David Mittelman, PhD

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+ *Professional Summary*

Dr. David Mittelman is a renowned scientist and DNA testing expert with nearly 30 years of experience in genetics and genomics. He has co-authored nearly 50 peer-reviewed articles, with his work cited more than 6,900 times. Dr. Mittelman began his career with the Human Genome Project and trained in Human Genetics at Baylor College of Medicine. A pioneer in genome technology, he has advanced DNA sequencing and SNP microarray technologies, driving innovation in biomedical research, diagnostics, and forensic science.

+ *Professional Experience*

Year(s)	***Positions Held***	***Company***
10/01/2018 - Present	Founder and Chief Executive Officer	Othram The Woodlands, TX
09/01/2015 - 9/30/2018	Partner and Division President	Elite Surgical Affiliates The Woodlands, TX
01/01/2015 - 08/31/2015	Investor & Chief Scientific Officer	Tute Genomics Salt Lake City, UT
08/01/2013 - 12/31/2014	Partner and Chief Scientific Officer	Gene by Gene Houston, TX
10/01/2012 - 07/31/2013	Founder and Chief Scientific Officer	Arpeggi Austin, TX

+ *Education*

Baylor College of Medicine
Houston, TX
Ph.D. Molecular Biophysics, 2007

University of Texas at Dallas
Richardson, Texas
B.S. Neuroscience, 2002

+ *Academic Experience*

Year(s)	***Title***
2026	**Visiting Senior Research Fellow,** Dept of Toxicology & Forensic Science, King's College London
2010-2013	**Associate Professor,** Dept of Basic Science, Virginia Tech Carilion School of Medicine. (from 2012)
	Associate Professor, Dept of Biological Sciences at Virginia Tech, Department Chair: Dr. Brenda Winkel, Ph.D. (from 2011)

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	Associate Professor, Virginia Bioinformatics Institute at Virginia Tech, Institute Director: Dr. Chris Barrett, Ph.D. (from 2010)
2009-2010	**Ruth L. Kirschstein NRSA Fellow**, Human Genome Sequencing Center at Baylor College of Medicine, Center Director: Dr. Richard Gibbs, Ph.D.
2008-2009	**Lecturer,** Department of Ecology and Evolutionary Biology at Rice University.
2007-2009	**Postdoctoral Fellow**, Department Molecular and Human Genetics at Baylor College of Medicine, laboratory of Juan Botas, Ph.D.
2002-2007	**Graduate Student**, Department of Biochemistry at Baylor College of Medicine, laboratory of John Wilson, Ph.D.
2002	**Scientific Programmer**, Department of Biochemistry at UT Southwestern Medical Center, laboratory of Nick Grishin, Ph.D.
1997-2002	**Research Assistant**, McDermott Center for Human Growth and Development at UT Southwestern Medical Center, laboratory of Harold Garner, Ph.D.

+ *Books*

1. ***D. Mittelman*** (ed) (2013) Stress-Induced Mutagenesis. New York, NY: Springer.

+ *Chapters & Collections (*Corresponding Author)*

2. *J. Wilson, C. Moye, and **D. Mittelman** (2016) Engineered Nucleases and Trinucleotide Repeat Diseases, a chapter in Genome Editing: The Next Step in Gene Therapy, Toni Cathomen, Matthew Hirsch, and Matthew Porteus, Springer.*

3. *R.M. Ward and **D. Mittelman*** (2013) Tandem repeat instability and genome evolution, in: eLS. John Wiley & Sons Ltd, Chichester.*

4. *K.J. Luebke, R.P. Balog, **D. Mittelman** and H.R. Garner (2002) Digital Optical Chemistry: A Novel System for the Rapid Fabrication of Custom Oligonucleotide Arrays, a chapter in Microfabricated Sensors, Application of Optical Technology for DNA Analysis, Usmani and Wai Tak Law, editors, ACS Publications.*

+ *Invited Reviews & Perspectives (*Corresponding Author)*

5. *R. Khan and **D. Mittelman*** (2018) Consumer genomics will change your life, whether you get tested or not, Genome Biology, 19(1):120.*

6. *R. Khan, L. Goodman, and **D. Mittelman*** (2014) Scientific Publishing Meets the 21st Century, Genome Biology, 15(12):556.*

