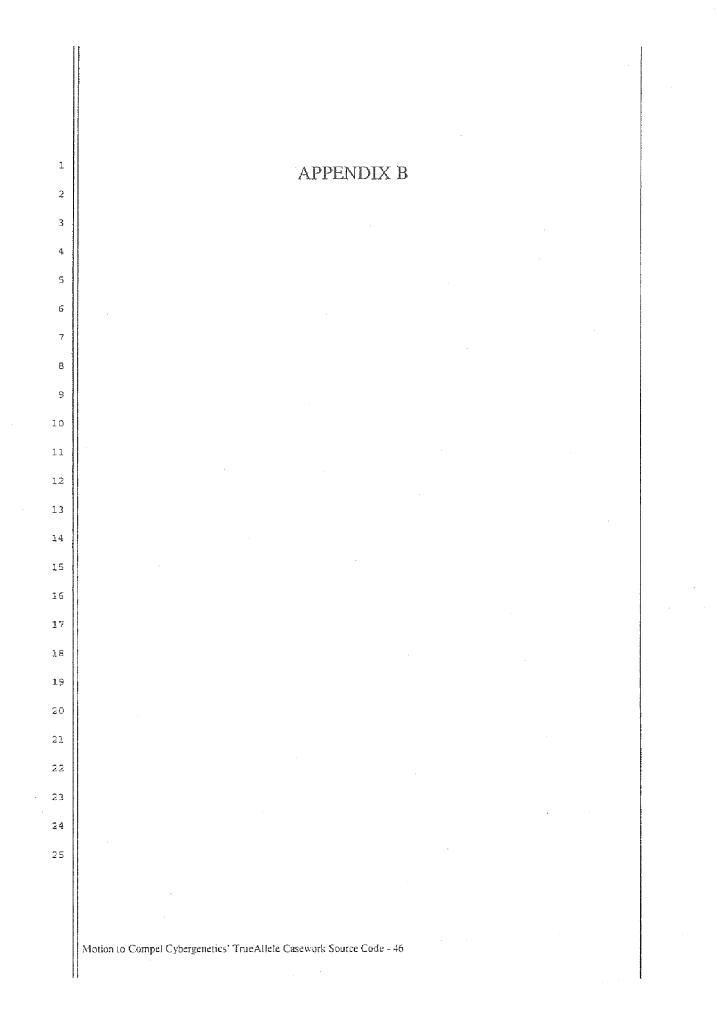
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	STATE OF WASHINGTON,	Case No. 10-1-09274-5 SEA
1.0	Plaintiff,	Case 110-1-07274-5 512A
11.		MOTION TO COMPEL
12	VS.	CYNERGENETICS' TRUEALLELE CASEWORK SOURCE CODE (PART 2)
13	Emanuel Fair,	
	Defendant	
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DECLARATION OF DR. DAN E. KRANE

I, Dan E. Krane, Ph.D., declare I have personal knowledge of the following, and if called upon to do so, could and would testify competently to the matters contained herein.

I am a Professor of Biological Sciences (with a courtesy appointment in the Department of Computer Science) at Wright State University in Dayton Ohio. I have recently completed a one-year term as a fellow of the American Council on Education at the University of Notre Dame in Notre Dame, Indiana. I have a B.S. degree with a double major in Biology and Chemistry from John Carroll University (Cleveland, Ohio), and a Ph.D. from the Biochemistry program of the Cell and Molecular Biology Department of the Pennsylvania State University (State College, Pennsylvania). I have also done postdoctoral research using the tools of molecular biology to answer questions in the fields of population genetics and molecular evolution in the Genetics Department of the Washington University Medical School (St. Louis, Missouri) and in the Department of Organismic and Evolutionary Biology of Harvard University (Cambridge, Massachusetts). I have published more than 50 scholarly papers in a variety of topics including population genetic studies of the genetic diversity of human populations at DNA typing loci, of organisms exposed to environmental stressors, and the use of DNA typing in forensic science. I am also the lead author of a widely used undergraduate textbook, Fundamental Concepts of Bioinformatics. I was a founding member of and two-time gubernatorial appointee to the Commonwealth of Virginia's Scientific Advisory Committee, a 12-member panel established by statute to provide oversight and guidance to the Virginia Department of Forensic Science (the crime laboratory for the Commonwealth of Virginia). I have testified in more than 110 criminal proceedings

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that have involved forensic DNA typing (in 23 different state and district courts, several courts martial, and in three different Federal courts within the United States, a Coronial Inquest in the State of Victoria in Australia, in Belfast Crown Court in Northern Ireland, the Black Friar's Court and the Central Criminal Court of London and in Oxford Crown Court in England).

I have been asked by attorney Ben Goldsmith to assist with the evaluation of results generated by TrueAllele® in the case of WA vs. Emanuel Demelvin Fair. I am familiar with the work of Dr. Mark Perlin and his expert system, TrueAllele®. I have reviewed results generated by TrueAllele's® in approximately ten criminal cases over the course of the past three years. I am very familiar with the conventional interpretation of DNA test results (e.g. as done by human experts without the assistance of probabilistic genotyping software like TrueAllele®).

I have read Dr. Perlin's publications regarding the TrueAllele® expert system. Among those publications is one in which Dr. Perlin describes TrueAllele®'s probability model
 ["Cybergenetics TrueAllele Technology Enables Objective Analysis of Previously Unusable DNA Evidence" (available at -

http://www.inathwersts.com.compenvinevisioners articles evbergenetics-inicalleletechnology-enables-objective-analysis-of-previously-unusable-dna-evidence.htmi)]. That publication states:

"This model incorporates several hundred variables, including the unknown genotypes of individuals contributing to the sample, DNA quantities, amplification artifacts that distort the signal, and the uncertainties of these variables. Many of the variables are hierarchical, which means they include submodels, each with their own

parameters and uncertainties."

Dr. Perlin has not provided any validation studies or published, third-party reviews of the hundreds of variables or their submodels and their associated uncertainties, boundaries, and interrelationships that constitute the underlying probability model of TrueAllele®. It is important to know how the value of each of these hundreds of variables and uncertainties is determined by TrueAllele®, how those values and uncertainties affect TrueAllele®'s analysis, and if an alternative implementation of this method would deliver a different, reasonable explanation of the data being evaluated.

4. The single best way to evaluate TrueAllele®'s probability model is through a review of its underlying source code. Source code is "a code written in a high-level or assembly language, which is converted into object code by a compiler, assembler, or interpreter; a program in a source language."⁴ Source code is the precise yet human-readable description of the sequence, branches, and loops of computer instructions that constitute a computer program. While peer-reviewed articles are important parts of demonstrating scientific *concepts*, source code serves as the *implementation* of those concepts. In this sense source code is directly analogous to the standard operating procedures that describe the implementation of the concepts that underlie a laboratory's testing methodology. It would be difficult to find a DNA profiling expert who felt that a list of the approaches that were used to generate a DNA profile (e.g. PCR amplification of short, tandem repeats followed by capillary electrophoresis) could possibly take the place of a review of a laboratory's standard operating procedures that describe the implementation of that

¹ from the Oxford English Dictionary.

methodology. In much the same way, it would be difficult to find a computer scientist that accepted that a computer program's reliability could be assessed without having access to the program's source code.

5.

Computer software can be validated at several different levels. In the most superficial sense, software can be tested by evaluating the results it generates when provided with certain inputs. More substantive validation studies evaluate the input and output of individual components of a program's subcomponents or of modules that contain multiple components. "Black box" and "white box" testing roughly describe these two different kinds of software testing approaches. Black box testing requires little or no knowledge of the internal components of a computer program. White box testing requires knowledge of the internal components of a computer program (typically a combination of software design documents and source code). Some software engineers advocate black box testing because it evaluates the correctness of the output with respect to only the input and not the working of internal components. However, software (like TrueAllele®) that produces likelihood ratios (LRs) cannot be validated with only black box testing because the *correct* answer cannot be known (and therefore cannot be compared to the results generated by the program). Christopher Steele and David Balding in the "Quality of Results" section of their article "Statistical Evaluation of Forensic DNA Profile Evidence" (available at -

http://www.annuslaeviews.org.doi.pdf/10.146/annurev-statistics-022f/03-115602) make this point:

"Laboratory procedures to measure a physical quantity such as a concentration can be validated by showing that the measured concentration consistently lies within an

acceptable range of error relative to the true concentration. Such validation is infeasible for software aimed at computing an LR [likelihood ratio] because it has no underlying true value (no equivalent to a true concentration exists). The LR expresses our uncertainty about an unknown event and depends on modeling assumptions that cannot be precisely verified in the context of noisy CSP [crime scene profile] data."

 Professor Balding makes the point again in 2013 in the prestigious Proceedings of the National Academy of Sciences, USA when he says:

> "There is no 'gold standard' test of an LR calculation for LTDNA profiles. Likelihoods reflect uncertainty, and even when the profiles of the true contributors are known in an artificial simulation, this does not tell us what is the appropriate level of uncertainty justified by a given observation affected by stochastic phenomena. Likelihoods depend on modeling assumptions, and there can be no 'true' statistical model for a phenomenon as complex as an LTDNA profile."²

7. "The Case for Open Computer Programs" (available at -

http://www.nature.com/nature/jagmal/y422/17586/pdf/nature1(836.pdf) summarizes the need for review of source code:

"Our view is that we have reached the point that, with some exceptions, anything less than release of actual source code is an indefensible approach for any scientific results that depend on computation, because not releasing such code raises needless, and needlessly confusing, roadblocks to reproducibility."

² D. J. Balding, "Evaluation of mixed-source, low-template DNA profiles in forensic science.," Proc. Natl. Acad. Sci. U. S. A., vol. 110, no. 30, pp. 12241-6, Jul. 2013. Available at - <u>http://www.pnas.org/content/110-30/12241.ful.</u>

 Steele and Balding (in "Statistical Evaluation of Forensic DNA Profile Evidence") also observe that:

> "Some progress can be made in evaluating the validity and performance of software. Courts need these kinds of evaluations to have confidence in the results of softwarebased forensic analyses. Open source software is highly desirable in the court environment because openness to scrutiny by any interested party is an invaluable source of bug reports and suggestions for improvement."³

9. An international body, the International Society for Forensic Genetics (ISFG), has also published a set of recommendations regarding probabilistic genotyping methods such as TrueAllele®. One of those recommendations speaks specifically to the desirability of openness to independent review of source code:

"(w)e do not advocate a 'black box' approach" and "(o)pen source is strongly encouraged since this solution offers unrestricted peer review and best assurance that the methods are fit for purpose."⁴

Others who have critically evaluated TrueAllele® have noted significant concerns about the model it uses and the implementation of that model even without access to the TrueAllele® source code. For instance, in a validation study conducted by the California Department of Justice, Steven Meyers noted:

"Precision was measured as the proportion of pairwise comparisons that were in the

⁴ Gill et al (2012) FSIG 6:679-688.

