SUPREME COURT, SUFFOLK COUNTY

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THE PEOPLE OF THE STATE OF NEW YORK,

ORDER

Case No. 73544-24

HON. RAYMOND A. TIERNEY
District Attorney, Suffolk County
ADA Nicholas Santomartino
ADA Andrew Lee
ADA Lawrence Opisso
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Riverhead, NY 11901

-against-

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REX A. HEUERMANN

Defendant.

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On March 28, 2025, April 2, 2025, April 3, 2025, April 15, 2025, April 16, 2025, April 17, 2025, June 17, 2025, June 18, 2025, and July 17, 2025, a hearing was conducted by the Court pursuant to Frye v United States, 293 F 1013 (DC Cir. 1923) as to the admissibility of nuclear DNA results as well as any expert testimony pertaining to said nuclear DNA results obtained from rootless hairs recovered from the person and/or crime scene of Maureen Brainard Barnes, Megan Waterman, Amber Costello, Sandra Costilla, Jessica Taylor and Valerie Mack

Findings of Fact

The People's Witnesses

Dr. Kelley Harris

Dr. Harris testified that she is a Population Geneticist and has been an Associate Professor of Genome Sciences at the University of Washington since 2018. Dr. Harris also holds

a position at the Fred Hutchinson Cancer Research Center where she gives research updates and exchanges ideas in computational biology. She has also published 40 peer-reviewed articles with most of them concentrating on whole genome sequencing, the process by which you obtain DNA from everywhere across the whole genome and analyze all or most of it. After receiving her Bachelor's Degree from Harvard University, Dr. Harris went on to receive her Master's Degree in biological science from Cambridge University's Genomic Center. Her Master's Degree thesis involved calculating the reliability of genetic identity over a stretch of the genome when you can assume that all of the sites of the genome you observe are likely the same because of recent ancestry. This is extremely helpful when the sample collected only contains a small amount of DNA and statistical analysis is used to check the reliability. Dr. Harris used the 1,000 Genomes Project in her research which is a reference panel containing sets of genomes from 2,504 different individuals around the world. It represents the genetic variation found in the entire population of the world and is publicly available for use. It has been used to calculate statistics for population genetics. In her testimony, Dr. Harris referred to a peer-reviewed article regarding the 1,000 Genome Project (People's 1E). After receiving her Master's Degree, Dr. Harris earned her doctorate in applied mathematics with an emphasis in computational biology from the University of California at Berkeley. During her studies, she used ratios to calculate how likely some observations were that she made under different scenarios to confirm or disprove her hypotheses. Dr. Harris then went on to complete a post-doctorate fellowship at Stanford University in their Department of Genetics. Dr. Harris further testified that she also has experience in bioinformatics, the process by which you have a small amount of DNA, place it through a DNA sequencer, receive an output of pieces of DNA, and then stitch it together so that the DNA is interpretable. A sequencer is a device which DNA is placed into that has been library prepped, and after being run through the machine, generates the sequence of all of the fragments of DNA that were placed into the sequencer. The Illumina sequencer is the dominant technology on the market and has been generally accepted by the scientific community to develop a DNA profile. Dr. Harris noted that she is not an expert in forensic science.

DNA contains four bases: adenine (A), cytosine ©, thymine (T) and guanine (G). Each individual has two copies of their nuclear DNA-one from their mother and one from their father. Each individual also can have hundreds or thousands of mitochondrial DNA depending on what type of cell in which it is located. Mitochondrial DNA is inherited by the individual from their mother. A short tandem repeat (STR) is when one, two, or three of the four of the bases of DNA (ACTG) repeat themselves in the genome. For example, if ACT or ACG or ATG, etc. were repeated several times when looking at the DNA in a genome. STRs have been used in forensic science since the 1980s. Whole genome sequencing focuses on these repeats after obtaining DNA from across the entire genome. The whole genome will often become amplified into multiple copies which then get cut up into pieces. The pieces are then placed into a genome sequencer and read out as a string of ACTGs by stitching them back together. Sometimes there are gaps in the string. Dr. Harris testified that whole genome sequencing can be used to create a nuclear DNA profile, and this has been generally accepted in the scientific community.

SNP (single nucleotide polymorphism) DNA refers to one base in the genome where a

variation has been observed. SNP DNA is used in medical genetics, forensic identification, etc. According to Dr. Harris, the best method to develop a DNA profile when you are dealing with a short fragment of DNA is whole genome sequencing. In addition, Dr. Harris testified that using a computer program to calculate a likelihood ratio of the statistical significance in whole genome sequencing DNA profiles is widely accepted in the scientific community.