7. *R. Khan and **D. Mittelman*** (2013) Rumors of the death of consumer genomics are greatly exaggerated, Genome Biology, 14(11):139.*

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8. *R.M. Ward, R. Schmieder, G. Highnam, and **D. Mittelman*** (2013) Big data challenges and opportunities in high-throughput sequencing. Systems Biomedicine, 1(1):23-28.*

9. ***D. Mittelman*** and J.H. Wilson (2013) The fractured genome of HeLa cells. Genome Biology, 4(4):111.*

10. *G. Highnam and **D. Mittelman*** (2012) Personal genomes and precision medicine, Genome Biology, 13(12):324.*

11. *N.C. Fonville, R.M. Ward, and **D. Mittelman*** (2011) Stress-induced modulators of repeat instability and genome evolution, J Mol Microbiol Biotechnol, 21:36-44.*

12. ***D. Mittelman*** and J.H. Wilson (2010) Stress, genomes, and evolution. Cell Stress Chaperones, 15(5):463-6.*

+ *Select Peer-Reviewed Publications (*Corresponding Author)*

13. *B. Budowle, S. Newman, N. Jones, M. Marra, K. Mittelman, & **D. Mittelman.*** (2026). Artificial intelligence enables scale, consistency, and rigor in forensic identity inference. Croatian Medical Journal, 67(3), 188.*

14. ***D. Mittelman***, B. Budowle, & K. Mittelman (2026). Terminology, retrieval bias, and field definition in forensic genetic genealogy. Forensic science international. Synergy, 12, 100679.*

15. *S. A. Bates, B. Budowle, M. Johnson, J. Ge, K. Mittelman, & **D. Mittelman.*** (2026). Large-scale analysis of DNA quantification metrics and SNP sequencing performance in unidentified human remains. Forensic Science International: Genetics, 84, 103470.*

16. *S. Newman, B. Budowle, K. Mittelman, & **D. Mittelman**.* (2026). Othram maps: a graph-powered platform for pedigree visualization and forensic intelligence. Bioinformatics, 42(2), btag047.*

17. *C. Lasyone, B. Budowle, K. Mittelman, & **D. Mittelman.*** (2025) Investigative and policy impacts of forensic genetic genealogy in the identification of human remains. Forensic Science International: Synergy, 11, 100651.*

18. *B. Budowle, K. Mittelman, & **D. Mittelman.*** (2025) Genomics will forever reshape forensic science and criminal justice. Genome Biology, 26(1), 296.*

19. *J. Ge, B. Budowle, M. Cariaso, K. Mittelman, & **D. Mittelman.*** (2025) A likelihood ratio framework for inferring close kinship from dynamically selected SNPs. Frontiers in Genetics, 16, 1635734.*

20. *R. A. Wickenheiser, J. Naugle, B. Hoey, R. Nowlin, C. Glynn, R. Valerio, L. Allen, S. Stoiloff, J. Kochanski, M. B. Schubert, M. Haas, D., Peters, R. Oefelein, R. Harmon, B. Llewellyn, T. Kacer, B. Patel, P. Panther, C. Fitzpatrick, G. Bombard, **D. Mittelman** ... T. Cober. (2025) National Technology Validation and Implementation Collaborative (NTVIC): Updated guidelines for establishing Forensic Investigative Genetic Genealogy (FIGG) programs. Forensic Science International: Synergy, 11, 100593.*

21. *B. Budowle, J. Ge, L. Baker, K. Mittelman, **D. Mittelman*** (2025) Analytical validation of the IBD segment-based tool KinSNP® for human identification applications. Biotechniques. 2025 Jan;77(1):9-22.*

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22. *S. A. Bates, B. Budowle, L. Baker, K. Mittelman,* ***D. Mittelman***** (2025) A Molecular framework for enhancing quality control and sample integrity in forensic genome sequencing. Forensic Science International: Genetics, 103179.*

23. *S. N. Mandape, B. Budowle, H. McKiernan, D. Slack, K. Mittelman,* ***D. Mittelman***** (2025) Dense SNP-based analyses complement forensic anthropology biogeographical ancestry assessments. Forensic Science International: Genetics, 74, 103147.*

24. *B. Budowle, L. Baker, A. Sajantila, K. Mittelman,* ***D. Mittelman***** (2024) Prioritizing privacy and presentation of supportable hypothesis testing in forensic genetic genealogy investigations, BioTechniques 76(9), 425-431.*