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³ C. D. Steele and D. J. Balding, "Statistical evaluation of forensic DNA profile evidence," Annu. Rev. Stat. Its Appl., vol. 1, pp. 361–384, 2014.

ranges of 0 - 0.3 and 0 - 1.0 log LR_H units. This corresponds to LRs within 2X and 10X of each other, respectively

Overall, TrueAllele Casework had 41.67% within 0.3 log units, and 70.09% of the pairwise comparisons within one log unit. These values are elevated somewhat by the pairs of interpretations that obtained identical LRs that should not have occurred given the randomness of the MCMC process. When the pairs with at least one LR = 0 result are removed from consideration, the maximum difference was 15.8 log units, which corresponds to a factor of - 6.5 quadrillion. As observed in the graphs, many deviations were observed that could lead to different conclusions about the strength of the evidence (e.g., $LR \ll 1$ in one interpretation becoming $LR \gg 1$ in another). It is acknowledged that some of these results may be due to interpretations where the MCMC process didn't explore the space well, or where the chains had not reasonably converged. A more in-depth examination of the Mx chains and genotype weights might have eliminated some runs from comparison. However, this highlights that more subjective evaluations and more computer interpretation time (3-4 days/interpretation for TrueAllele vs. < I day/per interpretation for STRmix) would be required for TrueAllele than for STRmix."5 This concern seems to specifically apply to the TrueAllele® results in the case of WA vs. Fair in that there are some reported LRs that are very different from others for the very same test results of individual samples.

⁵ Myers, Steven P. "STRmix V1.0.7.49 and V2.0 TrueAllele Casework, Interpretation of Complex DNA Mixtures – Part II: 3-Person Mixtures" (validation study). California Department of Justice. 2014.

 Similarly, an evaluation of TrueAllele®'s stutter models by a government testing laboratory in New South Wales, Australia found that:

> "there is a lack of consistency in stutter modelling. An example of this is seen in comparison of FGA in sample S0026 to D8 in the Foley case analysed and reported by Cybergenetics. The mixture in the Foley case was recovered from the fingernail of the victim and was of a very similar mixture proportion to S0026 with a minor contributor weight of 7%.

> Comparison of the pattern view for D8 (Foley) and FGA (SOO26) shows a different pattern of stutter. In Foley, the data for D8 can be seen to deal with peaks in stutter positions as expected by human review, but it does not seem to be modelling stutter in the same way for S0026....

The Cybergenetics response to a query in regard to Foley vs. S0026 was as follows: This 7% mixture (S0026) with two unknown contributor genotypes is a very different problem from the far simpler Foley case, where there was only one unknown genotype and a known victim reference profile was available. In Foley, coancestry was not considered: in that context, the match scores of the two S0026 repetitions (with theta = 0) were 10^6.2395 (1.74 million) and 10^3.5046 (3,196). In practice, since the larger objectively inferred LRs tend to be more accurate, we would have repeated the request to confirm the million fold LR result. The Explain window does not use the posterior probability distribution of stutter at a locus. Instead, it shows only an instant snapshot of the state of the memory less Markov chain. We only use the Explain interface for teaching purposes, and never to assess data or results.

The TrueAllele version 25 stutter models are the same in this problem as they were in Foley.⁹⁶

Stutter is a very commonly encountered technical artifact associated with short tandem repeat test results such as those that were analyzed by TrueAllele® in the case of WS vs. Fair.

- 12. A review of the TrueAllele® source code used in the case of WA vs. Fair would allow the following:
 - 12.1. A determination of what computations were performed by TrueAllele®.
 - 12.2. A determination of the scientific accuracy of the results of these computations by:
 - 12.2.i. Evaluating whether the computations performed by TrueAllele® and TrueAllele®'s resulting conclusions in the case of WA vs. Fair are consistent with the published claims of Dr. Perlin.
 - 12.2.ii. Evaluating whether these computations and conclusions are consistent with generally accepted principles that are routinely employed by human experts during the course of forensic DNA testing.
 - 12.3. A determination of if these methods were properly translated from concept to source code and that no mistakes were made during the writing of TrueAllele®'s code. This would allow it to be determined if translation

⁶ NSW Review Team. Phase 1 Evaluation Report of the Cybergenetics TrueAllele® Expert. System. New South Wales Police Force. 2011.

from concept to source code included any ambiguously described concepts that, in turn, led to unfounded assumptions in the source code.⁷

- 12.4. A determination of whether alternative explanations of the observed data could have produced similar results to those produced by TrueAllele® in this case.
- 13. Put simply, it is important to know precisely why and how TrueAllele® arrived at the results that it arrived at in the case of WA vs. Fair. A careful evaluation of the computational steps taken by TrueAllele® would allow it to be determined if the program: 1) reflects what is described by Dr. Perlin, 2) is consistent with the practices of the forensic DNA profiling community, 3) is free from bugs and errors, and 4) if TrueAllele® can and does provide sufficient explanations for the observed data in this case.

14. In addition to the source code of TrueAllele®, it is important to evaluate the data

⁷ "The Case for Open Computer Programs" describes this as "the curse of ambiguity." "Ambiguity in program descriptions leads to the possibility, if not the certainty, that a given natural language description can be converted into computer code in various ways, each of which may lead to different numerical outcomes. Innumerable potential issues exist, but might include mistaken order of operations, reference to different model versions, or unclear calculations of uncertainties. The problem of ambiguity has haunted software development from its earliest days... [It] is not necessarily the result of incompetence or bad practice. It is a natural consequence of using natural language and is unavoidable."

generated by TrueAllele & during the course of its analysis of the evidence in the case of WA vs. Fair and to evaluate how it progressed through the program. This preserved data serves as a snapshot of the state of the running TrueAllele® program at each point during the course of its analysis. The intermediate data is especially important in the evaluation of non-deterministic algorithms like the Metropolis-Hastings Markov chain Monte Carlo (MCMC) that are used by TrueAllele®. By their very nature algorithms such as these are very unlikely to arrive at the same exact answer twice. The degree to which a program's intermediate results vary and the methods that are used to "hone in" on the final result are critically important in such analyses and must be assessed for there to be confidence in the program's final conclusions. The variance of results produced by this type of algorithm can be affected by the starting value used for its Markov Chain: its acceptance ratio; the number of cycles performed; the number of cycles whose data were discarded; any fixed values that might serve as Markov Chain starting points, and many other factors that are not described in any of Dr. Perlin's publications. The approach used by TrueAllele® requires components so numerous that they could be adequately described in peer-reviewed publications.

15. Every software program has boundaries and limitations as to what it can do when given a specific task and a set of data as input. A description of a system's limitations plays a fundamentally important role in establishing an appropriate degree of confidence in its operation and results. A code review should include an evaluation of pre- and post-conditions that serve as self-checks within the program to ensure proper operation. If these conditions are not met by any component during a program's operation, then the program must either avoid using that component or (if no other computational pathway is

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available) report an error. I am unaware of any reported errors during the operation of TrueAllele® in the case of WA vs. Fair or of what, if any, self-checks were conducted by TrueAllele® that resulted in TrueAllele® performing corrections on its own data or avoiding potential computational pathways. Human experts are expected to explain how they arrive at a conclusion using alternative approaches when their preferred means of analysis fail in the context of a specific case's data. This same expectation can and should apply to a computer program such as TrueAllele®.

One deliverable from a review of the TrueAllele® source code that is likely to be particularly helpful to Mr. Goldsmith in his understanding of Dr. Perlin's supplemental report in this case would be a detailed flow chart that outlined what operations were performed and in what order as TrueAllele® evaluated the test results that were provided to it as input. A fair characterization of the understanding of that flow chart that can be made at the present time is "TrueAllele® was given input data that human analysts felt was sufficiently complicated that it was not suitable for conventional interpretation; TrueAllele® evaluated many different aspects of that data; TrueAllele® arrived at a conclusion regarding that data." A human expert that used that approach to explain how they arrived at a conclusion regarding a complicated analysis would not (and should not) be considered to be credible. It is not possible to assess or confront TrueAllele®'s conclusions without a particularized understanding of the analysis it performs and that cannot be accomplished without a review of its source code.

I have no interest in infringing upon Dr. Perlin's proprietary interest in the TrueAllele® 17. source code. However, scientific principles dictate that new manners of applying methodologies should be made available for outside review and confirmation before they 12

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are relied upon for any significant finding. It is essential that the TrueAllele® model and the specific implementation of that model are carefully evaluated before they are relied upon in a criminal proceeding such as WA. vs. Fair.

I declare the above is true and correct under the penalty of perjury under the laws of the State of Washington, executed this 4th day of March, 2016, in Dayton Ohio.

Dan E. Harane

Dan E. Krane

Curriculum Vitae

Name: Dan E. Krane

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Phone: (937) 775-2257 (lab) (937) 775-3320 (FAX) (937) 426-9270 (office)

Educational background:

B.S. (1985) in Biology and Chemistry at John Carroll University, University Heights, OH

Ph.D. (1990) Biochemistry program of the Department of Molecular and Cell Biology, The Pennsylvania State University, University Park, PA

Research interests: Molecular and genome evolution; human population substructuring; forensic DNA profiling; bioinformatics.