Dr. Harris peer-reviewed Dr. Richard Green's paper entitled, "A Computational Approach for Positive Genetic Identification and Relatedness Detection From Low-Coverage Shotgun Sequencing Data." (Defendant's B). This paper discussed whole genome sequencing of rootless hairs as compared to a higher quality DNA sample taken from a lab including the use of a computer software entitled IBDGem, created by Dr. Green, which calculated the likelihood ratio, and found that his system was reliable. She based this opinion upon her review of Dr. Green's paper, the study he performed, and his results. She noted that she co-authored peer-reviewed articles with both Dr. Green and his wife, Dr. Beth Shapiro. Dr. Harris explained that IBDGem uses the 1,000 Genomes Project as a reference sample. IBDGem examines hundreds of SNP locations at a time in a window and then combines information across millions of SNP locations genome-wide. Dr. Harris explained a test where IBDGem was used to compare a hair sample to the saliva of the person whom the hair sample came from as well as another test where IBDGem was used to compare a hair sample from an individual with the saliva of a different individual who did not give the hair sample. The likelihood ratio for the first test (the hair sample and saliva sample from the same individual) was up to 200 times more likely that the hair and saliva came from the same individual. In contrast, the likelihood ratio for the second test (hair and saliva from two different individuals) was up to 400 times more likely that each sample was not from the same individual. Based on this, Dr. Harris concluded that the IBDGem method using its likelihood ratio was confident about both outcomes, and was accurate. Dr. Harris testified that it is possible that IBDGem could overestimate a SNP profile and have a margin of error, and that the results are based on a likelihood ratio or probability. She further testified that while all individuals share short DNA sequences with each other which come from our ancient gene pool of common ancestors, close relatives share long DNA sequences which were inherited from recent ancestors. She further testified that while using a large reference panel like the 1,000 Genomes Project–which IBDGem uses–is important, IBDGem also tested a smaller reference table of 50 individuals–which was published in Dr. Green's peer-reviewed article–and was still accurate when comparing identity from non-identity.

Dr. Harris testified that the 1,000 Genomes Project is the best public reference panel to use when calculating likelihood ratios in population genetics, and that Dr. Green's IBDGem software's use of the 1,000 Genomes Project is not the only time that the 1,000 Genomes Project has been used by scientists to calibrate statistical significance of SNP DNA testing and comparisons. Dr. Harris testified that in the scientific field, there have been many thousands of peer-reviewed articles using the data from the 1,000 Genomes Project. In addition, she testified with respect to a peer-reviewed article (People's 1B) discussing linkage disequilibrium which is also incorporated in IBDGem. She further testified with respect to another peer-reviewed article (People's 1E) which notes that no two persons have similar genomes which she testified is

exactly what IBDGem is sensitive to. In her opinion, whole genome sequencing and IBDGem are suitable for forensic use and are generally accepted in the scientific community. She based her conclusion on all the tests run by Dr. Green and the correct outcomes that he received.

Dr. Nicole Novroski

Dr. Novroski testified that she is the Associate Director of the Center for Human Identification (CHI) at the University of North Texas. CHI is an accredited leading globally recognized forensic research, development and casework lab. It contains a forensic unit, a missing persons unit and a forensics genealogy unit. Dr. Novroski oversees all active research projects. CHI not only conducts its own research but also collaborates with other academic institutions and biotech companies in testing newly-developed chemistries to ensure that they are suitable for public lab operations as well as the forensic scientific community. At CHI, Dr. Novroski's role is the developmental validation of whole genome sequencing using SNPs for genetic genealogical applications. Dr. Novroski published a paper on mitochondrial whole genome sequencing. In addition, Dr. Novroski is an Associate Professor at the University of North Texas Health Science Center in its College of Biomedical and Translational Sciences, and was also employed by the University of Toronto as a professor for seven years where she taught forensic biology courses.

After receiving her Bachelor's Degree from the University of Toronto where she received a BS in both biology and forensic science, she then received a Master's Degree in forensic molecular biology from the State University of New York at Albany. The emphasis of her Master's Degree was in genetics and molecular biology with a forensic emphasis. As part of her Master's Degree, she completed an external internship with the Minnesota Bureau of Criminal Apprehension in Minnesota. During that time, she completed two projects. The first was entitled, "The Evaluation of Possible False Positives with Detergent when Performing Amylase Serological Testing on Clothing," and tested whether or not the transfer of saliva took place on garments while they were being laundered together. The second project was entitled, "The Feasibility of Using the Erase Sperm Isolation Kit to Develop an Improved Differential Extraction Procedure," and tested whether the new chemical was viable to use in the Minnesota's Bureau of Criminal Apprehension Workflow. Dr. Novroski's first position after receiving her Master's Degree was as a Criminalist in the New York City Office of the Chief Medical Examiner. She analyzed evidence, and conducted over one thousand DNA extractions where she would attempt to develop a DNA profile from a sample. Dr. Novroski then worked for the Centre of Forensic Sciences, a globally-recognized lab in Toronto, where she processed DNA samples through a rapid DNA workflow. After that, Dr. Novroski went on to obtain her doctoral degree in biomedical sciences with a focus on forensic and investigative genetics from the University of North Texas Health Science Center. Her thesis for her doctoral degree was focused on polymorphic short tandem repeats (STRs) for enhanced DNA deconvolution, or STRs that contain SNP information within their DNA fragment. During her thesis project, she had to develop DNA profiles which involved her becoming an expert in massive parallel sequencing. Dr. Novroski has published approximately 33 peer-reviewed articles. Her articles have been