25. *S. Mandape, B. Budowle, K. Mittelman,* ***D. Mittelman***** (2024) Dense single nucleotide polymorphism testing revolutionizes scope and degree of certainty for source attribution in forensic investigations, Croatian Medical Journal, 65(3):249-260.*

26. *H. Fang, Y. Wu, H. Yang, M. Yoon, L.T. Jiménez-Barrón,* ***D. Mittelman****, R. Robison, K. Wang, G.J. Lyon (2017) Whole genome sequencing of one complex pedigree illustrates challenges with genomic medicine, BMC Med Genomics, 10(1):10.*

27. *G.D. Poznik et al. (2016) Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences, Nature Genetics, 48(6):593-9.*

28. *J. Quilez, A. Guilmatre, P. Garg, G. Highnam, M. Gymrek, Y. Erlich, R.S. Joshi,* ***D. Mittelman,*** *A.J. Sharp (2016) Polymorphic tandem repeats within gene promoters act as modifiers of gene expression and DNA methylation in humans, Nucleic Acids Res, 44(8):3750-62.*

29. *J.A. O'Rawe, Y. Wu, M.J. Dörfel, A.F. Rope et. al. …* ***D. Mittelman*** *… M. Rosello, C.E. Keegan, G.J. Lyon (2015) TAF1 Variants Are Associated with Dysmorphic Features, Intellectual Disability, and Neurological Manifestations, Am J Hum Genet, 97(6):922-32.*

30. *1000 Genomes Project Consortium (2015) A global reference for human genetic variation, Nature, 526(7571):68-74.*

31. *S.T. Bilgin, T. Carvalho, M.D. Robinson, M.P. Greminger, M. Krützen, D. Comas,G. Highnam,* ***D. Mittelman****, A. Sharp, T. Marques-Bonet, A. Wagner (2015) Tandem repeat variation in human and great ape populations and its impact on gene expression divergence, Genome Res, 25(11):1591-9.*

32. *G. Highnam, J. Wang, D. Kusler, J. Zook, V. Vijayan, N. Leibovich, and* ***D. Mittelman***** (2014) An analytical framework for optimizing variant discovery from personal genomes, Nat Commun, 6:6275.*

33. *B.A. Santillan,C. Moye,* ***D. Mittelman****, Wilson JH (2015) GFP-based fluorescence assay for CAG repeat instability in cultured human cells, PLoS One, 9(11):e113952.*

34. *T.F. Willems, M. Gymrek, G. Highnam,* ***D. Mittelman****, and Y. Erlich (2014) Landscape of Human STR Variation. Genome Research, 24(11):1894-904.*

35. *S.N. Porter, L.C. Baker,* ***D. Mittelman****, M.H. Porteus (2014) Lentiviral and targeted cellular barcoding reveals ongoing clonal dynamics of cell lines in vitro and in vivo. Genome Biology, 15(5):R75.*

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36. *W. Huang, A. Massouras, Y. Inoue, J. Peiffer et. al. ... **D. Mittelman,** D. Muzny, R.A. Gibbs, A. Barbadilla, S. Johnston, E. Stone, S. Richards, B. Deplancke, and T.F.C. Mackay (2014) Natural variation in genome architecture among 205 Drosophila melanogaster Genetic Reference Panel lines. Genome Research, 24(7):1193-208.*

37. *J. Zook, B. Chapman, J. Wang, **D. Mittelman**, O. Hofmann, W. Hide, and M. Salit (2014) Integrating sequencing datasets to form highly confident SNP and indel genotype calls for a whole human genome. Nature Biotech, 32(3):246-51.*

38. *A. Guilmatre, G. Highnam, C. Borel, **D. Mittelman**, and A.J. Sharp (2013) Rapid multiplexed genotyping of simple tandem repeats using capture and high-throughput sequencing. Human Mutation, 34(9):1304-11.*

39. *G. Highnam, C. Franck, A. Martin, C. Stephens, A. Puthige, and **D. Mittelman*** (2013) Accurate human microsatellite genotypes from high-throughput resequencing data using informed error profiles. Nucleic Acids Res, 40(1):e32.*

40. *J. Li, R. Schmieder, R.M. Ward, J. Delenick, E.C. Olivares, and **D. Mittelman*** (2012) SEQanswers: An open access community for collaboratively decoding genomes. Bioinformatics, 28(9):1272-3.*