Training and positions held:

- Undergraduate researcher (1984-1985) Department of Chemistry, John Carroll University
- Graduate assistant (1985-1990) Department of Molecular and Cell Biology, The Pennsylvania State University
- Participant (1988) UCLA International School on Molecular Evolution

Research Associate (1990-1991) Howard Ochman and Daniel L. Hartl's laboratory, Department of Genetics, Washington University School of Medicine

- Research Associate (1991-1993) Daniel L. Hartl's laboratory, Department of Organismic and Evolutionary Biology, Harvard University
- Assistant Professor (1993-2000) Department of Biological Sciences, Wright State University.
- Affiliate Member of the Biomedical Sciences faculty (1994-1995) Wright State University,
- Associate Member of the Biomedical Sciences faculty (1995-present) Wright State University.
- Associate Professor (2000-2007) Department of Biological Sciences, Wright State University.
- Associate Director, Biomedical Sciences PhD program (2000-2002) Wright State University.
- President, CEO and Senior Analyst, Forensic Bioinformatics, Inc. (2002-present).
- Graduate Faculty, Wright State University Microbiology and Immunology Program (2003-present) Environmental Sciences Ph.D. Program (2003-present).

Professor (2007-present) Department of Biological Sciences, Wright State University.

University Faculty President (2011-present), Wright State University.

Awards, honors and grant support:

- American Institute of Chemists Student Research and Recognition Foundation Award (1985).
- Pella Fay Braucher Scholarship from The Pennsylvania State University College of Science (1985).
- UCLA International School on Molecular Evolution Fellowship (1988).
- The R. Adams Dutcher Fund Award from The Pennsylvania State University Biochemistry Program (1990).
- The W. R. Keck Fellowship from the Washington University School of Medicine (1990).

Collegium Summer Institute on Faith and Intellectual Life Fellowship (1993).

- Wright State University Alumni Grant for "Computer assisted DNA analysis" for \$2,650 (1993).
- Research Challenge Grant for \$25,000 from Wright State University (1994) for "The influence of regional GC-content on neutral substitutions".
- Finalist, "Teacher of the Year Award," Wright State University, College of Science and Mathematics (1994, 1995, 1997 and 2002).
- The Dean of the College of Science and Mathematics "Special Award for Outstanding Teaching." Wright State University, College of Science and Mathematics (1995).
- Principal investigator: Ohio biological survey for \$500 for "Molecular characterization of Black and Sugar Maples in Ohio." (1995-1996).
- Honorary induction into Alpha Lambda Delta, the National Academic Honor Society for Freshmen (1996).
- "Teacher of the Year Award," Wright State University, College of Science and Mathematics (1997 and 2008).
- Co-investigator (G. Allen Burton, project director): U.S. EPA grant for \$61,814 for "Assessment of sediment quality in the Black River." (1997).
- Co-investigator (G. Allen Burton, project director): U.S. EPA grant for \$449,499 for "Sediment contamination assessment methods: Validation of standardized and novel approaches." (1997).
- Principal investigator: U.S. EPA grant for \$420.277 for "Intraspecies genetic diversity measures of environmental impacts." (1998-2002).
- Principal investigator: Wright State University Early Start/Augmentation grant for \$17.998 for "DNA quantification center for assessing changes in genetic diversity levels" (1999).
- Principal investigator: Ohio biological survey for \$500 for "Survey of the terrestrial isopods of Ohio." (1999-2000).
- Principal investigator: Ohio biological survey for \$500 for "Survey of the Chironomid species of Ohio." (2001-2002).

Awards, honors and grant support (continued):

- Principal investigator: Various sources of compensation for consulting regarding forensic DNA analyses made payable to Wright State University for approximately \$125,000. (1993-2002).
- Principal investigator: Wright State University Technology Commercialization Initiative Grant for \$99,985 for "Commercialization of DNA profiling expertise." (2001-2002).
- Co-investigator (Mike Raymer, PI): National Science Foundation (Computer Science Directorate) grant for \$542,056 (\$47,254 under the direct control of D. E. Krane) for "Crossing the interdisciplinary barrier: An integrated undergraduate program in bioinformatics." (2001-2005).
- Co-investigator (Keith Grasman, Pl): Wright State University College of Science and Mathematics Research Incentive Fund project for \$30,000 for "Environmental health assessments using toxicogenomic technologies." (2001-2003).
- Co-investigator (Gerald Alter, PI): Wright State University College of Science and Mathematics Research Incentive Fund project for \$30,000 for "Establishing an applied biomedical computing center: Using the nucleotide excision repair complex as a paradigm." (2001-2003).
- Co-investigator (with Keith Grasman): Canadian Wildlife Service (Toronto, ON office) for \$5,000 for "The effects of environmental contaminants on sex ratios in young herring gulls in areas of concern." (2001-2002).
- Co-Investigator: State of Ohio Biotechnology Research and Technology Transfer grant for \$5.5 million (\$1.9 million to Wright State University; \$600,293 for bioinformatics work; \$33,273 under the direct control of D. E. Krane) (2002-2005).
- Principal investigator: Wright State University Technology Commercialization Initiative Grant for \$9,007 for "Developing software that generates forensic DNA profiles and meaningful statistics from mixed evidence samples." (2006).
- Co-investigator (with Joe Bartoszek): Systematics Research Fund for \$1,122 for "Phylogeny of hybrid unisexual Ambystomatid salamanders, a new genome." (2008-2009).
- Principal investigator: Research Initiative Grant from Forensic Bioinformatics, Inc. for \$53,338 for "Persistence and Transfer of STR DNA profiles." (2010-2012).
- Principal investigator: Wright State University Teaching Innovation Grant for \$4,270 for "Engaging students in forensic DNA profiling." (2012-2013).
- Omnicron Delta Kappa, Honorious Causa member, Wright State University Circle, National Leadership Honorary Society, 2012.

Fellow, American Council on Education Leadership Development Program, 2014-2015 cohort.

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- Krane, D. E. and R. C. Hardison. 1990. Short interspersed repeats in rabbit DNA can provide functional polyadenylation signals. Mol. Biol. Evol. 7:1-8.

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- Hardison, R. C., D. E. Krane, D. J. Vandenberg, J.-F. Cheng, J. Mansberger, J. A. Taddie, S. Schwartz, X. Huang and W. Miller. 1991. Sequence and comparative analysis of the rabbit alpha-like globin gene cluster reveals a rapid mode of evolution in a G+C rich region of mammalian genomes. J. Mol. Biol., 222:233-249.
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 Hardison. 1991. Intragenic sequences and proteins regulating the rabbit α-globin gene. Pp. 220-234 in G. Stamatoyannopoulos and A. W. Nienhuis, eds. The regulation of hemoglobin switching. Johns Hopkins University Press, Baltimore.
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Presentations:

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- Krane D. E. July, 1988. Subfamily relationships and the structure of rabbit C repeats. UCLA school on molecular evolution, The University of California, Los Angeles.
- Krane D. E., and R. C. Hardison. July, 1989. Rabbit C repeats and their role in the evolution of the rabbit genome. Eighth summer symposium in molecular biology – DNA protein interactions. The Pennsylvania State University.
- Krane D. E. April, 1990. The molecular evolution of a short repetitive element in rabbits. Biology departmental seminar, University of Illinois at Champagne-Urbana.

- Krane, D. E. and R. C. Hardison. May, 1990. Short interspersed repeats in rabbit DNA propagated by successive waves of retrotransposition. ASMBM/AAI 1990 Meeting.
- Hardison, R. C., S. E. Yost, M. James-Pederson, D. E. Krane and J. Xu. May, 1990. Intragenic sequences and protein factors regulating expression of the rabbit alpha-globin gene. ASMBM/AAI 1990 Meeting.
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- Krane, D. E. February, 1991. A new method for the analysis of the compartmentalization of vertebrate genomes. Biology and Chemistry Departments, John Carroll University, University Hts., OH.
- Krane, D. E. July. 1991. Analyses of the isochore structure of eukaryotic genomes. St. Louis Red Cross, St. Louis. MO.
- Krane, D. E. June, 1992. DNA profiling and the implications of population substructuring. Merimac Community College summer seminar series for gifted students, St. Louis, MO.
- Krane, D. E. October, 1992. Population genetics and forensic DNA typing. North Carolina Biotechnology Center/BASF Corporation Lecture Series in Biotechnology, The University of North Carolina at Charlotte.
- Krane, D. E. December, 1992. DNA profiling: A primer. Special seminar for the Missouri State Trial Lawyers Association, St. Louis, MO.
- Krane, D. E. March. 1993. Unresolved issues in the forensic application of DNA profiling. Department of Biology, Morehead State University, Morehead, KY.
- Krane, D. E. February, 1994. The structure and evolution of warm-blooded vertebrate genomes. Department of Biochemistry and Molecular Biology, Wright State University, Dayton, OH.
- Krane, D. E. April, 1994. A homogenating bias in the accumulation of mutations in primate isochores. Museum of Comparative Zoology, Harvard University, Cambridge, MA.
- Krane, D. E. and D. Barr. May, 1994. Evolutionism vs. Creationism on "Current Perspectives: WAZU (102.9 FM), Dayton, OH.
- Krane, D. E. and R. Keyes. May, 1994. Evolution/Creation Discussion, sponsored by the Wright State University Campus Crusade for Christ, Dayton, OH.
- Krane, D. E., M. Malinowski, E. W. Morgan and B. Gorman. January, 1995. Scientific Evidence on Trial. Wright State Policy Forum, Dayton, OH.

- Krane, D. E. February, 1995. Forensic applications of DNA. The Dayton Sertoma Club, Dayton, OH.
- Krane, D. E. April, 1995. DNA forensics. 1995 Bi-state conference of the Indiana and Ohio Societies for Clinical Laboratory Science, Fairborn, OH.
- Krane, D. E. June, 1995. Computer applications in DNA analyses. 1995 Regional meeting of the Academic Computing Society, Dayton, OH.
- Krane, D. E. December, 1995. Forensics in the '90's. The University of Cincinnati and Benjamin/Cummings. Cincinnati, OH.
- Krane, D. E. February, 1996. Polymorphisms at hypervariable loci and human population substructuring. Heidelberg College, Tiffin, OH.

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- Krane, D. E. January, 1997. Minor shifts in genomic GC-content alter amino acid fixational bias. International Society of Molecular Evolution meeting, Guanacaste, Costa Rica.
- Krane, D. E. February. 1997. The potential and pitfalls of DNA profiling. The Harvard Club of Dayton, Dayton, OH.

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Krane, D. E. March, 1998. The influence of large-scale genomic context upon amino acid replacements. The Pennsylvania State University, Department of Biology, State College, PA.

Stemberg, D. V., G. A. Burton, D. E. Krane and K. Grasman. April, 1998. Randomly amplified polymorphic DNA markers in determinations of genetic variation in aquatic species affected by stressors. Annu. Meeting Central Great Lakes Regional Chapter Society of Environmental Toxicology and Chemistry. East Lansing, MI.

