ChIP), mRNA and microRNA expression, transcriptional promoter and methylation measurements, and computational and statistical tools to study human biology. We are one of the initial groups who comprise the ENCODE Consortium, which has the goal of identifying and understanding all the functional elements in the human genome. The techniques and knowledge we have gained from this work are important components of our projects to understand diseases and our interactions with the environment, including variable responses to drugs, as discussed below.

HudsonAlpha Institute

In 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, uses genomics and genetics to make and apply discoveries for solving important problems in human health, energy and environmental science. At HudsonAlpha Institute, we have continued work that my laboratory started at Stanford, while

working collaboratively with faculty at the institute and with other researchers on a wide range of scientific and biomedical problems.

A large part of our efforts are towards the study of an array of human diseases. These include disorders of the nervous system, notably Parkinson disease, bipolar disorder, schizophrenia, major depression and ALS, as well as several types of cancer, including breast, prostate, kidney, and pancreatic cancer. We also work on autoimmune diseases, with emphasis on rheumatoid arthritis, Crohn's disease, lupus and psoriasis. These studies involve identifying DNA sequence differences, as well as differences in functional readout of the genome, between affected and unaffected individuals in an effort to understand the genetic basis of the disease.

My lab is part of the Pritzker Consortium, a collaboration between six laboratories around the U.S., where we study psychiatric disorders by assessing gene expression and DNA methylation patterns in post mortem brain tissues, as well as blood specimens, from people with the disease compared to individuals who are not affected. With Shawn Levy at HudsonAlpha, we also collaborate with Dr. Mike Boehnke, Dr. Goncalo Abecasis, and colleagues at the University of Michigan and several other universities to study the genetics of bipolar disorder, in a very large study where we sequenced the entire genomes of 4,000 people, half with bipolar and half without. The goals of our psychiatric research are to understand the genetic and genomic bases of the disorders, in hopes of identifying pathways that will lead to predictive biomarkers for the disorders and responses to treatments, as well as to new targets for therapies.

In collaboration with scientists at HudsonAlpha, Stanford University, the University of Alabama at Birmingham, and the Mitchell Cancer Center at the University of South Alabama in Mobile, we are applying these approaches to several cancer projects to provide a comprehensive genomic comparison of tumors compared to non-tumor tissues. These studies include breast cancer (ER+PR+ as well as triple negative breast cancer), kidney cancer, prostate cancer and pancreatic cancer. In the case of breast cancer, we are also using genomic approaches to understand the basis of response and non-response to new therapies in clinical trials; these are in collaboration with Drs. Andres Forero, Al LoBuglio and Don Buchsbaum at UAB and with Dr. K-T Varley, a former postdoc in my lab now on the faculty at the University of Utah. These experiments include measuring copy number variation, exome sequence variants, the immune repertoire, and genome-wide DNA methylation, mRNA, microRNA, and chromatin modifications. With Drs. Devin Absher and Shawn Levy at HudsonAlpha, we have also begun to apply this type of comprehensive genomic analysis to autoimmune disease, including lupus, rheumatoid arthritis (with Dr. Sara Marsal at Vall d'Hebron Hospital in Barcelona, Spain and Dr. Louis Bridges at UAB) and Parkinson disease (with Dr. David Standaert and colleagues at UAB). With Dr. David Goldstein, then at Duke University, and Dr. Tim Harris, at Biogen Idec, Inc. in Cambridge, MA, we sequenced the exomes of thousands of individuals with ALS, and these studies identified new genes that contribute to the disease that are also potential targets for new drugs. In related studies, we have collaborated with Drs. Tom Maniatis and Neil Shneider at Columbia University to apply functional genomics methods to human cells and mouse models of ALS to elucidate the mechanisms of the disease.

The sequencing group we built at the Stanford Human Genome Center moved to HudsonAlpha as well, now led by HudsonAlpha faculty investigators Jane Grimwood and Jeremy Schmutz. They continue to collaborate with the Joint Genome Institute and have developed their own research programs, mostly concerned with the genomics of plants, organisms with complex and difficult-to-sequence genomes, with particular interests in crop improvement, other agricultural problems, bioenergy and the environment.

We have continued our basic science interest in gene expression, applying genetics and functional genomics methods to probe a wide range of human cells for both cis- and trans-acting elements that regulate transcription. We continue to collaborate with Dr. Barbara Wold and others on the ENCODE Project. In addition to contributing to the ENCODE encyclopedia, we are studying particular transcription factors and networks of factors involved in interesting human biological problems, including responses to hormones such as glucocorticoids and sex hormones, the stress response, and neuronal development.

In addition to my research, I participate in a 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, as well as to non-science majors. I helped established a partnership between the Department of Genetics and the San Jose Tech Museum, which develops scientific exhibits as well as providing a venue for training graduate students and postdoctoral fellows in the art of teaching to the public. I have had a long-standing special interest and have participated in numerous activities to increase and foster diversity in research and education, with particular emphasis in under-represented groups. We have continued and greatly expanded these types of activities at HudsonAlpha Institute, where we have a team of science education professionals, led by Dr. Neil Lamb, who work with faculty, students and postdocs at HudsonAlpha to develop, test, and implement a wide variety of programs that teach the importance of science in our everyday lives at every age level, from young children to adults. These programs provide services, ideas, excitement and tools throughout the State of Alabama and the country (see <http://www.hudsonalpha.org/education>).

I serve on a variety of advisory panels and editorial boards, including panels for the National Institutes of Health, the Department of Energy, several universities, and the Pharmacogenomics Research Network. I am a member of the HeLa Genome Data Access Working Group, led by the National Institutes of Health. I am an Associate Editor of Genome Research and participate in strategic planning and grant reviews for the NIH, DOE and other agencies. I am also an advisor to two biotech companies that work on genomics-related problems; these are Kailos Genetics, Inc., located on the HudsonAlpha campus, and DNAnexus, Inc. in Mountain View, CA. I serve on the Scientific Advisory Boards of Bay City Capital and Decheng Capital, both in San Francisco, CA.