41. *J. Fondon III, A. Martin, S. Richards, R.A. Gibbs, and **D. Mittelman*** (2012) Analysis of microsatellite variation in drosophila melanogaster with population-scale genome sequencing. PLoS One, 7(3): e33036.*

42. *T.F.C. Mackay, S. Richards, E.A. Stone, A. Barbadilla, J.F. Ayroles, D. Zhu, S. Casillas, Y. Han, M.M. Magwire, J.M. Cridland et. al. ... **D. Mittelman**, and R.A. Gibbs (2012) The Drosophila Genetic Reference Panel: A Community Resource for Analysis of Population Genomics and Quantitative Traits. Nature, Feb 9;482:173-8.*

43. ***D. Mittelman,** K. Sykoudis, M. Hersh, Y. Lin, and J.H. Wilson (2010) Hsp90 modulates CAG/CTG repeat instability in human cells. Cell Stress Chaperones, 15(5): 753-9.*

44. ***D. Mittelman,** C. Moye, J. Morton, K. Sykoudis, Y. Lin, D. Carroll, and J.H. Wilson (2009) Zinc-finger directed double-strand breaks within CAG repeat tracts promote repeat instability in human cells. P. Natl. Acad. Sci. USA,106:9607-12.*

45. *D.H. Morgan, D.M. Kristensen, **D. Mittelman**, and O. Lichtarge (2006) ET Viewer: An Application for Predicting and Visualizing Functional Sites in Protein Structures. Bioinformatics, 22(16):2049-50.*

46. *V. Gorbunova, A. Seluanov, **D. Mittelman**, and J.H. Wilson (2004) Demethylation of the genome strongly destabilizes CAG/CTG trinucleotide repeats in mammalian cells. Hum. Mol. Genet., 13(23):2979-2989.*

47. *A. Seluanov, **D. Mittelman,** O.M. Pereira-Smith, J.H. Wilson, and V. Gorbunova (2004) DNA end joining becomes less efficient and more error-prone during cellular senescence. P. Natl. Acad. Sci. USA, 101(20):7624-9.*

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48. ***D. Mittelman,*** *R. Sadreyev, and N. Grishin (2003) Probabilistic scoring measures for profile-profile comparison yield more accurate short seed alignments. Bioinformatics, 19(12): 1531-1539.*

49. *R.P. Balog, Y. Ponce de Souza, H. Tang, G. DeMasellis, B. Gao, A. Avila, D. Gaban,* ***D. Mittelman****, J.D. Minna, K.J. Luebke, and H.R. Garner (2002) Parallel assessment of CpG methylation by two-color hybridization with oligonucleotide arrays. Analytical Biochemistry, 309(2):301-310.*

50. *A. Kulkarni, N. Williams, Y. Lian, J.D. Wren,* ***D. Mittelman****, A. Pertsemlidis, and H.R. Garner (2002) ARROGANT: an application to manipulate large gene collections. Bioinformatics, 18(11): 1410-1417.*

51. *J.D. Wren,* ***D. Mittelman****, and H.R. Garner (2002) SIGNAL: Sequence Information and Genomic Analysis. Comput Meth Prog Bio, 68(2):177-181.*

52. *Pertsemlidis, B. Miller, A. Pande,* ***D. Mittelman,*** *P. Schilling, M. Wei, M. Lerman, J. Minna, and H. Garner (2000) PANORAMA - An Integrated Web- Based Sequence Analysis Tool and Its Role in Gene Discovery. Genomics, 70(3): 300-30.*

+ *Forensic Genetic Genealogy Testimony*

The cases in the below table signify a sampling of cases in which Othram's technology was cross-examined in court, specifically on the topic of forensic genetic genealogy. As of July 2026, Othram is the only United States-based forensic laboratory to defend this technology in a jury trial. An asterisk indicates that Dr. Mittelman took the stand.

Year	***Defendant***	***Court***	***Expertise***	***Verdict***
2024	Clayton Bernard Foreman	Jefferson County, Texas	SNP Testing, Forensic Genetic Genealogy*	Guilty
2021	Glen Samuel McCurley, Jr.	Tarrant County, Texas	SNP Testing, Forensic Genetic Genealogy	Guilty