York, Allen J. and D. E. Krane. April, 1997. Evolution and function of highly repeated short sequences within the rabbit genome. (OH. J. Sci., 98:7). 107th meeting of the Ohio Academy of Science, Middletown, OH.

Skepner, Adam P. and D. E. Krane. April, 1997. Molecular analyses
 reveal genetic similarity of *Acer saccharum* and *Acer nigrum*. (OH. J. Sci., 98:14). 107th meeting of the Ohio Academy of Science, Middletown, OH.

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Grunwald, B., S. A. Roush, and D. E. Krane. November, 1999. Genetic diversity measures of terrestrial isopods as ecoindicators. Society of Environmental Toxicology and Chemistry 20th annual meeting, Philadelphia, PA.

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Krane, D. E. May, 2000. Genetic diversity measures of environmental impacts. 2000 STAR Ecosystem Indicators Progress Review Workshop, Las Vegas, NV.

- Krane, D. E. May, 2000. Effects of stressors on genetic diversity in naturally occurring populations, Ohio Valley Chapter of SETAC, 17th annual meeting, College Corner, OH.
- Newburn, E. and D. E. Krane. August. 2000. Molecular Identification Markers of Chironomid Species for Use as an Ecoindicator of Aquatic Systems, Poster and abstract, American Chemical Society National Meeting, Washington D.C.
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- Krane, D. E. December, 2000. Correlations between genetic diversity and exposure to stress, Biology Departmental Seminar, Akron University, Akron, OH.
- Krane, D. E. January, 2001. Business opportunities in the area of DNA consulting. Information Technology Research Initiative. Executive Board Meeting, Wright State University, Dayton, OH.
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- Schmidt, S., D. Cipollini, and D. E. Krane. April, 2001. RAPD-PCR assessment of the genetic diversity within *Alliaria petiolata*. Ohio Academy of Sciences 111 th meeting, Tippin, OH.
- Burton, G. A., M. Morris, D. E. Krane, K. Grasman, W. Carmichael, S. Berberich, D. Organisciak and J. Lucot. April, 2001. Human and environmental risk assessment related research at Wright State University. EPA/DOD special conference on toxicology, Dayton. OH.
- Krane, D. E. May, 2001. Hallmarks of research and forensic science. Third annual DePaul University Law School and Cook County Public Defenders' short course on DNA analysis, Chicago, IL.
- Krane, D. E. August, 2001. Genomes as information storage systems. Summer Institute on Advanced Computation, Wright State University, Dayton, OH.
- Krane, D. E. September 2001. Genetic diversity of naturally occurring populations as an ecoindicator. Biology Departmental Seminar, Northern Kentucky University. Highland Heights, KY.
- Krane, D. E. September, 2001. The potential and pitfalls of forensic DNA profiling. Sigma Xi Distinguished Lecturer Series. Northern Kentucky University, Highland Heights, KY.
- Krane, D. E. September, 2001. The science behind forensic DNA profiling. Engineer's Club of Dayton Sertoma lecture series. Dayton, OH.
- Doom, T, M. Raymer, D. Krane and O. Garcia. February, 2002. A proposed undergraduate bioinformatics curriculum for computer scientists. Proceedings of the 2002 ACM Special Interest Group on Computer Science Education (SIGCSE 2002), Covington, KY.
- Krane, D. E. May. 2002. Genophiler: Advantages of automated review of forensic DNA evidence. Fourth annual DePaul University Law School and Cook County Public Defenders' short course on DNA analysis, Chicago, IL.
- Krane, D. E. June, 2002. Reaching out to computer science and biology majors interested in bioinformatics – at the same time. Introducing Bioinformatics to Undergraduate Curricula Conference, hosted by Wheaton College, Norton, MA.
- Krane, D. E. March, 2003. Commercialization: Why do it? Ohio Valley Affiliates for Life Sciences, Kingsgate Conference Center, Cincinnati, OH.
- Gilder, J. R., D. E. Krane, T. E. Doom and M. L Raymer. April, 2003. Identifying patterns in DNA change. Proceedings of the 2003 Midwest Artificial Intelligence and Cognitive Science Conference (MAICS 2003; 34, 78-84). Cincinnati, OH.

- Gilder, J., S. Ford, M. Raymer, T. Doom and D. Krane. September, 2003. Differences in electropherogram peak heights reported by different versions of the GeneScan software. Promega Meeting. Phoenix, AZ.
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- Krane, D. E. October, 2003. Evaluating forensic DNA evidence. Indiana State Investigators Meeting, Indianapolis. IN.
- Krane, D. E. October, 2003. Bioinformatics education: Crossing the interdisciplinary boundary. Keynote address; Bio21: Teaching Biology with Bioinformatics, Chapel Hill, NC.
- Krane, D. E. November, 2003. Evaluating forensic DNA evidence. Virginia State Bar Association Capital Litigation Meeting, Richmond, VA.
- Krane, D. E. December, 2003. Evaluating forensic DNA evidence. Indiana Public Defender's Capital Litigation Meeting, Indianapolis, IN.
- Krane, D., M. Raymer and T. Doom. March, 2004. Bioinformatics at Wright State University. Ohio Valley Affiliates for Life Sciences, University of Louisville, Louisville, KY.
- Converse, K. and D. Krane. March, 2004. Forensic DNA testing and review. "Life in the Balance" conference and annual meeting of the National Association of Criminal Defense Lawyers, Memphis. TN.
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- Krane, D. E. April. 2004. Evaluating forensic DNA evidence. "Mindful Explorations" seminar series funded by the William H. and Jean R. Reller Endowment, Indiana University East, Richmond, IN.
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- Krane, D. E. October, 2004. Evaluating forensic DNA evidence. Mississippi Public Defenders' Capital Litigation Meeting. Biloxi, MS.
- Thompson, W. C. and D. E. Krane. February, 2005. Evaluating forensic DNA evidence. National Association of Criminal Defense Lawyers Annual Meeting. featured presentation, New Orleans, LA.
- Krane, D. E. April, 2005. Evaluating forensic DNA evidence. Cuyahoga County Capital Litigation Seminar, Cleveland, OH.

- Krane, D. E. April, 2005. The strengths and weakness of forensic DNA profiling techniques. Biology departmental seminar, John Carroll University, University Heights, OH.
- Krane, D. E. April, 2005. Deciphering the human genome with bioinformatics techniques. Café Scientifique Seminar Series. Cox Arboretum, Dayton, OH.
- Krane, D. E. May, 2005. Objective interpretation of forensic DNA testing evidence. Seventh annual DePaul University Law School and Cook County Public Defenders' short course on DNA analysis, Chicago, IL.
- Krane, D. E. and W. C. Thompson. July, 2005. Evaluating forensic DNA evidence. North Carolina Academy of Defense Lawyers, Sunset Beach, NC.
- Krane, D. E., T. E. Doom and M. L. Raymer. August, 2005. Assessing the implications for close relatives in the event of similar but non-matching DNA profiles. Fourth annual Expert Forum on the Science of DNA Profiling, University of Dayton School of Law, Dayton, OH.
- Heizer, E. and D. Krane. September. 2005. Correlation between major codon usage and amino acid biosynthetic costs in eight prokaryotic species. Wright State University Biology Department Research Forum, Dayton, OH.
- Sharma, M. and D. Krane. September, 2005. Molecular characterization of Chironomid Species and their use as bioindicators. Wright State University Biology Department Research Forum, Dayton, OH.
- Gilder, J. R. and Krane, D. E. October, 2005. Objective evaluation of DNA evidence. Indiana University East. Richmond, IN.
- Krane, D. E. October, 2005. Evaluating forensic DNA evidence: What software can and cannot do. Illinois Institute for Continuing Legal Education Death Penalty Litigation Seminars, Springfield, IL.
- Rowland, C, R. Van Trees, M. Taylor, and D. Krane. February, 2006. Was the Shawnee war chief Blue Jacket a Caucasian? 58th Annual Meeting of the American Academy of Forensic Sciences, Seattle, WA.
- Krane, D. E. March, 2006. Essential elements of a review of forensic DNA profile evidence. National Legal Aid and Defender Association National Meeting, Philadelphia, PA.
- Krane, D. E. March, 2006. Objective characterization of technical artifacts in forensic DNA profiles. Illinois Institute for Continuing Legal Education Scientific Evidence Seminars, Chicago, IL.
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- Gilder, J. R., T. E. Doom, M. L. Raymer, K. Inman, and D. E. Krane. April, 2006. Resolution of forensic DNA mixtures. Annual Meeting of the Ohio Academy of Science, Dayton, OH.
- Krane, D. E. May, 2006. Familial searches and debating the significance of DNA database "cold hits." Illinois Institute for Continuing Legal Education Death Penalty Litigation Seminars, Springfield, IL.

- Krane, D. E. May, 2006. GenoStat®: A user-friendly alternative to PopStats for calculating random match probabilities. Eigth annual DePaul University Law School and Cook County Public Defenders Seminar Series on DNA Analysis, Chicago, IL.
- Raiford, D. W. D. E. Krane, T. E. Doom and M. L. Raymer. July, 2006. An investigation of codon usage bias: Isolation and visualization of translation bias in organisms exhibiting multiple biases. The Ohio Collaborative Conference on Bioinformatics, Athens, OH.
- Krane, D. E., T. E. Doom and M. L. Raymer. August, 2006. Run-specific limits of quantitation and detection (an alternative to minimum peak height thresholds for DNA profile analyses). Fifth annual Expert Forum on the Science of DNA Profiling, Sinclair Center, Dayton, OH.
- Krane, D. E. September, 2006. Evaluating forensic DNA evidence. Wright State University Department of Biological Sciences departmental seminar, Dayton, OH.
- Krane, D. E. and R. Cassanova. September, 2006. Evaluating forensic DNA evidence. Indiana Public Defender's Capital Litigation Meeting, Indianapolis, IN.
- Raiford, D. W., D. E. Krane, T. E. Doom, and M. L. Raymer. October, 2006. Isolation and visualization of codon usage biases. Proceedings of the 6th IEEE Symposium on Bioinformatics and Bioengineering (BIBE 2006), Washington, DC.
- Krane, D. E. October, 2006. Evaluating forensic DNA evidence. Illinois Continuing Legal Eduction (ICLE) program, Springfield, IL.
- Krane, D. E. December, 2006. Amino acid cost and codon usage biases in six prokaryotic genomes: A whole genome analysis. Oklahoma State University Microbiology Department Seminar, Stillwater, OK.
- Krane, D. E. February, 2007. Run-specific limits of quantitation and detection (an alternative to minimum peak height thresholds). American Academy of Forensic Sciences (AAFS) 59th annual meeting, San Antonio, TX.
- Krane, D. E. and J. R. Gilder. November. 2006. Essential elements of a defense review of DNA testing results. Midwestern Academy of Forensic Sciences (MAFS) annual meeting. Indianapolis, IN.
- Krane, D. E. January, 2007. Evaluating forensic DNA evidence. National Association of Criminal Defense Lawyers Annual Meeting, New Orleans, LA.
- Krane, D. E. February, 2007. Assessing the implications for close relatives in the event of similar but non-matching DNA profiles. American Academy of Forensic Sciences (AAFS) 59th annual meeting. San Antonio, TX.
- Krane, D. E. February, 2007. Empirical analysis of the STR profiles resulting from conceptual mixtures. American Academy of Forensic Sciences (AAFS) 59th annual meeting, San Antonio, TX.

- Krane, D. E. March, 2007. Some of the problems associated with LCN (Low Copy Number) DNA testing. The Forensic Institute 2007 Forensic e-Symposium on Human Identification: Profiling of degraded and low amounts of DNA.
- Krane, D. E. March, 2007. The statistics of DNA profiling a day long workshop. The Washington, DC Public Defenders' Office, Washington, DC.
- Krane, D. E., J. R. Gilder, E. Ungvarsky and A. Jamieson. May, 2007. Essential elements of a defense review of DNA testing results. Mid-Atlantic Academy of Forensic Sciences (MAAFS) annual meeting. Washington, DC.
- Krane, D. E., T. E. Doom and M. L. Raymer. August, 2007. Run-specific limits of quantitation and detection: an alternative to minimum peak height thresholds for DNA profile analyses. Sixth annual Expert Forum on the Science of DNA Profiling. Sinclair Center, Dayton. OH.
- Krane, D. E., T. E. Doom and M. L. Raymer. August, 2007. Familial searches and cold hit statistics. Sixth annual Expert Forum on the Science of DNA Profiling, Sinclair Center, Dayton, OH.
- Raiford, D. W., D. E. Krane, T. E. Doom, and M. L. Raymer. October, 2007. A multi-objective genetic algorithm that employs a hybrid approach for isolating codon usage bias indicative of translational efficiency. Proceedings of the 7th IEEE Symposium on Bioinformatics and Bioengineering (BIBE 2007), volume 1, pages 278-285, Cambridge, MA.
- Krane, D. E. and W. C. Thompson. October, 2007. Evaluating forensic DNA evidence – a day-long workshop. Northern Ireland Criminal Bar Association, Belfast, Northern Ireland.
- Krane, D. E. and Angel Carracedo. December, 2007. Forensic DNA profiling a two day-long workshop. Chilean Department of Forensic Sciences, Santiago, Chile.
- Krane, D. E. April, 2008. Expert witnesses: What are they thinking? Mad Anthony Writers' Convention. Hamilton. OH.
- Krane, D. E. May, 2008. Familial searching in policy and practice. Science in the Courtroom for the 21st Century: Issues in Forensic DNA, DePaul Center for Science and the Cook County Public Defender, Chicago, IL.
- Krane, D. E. May, 2008. Y-STR testing validation and the Virginia example.
 Science in the Courtroom for the 21st Century: Issues in Forensic DNA,
 DePaul Center for Science and the Cook County Public Defender, Chicago,
 IL.
- Krane, D. E. May, 2008. The science and pseudoscience of DNA profiling. Cuyahoga County Bar Association, Cleveland, OH.
- Krane, D. E. September, 2008. Emerging issues in forensic DNA profiling: databases and advisory boards. National Center for State Legislatures Annual Meeting, Columbus, OH.
- Krane, D. January. 2009. Evaluating forensic DNA evidence. Fifth National Seminar on Forensic Evidence and the Criminal Law, Philadelphia, PA.

 Krane, D. E., S. Ford, J. R. Gilder, K. Inman, A. Jamieson, R. Koppl, I. L. Komfield, D. M. Risinger, N. Rudin, M. S. Taylor, W. C. Thompson, February 2009.
 Sequential unmasking: Determining what information is crucial and what is extraneous in a forensic analysis. American Academy of Forensic Sciences (AAFS) 61st annual meeting. Denver, CO.

Krane, D. May, 2009. Evaluating forensic DNA evidence. Virginia Public Defenders' continuing education seminar series. Richmond, VA.

- Krane, D. and J. Gilder. June. 2009. Evaluating forensic DNA evidence. The Netherlands Bar Association and Leiden University Law School, The Netherlands.
- Gilder, J. and D. Krane. May, 2009. Searching for (and finding) relatives in forensic DNA databases. Eleventh annual DePaul University Law School and Cook County Public Defenders' short course on DNA analysis, Chicago, IL.
- Gilder, J. and D. Krane. May, 2009. SWGDAM recommendations regarding familial searches. Eleventh annual DePaul University Law School and Cook County Public Defenders' short course on DNA analysis. Chicago, IL.
- Krane, D. and J. Gilder. May, 2009. New developments in DNA technology and litigation. Eleventh annual DePaul University Law School and Cook County Public Defenders' short course on DNA analysis, Chicago, IL.
- Krane, D. July, 2009. Evaluating forensic DNA evidence. National Association of Death Penalty Litigators annual meeting. Airlie, VA.
- Krane, D. November, 2009. Evaluating forensic DNA evidence. Ohio Academy of Criminal Defense Lawyers Death Penalty Seminars, Columbus, OH.
- Krane, D. January, 2010. The science (and pseudoscience) of forensic DNA profiling. Pub-Science series. sponsored by the Boonshoft Museum of Discovery, Dayton, OH.
- Rowland, C. and D. Krane. February, 2010. The National Academy of Sciences report and the Law Commission Consultation paper: Differences and similarities between the United States and England and Wales. The American Academy of Forensic Sciences 63rd Annual Scientific Meeting, Seattle, WA.
- Gilder, J. and D. Krane. February, 2010. Examining of the case of the Deventer murder in the Netherlands. The American Academy of Forensic Sciences 63rd Annual Scientific Meeting. Seattle, WA.
- Gilder, J. and D. Krane. February, 2010. Beer, Wine, and Forensic Science. The American Academy of Forensic Sciences 63rd Annual Scientific Meeting, Seattle, WA.
- Gilder, J. and D. Krane. February, 2010. Discovering relatives in STR DNA databases. The American Academy of Forensic Sciences 63rd Annual Scientific Meeting, Seattle, WA.
- Krane, D. March, 2010. Low copy number (LCN) DNA profiling. The Innocence Project, Cardozo Law School, New York, NY.
- Krane, D. April, 2010. Evaluating forensic DNA evidence. Steelman Visiting Scientist Lecture Series, Lenoir-Rhyne University, Hickory, NC.

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- Krane, D. April, 2010. Establishing parameters for objective interpretation of DNA profile evidence. Steelman Visiting Scientist Lecture Series, Lenoir-Rhyne University, Hickory, NC.
- Krane, D. May, 2010. Low Copy Number DNA Testing and New developments in DNA technology. Twelfth annual DePaul University Law School and Cook County Public Defenders' short course on DNA analysis, Chicago, IL.
- Krane, D. and K. Inman. August, 2010. The science (and pseudoscience) of forensic DNA profiling. A day-long workshop held for an international audience in St. Croix, The United States Virgin Islands.
- Krane, D. September, 2010. Forensic DNA profiling at the 2010 Annual Meeting of the Ohio Judicial Conference: The intersection of law, science and ethics. September, 2010, Dublin, OH.
- Krane, D. September, 2010. The science (and pseudoscience) of forensic DNA profiling. A day-long workshop sponsored by the Office of the Attorney General, St. Thomas, The United States Virgin Islands.
- Krane, D. November, 2010. Low copy number (LCN) DNA profiling. Promega Meeting on Human Identification, San Antonio, TX.
- Krane, D. April, 2011. Forensic DNA profiling: interpretation, statistics and challenges (a series of three presentations), New York City DNA College, New York, NY.
- Krane, D. May, 2011. Suspect-centric combined probabilities of inclusion. Thirteenth annual Cook County Public Defenders' short course on DNA analysis, Chicago, IL.
- Krane, D. October, 2011. Forensic DNA profiling and the use of Y-STRs in casework. Mississippi Public Defender Conference, Choctaw, MS.
- Krane, D. November, 2011. Forensic DNA profiling. Federal Bar Council, Mohonk Mountain House, New Paltz, NY.
- Krane, D. November, 2012. Attaching weight to DNA profiles. Doughty Street Chambers, London, England.
- Krane, D. November. 2012. Evaluating Forensic DNA profiling. Missouri Bar Fall Continuing Legal Education Workshop, Kansas City, MO.
- Krane, D. December, 2012. DNA technology in court. Forensic DNA Profiling Video Series, http://youtube/Xz3mQS5V/wlM.
- Krane, D. December, 2012. Generating forensic DNA profiles. Forensic DNA Profiling Video Series. <u>http://youtu.be/ksXzsL2Y2i</u>.
- Krane, D. December, 2012. Statistical weight of single source DNA profiles. Forensic DNA Profiling Video Series, http://voutu.be/EVf4HgUl0Hk.
- Krane, D. December, 2012. Statistical weight of mixed DNA profiles. Forensic DNA Profiling Video Series, <u>http://youtu.be/daRBTopFA1A</u>.
- Krane, D. December, 2012. Implications of database searches for DNA profiling statistics. Forensic DNA Profiling Video Series, <u>http://youtu.be/eY4s1cEk-BQ</u>.

- Krane, D. December, 2012. Artifacts and noise in DNA profiling. Forensic DNA Profiling Video Series, <u>http://youtu-be/94NnYCKesOU</u>.
- Krane, D. December, 2012. Observer effects in DNA profiling. Forensic DNA Profiling Video Series, <u>http://youtu.be/XoXxUrhDUi4</u>.
- Krane, D. December. 2012. What can go wrong with DNA profiling. Forensic DNA Profiling Video Series, http://youtu.be/g4ZU6wb76pU.
- Krane, D. March, 2013. Forensic DNA profiling. Take Our Daughters and Sons to Work Day. Wright State University, Dayton, OH.
- Krane, D. May. 2013. Advances in forensic DNA profiling. Fourteenth annual Cook County Public Defenders' short course on DNA analysis, Chicago, IL.
- Krane, D. September. 2013. The science (and pseudoscience) of forensic DNA profiling. Special guest presenter, Writer's Police Academy, Jamestown, NC.
- Krane, D. September, 2013. Statistical weights for mixed DNA profiles. Doughty Street Chambers, London, England.
- Krane, D. September, 2013. Bayesian approaches to weighting DNA profile evidence. Northern Ireland Criminal Bar Association, Belfast, Northern Ireland.
- Krane, D. February, 2014. The time has come to analyze DNA profile databases.
 Annual meeting of the American Academy of Forensic Sciences, Jurisprudence section platform presentation, Seattle, WA.
- Krane, D. February. 2014. Suspect-Centric Combined Probability of Inclusion: A means of attaching objective statistical weights to mixed DNA profiles where drop out may have occurred. Annual meeting of the American Academy of Forensic Sciences. Criminalistics section platform presentation, Seattle, WA.
- Houston, E., and D. Krane. February, 2014. Effect of machine laundering additives on human blood. Annual meeting of the American Academy of Forensic Sciences, Poster presentation, Seattle, WA.
- Krane, D. April. 2014. Forensic DNA profiling. Take Our Daughters to Work Day, Wright State University, Dayton, OH.
- Krane, D. May, 2014. The science (and pseudoscience) of forensic DNA profiling. Biology Departmental Seminar. Youngstown State University, Youngstown, OH.
- Krane, D. May, 2014. Attaching statistical weights to mixed DNA profiles where drop out may have occurred. Fifteenth annual Cook County Public Defenders' forensics forum, hosted by DePaul University, Chicago, IL.
- Krane, D. May, 2014. The implications of database analyses to CODIS searches. Fifteenth annual Cook County Public Defenders' forensics forum, hosted by DePaul University, Chicago, IL.
- Krane, D. June, 2014, Attaching statistical weights to DNA profiles. Kingsley Napley Chambers, London, England.
- Krane, D. June, 2014. Statistical weights for low-level mixed DNA profiles. Doughty Street Chambers. London, England.

- Krane, D. June, 2014. Attaching statistical weights to DNA profiles. University College London Crime and Forensic Science distinguished lecturer seminar program. London, England.
- Krane, D. and W. C. Thompson. June 2014. Complex, mixed DNA profiles. The National Innocence Project's DNA College, hosted by Yeshiva University, New York, NY.
- Krane, D. and W. C. Thompson. June 2014. Low copy number DNA profiling. The National Innocence Project's DNA College, hosted by Yeshiva University, New York, NY.
- Krane, D. June 2014. Software approaches for attaching statistical weights to complex mixed DNA profiles. The National Innocence Project's DNA College, hosted by Yeshiva University, New York, NY.
- Krane, D. January, 2015. The science (and pseudoscience) of forensic DNA profiling. Montgomery County Library seminar series, Kettering, OH.
- Krane, D. September, 2014. Exploring bias in forensic DNA profiling. TEDxDayton, Dayton, OH.
- Krane, D. January, 2015. The science (and pseudoscience) of forensic DNA profiling. Biology Departmental Seminar, University of Notre Dame, Notre Dame, IN.

Graduate students and post-doctoral fellows mentored:

- David P. Hostler, III. 1993-1995, M.S.: The dependence of rate and mode of evolution on genomic context within primates.
- Adam P. Skepner. 1994-1996, M.S.: The application of random amplification of polymorphic DNA to phylogenetic reconstructions.
- Keri Steinbrugge. 1994-1997, M. S. candidate: The role of the predominant SINE within lagomorph genomes.
- Krista E. Bloniarz, 1995-1996, M.S., non-thesis option: The application of RAPD-PCR in genome analyses.
- Cynthia Kiefer. 1996-1999, M.S., non-thesis option: The influence of genome compartmentalization on nucleotide substitutions.
- Allen J. York. 1997-2000, M.S. candidate: The subfamily relationships and functional roles of repetitive elements.
- Dalana Barnett, 1997-2000, M. S. recipient: Characterization of a novel, short and highly repeated sequence in carnivores.
- Terry Oroszi. 1998-2000. M.S. candidate: Characterization of a novel, short and highly repeated sequence in pigs.
- Billy Grunwald. 1998-present, M.S. candidate: Utilization of genetic diversity measures a means of assessing terrestrial environmental impacts.
- John F. Sojda, III. 1999, post-doctoral research fellow: Sequence variation in the superoxide dismutase gene in Caribbean *Drosophila* populations.

Graduate students and post-doctoral fellows mentored (continued):

- Emmanuel Aigbokhan. 1999-2000, post-doctoral research fellow: Utilization of genetic diversity measures a means of assessing aquatic environmental impacts.
- Lee Ott. 1999-2002, M.S. recipient: Genetic population structures of Pacific Coast herring populations exposed to anthropogenic stressors.
- Erin Newburn, 1999-2002, M.S. recipient: Molecular identification of Chironomid species.
- Balasubramanian Abiramikumar. 1999-2003. M.S. recipient: Characterization of a novel, short and highly repeated sequence in African elephants.
- Michael C. Kuneman, 2001-2003. M.S., non-thesis: Progress in understanding genetic diversity: The use of genetic diversity for assessment, conservation and protection purposes.
- Randall J. Loges. 2000-2003. M.S. candidate: Genetic diversity and characterization of *Hyallela azteca* from Ohio, Montana and commercial suppliers.
- Krista Jastremski. 2000-2004. M.S. recipient: Changes in genetic diversity within pill bug populations at historically impacted terrestrial sites.
- Norman Scott Blair. 2000-2004. M.S. candidate: Molecular characterization of the sex of Great Lakes birds.
- Joseph Bartozcek. 2001-2010. Biomedical Sciences Ph. D. recipient: Effects of habitat loss/fragmentation on Ambystomatid salamanders.
- Esley Heizer. 2003-2005. M.S. recipient: Correlation between major codon usage and amino acid biosynthetic costs in eight prokaryotic species.
- Monita Sharma, 2004-2006, M.S. recipient: Molecular characterization of chironomid species.
- Peichang Shi, 2006, M.S., non-thesis option: Gene expression patterns as an indicator of exposure to environmental stresses.
- Chad Ferguson, 2004-2009, Environmental Sciences Ph. D. recipient: Using chironomids for environmental impact assessment.
- Nina Archie, 2004-2006, M.S. recipient: Characterization of n+4 stutter artifacts in forensic DNA profiles.
- Esley Heizer. 2005-2010. Biomedical Sciences Ph.D. recipient: Correlation between major codon usage and amino acid biosynthetic costs in prokaryotes and eukaryotes.
- Uohna Foster, 2010-2013, Biomedical Sciences Ph.D. candidate: Persistance and transfer of forensic DNA samples.
- Erin Berdanier, 2011-present, M.S. candidate: Laundry transfer of DNA from blood stains.
- Taryn Hunt, 2011-present, M.S. candidate (non-thesis option): Laundry transfer of DNA from epithelial cells.

Graduate thesis committees served upon:

Keri Pedly. 1993-1994. M.S. recipient.
Liang Shi. 1993-1996. Ph.D. recipient.
Melissa Goldman. 1994-1996. M.S. recipient.
Lou Li. 1994-1997. Ph.D. recipient.
Adrienne Moran. 1994-1996. M.S. recipient.
Steve Hendrix. 1994-1996. M.S. recipient.
David Brown. 1994-1996. M.S. recipient.
Michelle Malotte. 1994-1999. Ph.D. recipient.
David Ellis. 1995-2000. M.S. student.

Graduate thesis committees served upon (continued):

Scott Rousch. 1995-1997. M.S. recipient. Elizabeth Smucker. 1996-1999, M.S. recipient. David Sternberg. 1995-2002. M.S. recipient. Deborah Vallance. 1995-1996. M.S. student. Andrea Alexander, 1999-2002, M.S. recipient. Patricia Morgan. 1997-present. Ph.D. candidate. Billy Grunwald, 1998-2001, M.S. student. Terry Oroszi. 1998-2001. M.S. student. Kelly Jo Peterson, 1998-2003. Ph.D. recipient. Lee Ott. 1999-2002. M.S. recipient. Erin Newburn, 1999-2002, M.S. recipient, Balasubramanian Abiramikumar. 1999-2003. M.S. recipient. Norman Scott Blair. 2000-2005. M.S. candidate. Randall Loges. 2000-2004. M.S. candidate. Marc Greenberg. 2001-2002. Ph.D. recipient. Michael C. Kuneman. 2001-2003. M.S. recipient. Joseph Bartozcek. 2001-present. Ph.D. candidate. David Paoletti, 2001-2006. Ph.D. recipient. Gina Cooper. 2001-2009. Ph.D. recipient. Jason Gilder, 2001-2003. M.S. recipient. Sundeep "Sunny" Anand. 2001-2003. M.S. recipient. Sharon Reilly. 2002-2004. M.S. candidate (non-thesis option). Prashanth Athri. 2002-2004. M.S. recipient.

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Graduate thesis committees served upon:

Balasubramanian Abiramikumar, 2002-2004, M.S. recipient, Jeanette Frey. 2003-2005. M.S. recipient. Esley Heizer, 2003-2005. M.S. recipient. Doug Raiford. 2003-2005. M.S. recipient. Ryan Flynn, 2003-2009. M.S. recipient (non-thesis option). Sridhar Ramachandran, 2003-2007, Ph.D. recipient, Jason Gilder. 2004-2007. Ph.D. recipient. Monita Sharma. 2004-2007. M.S. recipient. Doug Raiford. 2005-2008. Ph.D. recipient. Chad Ferguson. 2004-2010. Ph.D. recipient. Esley Heizer. 2005-2010. Ph.D. recipient. Peichang Shi. 2006. M.S. recipient (non-thesis option). Adam Guess. 2007-2008. M.S. recipient. Amanda Hanes. 2007-2009. M.S. recipient. Sushant Taksande. 2008-present. M.S. candidate. Uohna Foster, 2010-2013, Ph.D. candidate, Taryn Hunt, 2011-present, M.S. candidate. Erin Berdanier. 2011-present. M.S. candidate. Sara Seibert. 2011-present. M.S. candidate.

Undergraduate honors thesis advisees:

Carri Eagler: 1993-1996.	Libby Provci: 1994-1996.
Michelle Gnam: 1994-1996.	Jeanne Uy: 1994-1996
Michelle Lawhun: 1995-1998.	Lora Dodson: 1996-1998.
Jason Soderquist: 1997-1999.	Elizabeth Zimmer: 1998-1999.
Sarah Schmidt: 2000-2001.	Melissa Strain: 2000-2001.
Denada Sharra: 2001-2004.	Roger Fecher: 2005-2006.
Leah Kershner: 2007-2009.	Krista Dona: 2013-present.

Courses taught/developed:

Molecular Genetics (BIO 211). An introduction to molecular biology and genetics for majors in Biological Sciences at Wright State University. Winter, 1994 through 2012; Summer 1998 through 2012.

Cells and Genetics (BIO 112). An introduction to biology for majors in Biological Sciences at Wright State University. (Extensively redeveloped in Summer, 1993) Fall, 1994 through 2000; 2002; 2008 through 2010.

Courses taught/developed (continued):

- Molecular and Cell Biology Laboratory (BIO 410). An introduction to molecular and cell biology laboratory techniques for majors in Biological Sciences at Wright State University. (Developed course in Winter, 1994) Spring, 1994; (redeveloped in Spring, 2003) Spring, 2003.
- Molecular Evolution (BIO 461/661). A senior/graduate level course describing the basis of evolutionary inferences using molecular data including phylogenetic reconstruction and mutational tendencies. Biological Sciences at Wright State University. (Developed course in Winter, 1995) Spring, 1996, 1997, 1999, 2001, 2004 and 2007.
- Population Genetics (BIO 460/660). A senior/graduate level course focusing on the statistical basis of changes in allele frequencies within populations of organisms. Biological Sciences at Wright State University. (Developed course in Winter, 1998) Spring. 1998, 2000, and 2003.
- Human Genetics (BIO 426/626). A senior/graduate level course on the special considerations and approaches used to study the patterns of inheritance in humans. Biological Sciences at Wright State University. (Developed course in Winter, 2002) Spring, 2002.
- Advanced Cell Biology (BMS 991/BIO 701). An advanced literature based course survey on the principles of cell structure and function for incoming biomedical sciences PhD students and graduate students in Biology. (Co-developing course in Summer, 1998) Fall, 1998 and 1999.
- Introduction to Research Biology (BIO 702). A graduate level course on current research in biological sciences at Wright State University. Fall, 1993 and 1996.
- Independent Studies in Biology (BIO 499). A senior level course of guided independent, laboratory research for majors in Biology. Winter, 1994 to present.
- Introduction to Bioinformatics (BIO 371/CS 271). A sophomore level course that introduces computer science and biology majors to the most important algorithms and current problems in bioinformatics. Spring, 2002 through 2012.
- Bioinformatics algorithms (BIO 471/CS 471). A senior level, capstone course focusing on algorithm development for biology and computer science students in the Wright State bioinformatics program. Fall, 2002 through 2011.
- Honors Genetics (BIO 119). A course featuring selected readings on genetics and evolution for Honor's students. Biological Sciences at Wright State University. (Developed course in Summer, 1994) Fall, 1994 through 2000; 2002, 2004 through 2010.
- Bioinformatics algorithms (BIO 4710/CS 4710). A senior level, capstone course focusing on algorithm development for biology and computer science students in the Wright State bioinformatics program. Fall. 2012.
- Cells and Genetics (BIO 1120). An introduction to biology for majors in Biological Sciences at Wright State University. (Team taught with Dr. Emily Kramer) Fall, 2012.

Courses taught/developed (continued):

- Cells and Genetics (BIO 1120). An introduction to biology for majors in Biological Sciences at Wright State University. Fall, 2013.
- Honors Genetics (BIO 1190). A course featuring selected readings on genetics and evolution for Honor's students. Biological Sciences at Wright State University, Fall, 2012 and 2013.
- First Year Seminar (UVC 1010). A course introducing incoming students to college life. University College. Wright State University. Fall, 2012 and 2013.
- Senior Seminar (BIO 4920). A capstone course on presenting scientific information. Biological Sciences at Wright State University. Winter and Summer, 2013.
- Introduction to Bioinformatics (BIO 3710/CS 2710). A sophomore level course that introduces computer science and biology majors to the most important algorithms and current problems in bioinformatics. Spring, 2013 and 2014.
- Forensic DNA Profiling (BIO 4010/ATH 3800). Application of critical thinking skills to forensic DNA profiling in a scale-up setting. Cross-listed in Biology and Anthropology at Wright State University. Spring, 2013 and 2014.

Academic service at Wright State University:

- Biological Sciences Molecular and Cell Biology Curriculum Development Committee, 1993 to present.
- Science Apprenticeship Program for Women and Minority Students (mentor and coinvestigator, Prem Batra – founding program director), 1994 to 2005.
- Short Term Research Experience/Access for Minority Students (STREAMS) (faculty advisor and co-investigator. Robert Putnam program director), 1994 to 2003.
- Computer-assisted Learning Center Committee (elected chair), 1993 to 1996.

Ohio Science Fair Judge and Awards Presenter, 1994 to 1997.

- Biological Sciences Seminar Program Committee, 1994 to present (Chair in 2005 to 2011).
- College of Science and Mathematics Computer Network Facilitation Committee, 1994 to 1996.
- Biomedical Sciences PhD Program Nomination Committee, elected to terms running from 1994 to 1996, from 2005 to 2007 and from 2009 to 2011.

Developmental Biology Search Committee, 1994.

Biology Departmental Honors and Scholarships Committee, 1995 to 2001.

Cell Biology Search Committee, 1995.

Research and Sponsored Programs Associate Director Search Committee, 1995.

University Resident Life Committee, 1995 to 1996.

Computer-assisted Learning Center Committee, 1996 to 1999.

Space and Equipment Allocation Committee, 1997 to 2000.

Faculty liaison for Wright State University's varsity baseball team, 1997 to present.

Academic service at Wright State University (continued):

University Commencement Committee, 1998 to 2000.

University Honors' Committee, 1998 to 2001.

Biological Sciences Undergraduate Curriculum Committee, 1998 to 2001; 2003 to 2005; 2007 to 2009.

Plant Physiologist Search Committee, 1998.

College of Science and Mathematics Faculty Development Committee, elected 1999 to 2001; Appointed Biology Department Representative for 2007-2008 and for 2008-2009 and for 2012-2013.

Cell/Molecular Biologist Search Committees. 2000; 2008 (co-chair).

Information Technology Research Initiative, Research Committee, 2000 to 2004.

College of Science and Mathematics Scholarships Committee, 2000 to 2001.

College of Science and Mathematics Dean Search Committee, 2001 to 2002.

Assistant to the Director (Technology Transfer) of the Office of Research and Sponsored Programs Search Committee, 2002.

Aquatic Biologist Search Committee, 2002-2003.

University Athletics Council, elected to terms running from 2002 to 2004 and 2005 to 2006; Faculty Senate Appointee 2006 to 2007 (elected Vice-Chair in 2006 to 2007; elected Chair 2009-2011; past-chair 2011-2013); Senate representative (2013-2015).

Athletics Council Pre-game Lecture Committee (chair), 2007-2014.

Athletics Council Blackboard to Backboard Challenge Committee (2010-2013).

Athletics Council Gender Equity Sub-committee. 2003 to 2006, and 2008-2011.

Athletics Council Team Liaison Sub-committee, 2002 to 2008.

Athletics Council Athletic Director Review Sub-committee, 2002-2007 (Chair in 2005-2006).

Athletics Council Constitution and By-laws Sub-committee, 2006-2008 (Chair).

Athletics Council Student Welfare Committee, 2009-2014.

Research and Sponsored Programs Technology Transfer Director Search Committee, 2007.

Cell/Molecular Biologist Search Committee, 2007-2008 (Chair in 2008).

Steering Committee. College of Science and Mathematics, elected 2006 to 2007 and 2008 to 2009 (elected Chair for 2007-2008, 2008-2009, 2009-2010, 2010-2011 and 2011-2012 academic years).

Vice President for Advancement Search Committee, 2008.

College of Science and Mathematics Academic Mediation Committee, 2007-present.

College of Science and Mathematics representative (elected) to the Wright State University Faculty Senate, 2009-2010.

Director of the Wright State University Ervin J. Nutter Center Search Committee, 2010.

Academic service at Wright State University (continued):

Wright State University representative to the Ohio Faculty Council (secretary), 2010-2012. Wright State University representative to the Ohio Faculty Council (vice chair), 2012-2013. Wright State University representative to the Ohio Faculty Council (chair), 2013-2015. Faculty Senate ad hoc Committee on the Master Planning Process (chair), 2010-2011.

Semester Conversion Director Search Committee, 2010.

University Commencement Committee, 2011-2014.

Graduate Council, 2011-2014.

Vice President for Business and Fiscal Affairs Search Committee, 2011.

University Faculty Budget Priority Committee (chair), 2010-2014.

Faculty Senate Executive Committee (chair), 2010-2014.

Faculty Senate ad hoc committee on First Year Seminars. 2012-2014.

University President's Cabinet, 2012-2014.

University Mission Driven Allocation Budget Model Executive Committee, 2012-2014.

University Diversity Advisory Council, 2012-2014.

Permanent Provost Search Committee, 2012-2013.

Academic Integrity Conduct Review Panelist, 2012-2013.

President-elect of the Wright State University Faculty, 2010-2011.

President of the Wright State University Faculty, 2011-2013.

Court recognized expert in DNA profiling:

Missouri vs. Nethery (St. Charles, MO, 1991).

lowa vs. Ripperger (Burlington, IA, 1992).

North Carolina vs. Fisher (Charlotte, NC, 1992).

Illinois vs. Tynes (Kankakee, IL, 1992).

Nebraska vs. Bundy (Columbus, NE, 1992).

North Carolina vs. White (Edenton, NC, 1993)

North Carolina vs. Jones (Winnsboro, NC, 1993).

Ohio vs. Honzu (Columbus, OH, 1994).

Ohio vs. Saylors (Urbana, OH, 1994).

Ohio vs. McGuire (Dayton, OH, 1994).

Ohio vs. Brewer (Hillsoboro, OH. 1995).

South Carolina vs. Eubanks (Columbia, SC., 1995).

Ohio vs. Parks (Columbus, OH, 1995).

Ohio vs. Oldham (Hamilton, OH, 1995).

California vs. Strange (Nevada City, CA, 1996).

Court recognized expert in DNA profiling (continued): California vs. Wenger (Long Beach, CA, 1996). United States vs. Lowe (First Circuit, Boston, MA, 1996). Washington 13: Gore (Seattle, WA, 1996). Virginia vs. Gray (Martinsville, VA, 1996). Kentucky vs. Tipton (Stanton, KY, 1997). California vs. Allen (Compton, CA, 1997). Virginia vs. Brogan (Roanoke, VA, 1998). Missouri vs. Taylor (St. Louis, MO, 1998). Ohio vs. Sapp (Springfield, OH, 1998). Missouri vs. White (St. Louis, MO, 1998). Indiana vs. Smith (Middletown, IN, 1999). Indiana vs. Jones (Vincennes, IN, 2000). Florida vs. Estv (Pensacola, FL, 2000). Indiana vs. Williams (Terre Haute, IN, 2001). Minnesota vs. Roman Nose (St. Clair. MN, 2001). Massachusetts vs. Greineder (Welsley, MA, 2001). Indiana vs. Wilburn (Covington, IN, 2001). South Dakota vs. Luce (Aberdeen, SD, 2002). Minnesota vs. Bailey (Minneapolis, MN, 2002). California vs. Howard (Los Angeles, CA, 2002). California vs. Quinones (San Francisco, CA, 2002). Minnesota vs. Traylor (Minneapolis, MN, 2002). Ohio vs. Knott (Athens, OH, 2002). Indiana vs. Guffey (Tipton, IN, 2002) Indiana vs. Ward (Rockport, IN, 2002). California vs Robinson (Sacramento, CA, 2003). New Mexico vs. Arviso (Farmington, NM, 2003). California vs. Cheung (Orange County, CA, 2003). Ohio vs. Henderson (Athens, OH, 2003). Ohio vs. Fears (Lebanon, OH, 2003). Maryland vs. Daniels (Frederick and Rockville, MD, 2003). United States vs. Zephier (Sioux Falls, SD, 2003). Montana vs. Jones (Lewistown, MT, 2004). Indiana vs. Cooper (Goshen, IN, 2004).

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Court recognized expert in DNA profiling (continued):

New Mexico vs. Garcia (Albuquerque, NM, 2004).

New York vs. Alvarez (Schenectady, NY, 2004).

Ohio vs. Hines (Cleveland, OH, 2004).

Victoria State Coroner's Inquest into the Death of Jaidyn Leskie (Melbourne, Victoria, Australia, 2004 and 2005)

Montana vs. Misner (Great Falls, MT, 2005).

California vs. Avila (Orange County, CA, 2005).

Minnesota vs. Bailey (Minneapolis, MN, 2005).

United States vs. Jenkins (Washington DC District Court, 2005).

Iowa vs. LaMasters (Waterloo, IA, 2005).

Minnesota vs. Temple (Minneapolis, MN, 2005).

Michigan vs. Leiterman (Ann Arbor, MI, 2005).

Michigan vs. Spagnola (2nd Circuit Court of Appeals, Benton Harbor, MI, 2005).

Ohio vs. McClure (Batavia, OH, 2005).

Virginia vs. Davis (Norfolk, VA, 2005).

Maryland vs. Derr (La Plata, MD, 2006).

Colorado vs. Brownlow (Adams County, CO, 2006).

Maryland vs. Odom (Prince George's County, MD, 2006).

Virginia vs. Riddick (Hampton Circuit Court, Hampton, VA, 2006).

Illinois vs. Rivera (Chicago, IL, 2006).

California vs. Robinson (Los Angels, CA, 2006).

Regina vs. Sean Hoey (Northern Ireland High Court, Belfast, NI, 2006).

Arizona vs. Bigger (Tucson, AZ, 2007).

Ohio vs. Matthews (Xenia, OH, 2008).

United States vs. Davis (US District Court of MD, 2008).

United States vs. Garner (Fort Eustis, VA, 2008).

United States vs. Hennis (Fort Bragg, NC, 2008).

Colorado vs. Tunis (Golden, CO, 2008).

Regina vs. Broughton (Oxford Crown Court, Oxford, England, 2009)

California vs. Smith (Sacramento, CA, 2009).

New York vs. Megnath (Queens, NY, 2009).

Virgin Islands vs. Xavier (St. Croix, Virgin Islands District Court, 2010).

Regina vs. Canning (Belfast Crown Court, Belfast, Northern Ireland, 2010).

Regina vs. Broughton (Oxford Crown Court, Oxford, England, 2010).

Court recognized expert in DNA profiling (continued):

Regina vs. Walsh (Belfast Crown Court, Belfast, Northern Ireland, 2011).

Colorado vs. Rodriquez (Golden, CO: 2011).

Illinois vs. Gonzalez (Chicago, IL, 2011).

Regina vs. Duffy and Shivers (Belfast Crown Court, Belfast, Northern Ireland, 2011).

Regina vs. Dos Santos (Central Criminal Court, London, England, 2012).

Oregon vs. Garrett (Portland, OR, 2012).

Regina vs. Deacon (Central Criminal Court, London, England, 2013).

United States vs. McCluskey (US District Court of AZ, 2013).

Regina vs. Dos Santos (Central Criminal Court, London, England, 2013).

Regina vs. Colhoun (Newry Crown Court, Newry, Northern Ireland, 2013).

Ohio vs. McKenna (Dayton, OH, 2014).

Regina vs. Colhoun (Newry Crown Court, Newry, Northern Ireland, 2014).

Missouri vs. McBenge (St. Charles, MO, 2014).

Administrative responsibilities:

Faculty advisor, Wright State University Biological Sciences Association. (1994 to 2002).

Organizer and co-founder, Wright State University Molecular Biology Retreat. (1995 to 2003).

Chapter president, Sigma Xi (National Scientific Honor Society). (1997 to 2001).

Associate director's board member, The Engineers' Club of Dayton. (1997 to 2001).

Board of Directors, Chairman, Forensic Bioinformatic Services, Inc. (2002 to present).

Professional societies:

The Academy of Science of St. Louis (1992-2003)

The American Association for the Advancement of Science (1992-2003)

The Molecular Biology and Evolution Society (1992-2003)

The Engineers' Club of Dayton, OH (1993-2003)

Honorary member of Alpha Lambda Delta, National Academic Honor Society for Freshmen (1996)

Chapter president/member, Sigma Xi, National Scientific Honor Society (1996-2003)

International Society of Molecular Evolution (1997-2003)

The Ohio Academy of Sciences (1997-2003)

The American Chemical Society (2002-2004)

Professional service:

- Featured appearances on "Court TV." "CBS Nightly News," "Unsolved Mysteries," "BBC Newsnight." "BBC Panorama" and numerous appearances on all Dayton-area local TV broadcasts.
- Technical consultant for "Court TV," "CBS Nightly News," NBC's "Unsolved Mysteries," CBS's "Sixty Minutes," CBS's "Eye to Eye with Connie Chung," the Gannette News Service, "Weekly Reader Magazine," "The Washington Post," "The Los Angeles Times" and "The Dayton Daily News."
- Reviewer for the journals: "Appraisals," "Molecular Biology and Evolution," "Genetics," "Genomics," "Journal of Molecular Evolution" "The American Biology Teacher," "IEEE Bioinformatics," and "Accountability in Research."
- Presiding officer, Animal Molecular Biology Section, Ohio Academy of Science 107th Annual Meeting at Miami University-Middletown, April 1998.
- Review panel member, U. S. Environmental Protection Agency "Ecological Indicators Panel," 1999, 2000, 2001, 2002, 2004 and 2006.
- Review panel member, U. S. Environmental Protection Agency "Nanotechnology Panel," 2006.

Ad hoc reviewer for the Hudson River Foundation, 2002 and 2004.

- Fairness in Forensics," with Roger Koppl, op ed published in several newspapers, 12-17
 August 2008, including Newark Star-Ledger. The Olympian (Olympia, Washington), Hartford Courant (Sunday edition). Herald-Leader (Lexington, Kentucky: Sunday edition), Lake Wylie Pilot (Lake Wylie, South Carolina), Daily Herald (Provo, Utah). The Modesto Bee (Modesto, California), Tri-city Herald (south-central Washington), The News & Observer (Raleigh, Durham, and Chapel Hill, North Carolina). Belleville News-Democrat (Belleville, Illinois), The Bellingham Herald (Bellingham. Washington), The Fresno Bee (Fresno, California) and the Anchorage Daily News.
- *Science Rules the FBI Should Obey," with Roger Koppl, op ed published in several newspapers, 13-16 January 2010, including the Cleveland Plain Dealer, Fort Worth Star-Telegram Press Democrat (Santa Rosa, California), Bradenton Herald (Florida). Wake Forest News & Observer. The News Tribune (Tacoma, Washington), and The Fresno Bee (Fresno, California).
- David R. Hopkins and Dan E. Krane, "Higher education: An investment guaranteed to pay off." An op-ed piece published in major newspapers in Ohio during the month of September, 2013.
- David R. Hopkins and Dan E. Krane, "Education An equal opportunity path to the American dream." An op-ed piece published in major newspapers in Ohio during the month of November, 2013.
- National Event Supervisor (Forensic Science), Science Olympiad, Wright State University, Dayton, OH 2013.
- Gubernatorial appointee. Forensic Chemistry Representative to the Scientific Advisory Committee for the Virginia Department of Forensic Science. (appointed by Governor Mark Warner for a term of 2005-2006; reappointed by Governor Tim Kaine for a term of 2006 to 2010).

Professional service:

Familial Search Subcommittee of the Virginia Scientific Advisory Committee, Chair (2006 to 2007).

Y-STR Validation Subcommittee of the Virginia Scientific Advisory Committee, Chair (2008).

Ohio Board of Regents Faculty Credentials Committee (co-chair), 2012.