cited over 1,200 times and she is also the editor-in-chief of Forensic Genomics. She also wrote two chapters in different books about SNPs and advanced technologies with a focus on challenged samples or those not typically suitable for traditional STR analysis (ie. rootless hairs). Dr. Novroski was also consulted by the Canadian Criminal Convictions Review Board to review protracted DNA evidence and provide a report of her findings as to whether or not the conclusions initially drawn about a certain DNA sample was appropriate given the DNA evidence. She concluded they were not, and, as a result, the charges were dismissed, and an inmate, who had been incarcerated for years, was exonerated.

According to Dr. Novroski, whole genome sequencing is the chemistry utilized to capture the entire DNA information within a given DNA sample. It uses a library preparation of the DNA sample to prepare the DNA fragments for sequencing. The fragments are then placed into a sequencer to generate the DNA fragments that were in the original template sample and then a computational analysis is done to look at the entirety of an organism's genome. Whole genome sequencing has been used for decades, and has been used in forensic science for the past 5 to 7 years. It can be used to develop a nuclear DNA profile, and is generally accepted within the forensic science community. SNPs have also been used by scientists, including forensic scientists, for decades. When performing mitochondrial (the DNA inherited from your mother) DNA testing, a scientist examines SNP information to determine a mitochondrial DNA profile. According to Dr. Novroski, when using a degraded or challenged sample (ie. rootless hair), a scientist will use SNP information to uncover the information necessary to make an identity determination for ancestry or genealogy due to the fact that there is no large fragment of DNA so STRs cannot be used. In the 1,000 Genomes Project, SNPs were observed in more than one percent of the samples. Dr. Novroski explained that the steps for analyzing SNP DNA is to begin by extracting the DNA sample, and then quantifying how much DNA is present within the extracted sample. Thereafter, a scientist would move on to use a library preparation kit on the sample. Then sequencing would be conducted utilizing the targeted amplification of whole genome sequencing by placing it in a sequencer. The sequencer generates information in the form of DNA reads. At this point, the DNA can be compared to other SNP DNA profiles (such as GEDmatch or FamilyTreeDNA) and statistics are then performed on both DNA profiles. Dr. Novroski testified that targeted SNP testing of data observed from a DNA sample is generally accepted in the scientific community.

Dr. Novroski testified that Dr. Green is highly regarded in the scientific community, and CHI is currently evaluating Astrea Forensics' rootless hair DNA extraction protocol as established by Dr. Green. Dr. Green's extraction method uses an optimized protocol which maximizes that amount of DNA recovered from a rootless hair. Since CHI works with many unidentified human remains and challenged samples, CHI wants to use the best protocols which are reliable in generating DNA extracts for whole genome sequencing. In her opinion, Dr. Green's method of extracting DNA from rootless hairs is effective and that his method of extraction as well as the use of the Illumina sequencer is generally accepted in the forensic scientific community. Further, the 1,000 Genomes Project is accepted in the general scientific forensic community as being a sufficient reference panel and is best suited to capture global

genetic variation. Dr. Novroski referred to a peer-reviewed article (People's 2B) supporting the use of the 1,000 Genomes Project as a reference panel. There are labs across the country which utilize the 1,000 Genomes Project to solve cases. She was unsure if CHI was evaluating Dr. Green's IBDGem computer program. Dr. Novroski read Dr. Green's peer-reviewed article about his IBDGem computer program, and testified that she was not an expert in probabilistic genotyping and could not testify with respect to Dr. Green's IBDGem program, which is the computer program he uses to perform a statistical analysis and uses likelihood ratios. However, Dr. Novroski testified that there have been hundreds of cases where SNP DNA was used to identify previously unidentified human remains or a perpetrator in a criminal case using the genetic genealogical landscape in forensic science. Comparing the SNP DNA from a crime scene to public reference panels will likely result in some kind of kinship determination with the ultimate goal of identifying who the person of interest is. SNP DNA has been used in courtrooms before, including Kern County California as well as in an Innocence Project case in Idaho. Dr. Novroski testified that comparing a SNP DNA sample to a sample from a reference panel (such as the 1,000 Genomes Project) as well as attaching a statistical significance to that comparison is generally accepted by the forensic scientific community. Dr. Novroski testified that SWGDAM (Scientific Working Group DNA Analysis Methods) and the Quality Assurance Protocol provide validations for probabilistic genotyping systems, and she was not sure if Dr. Green or Astrea Forensics had complied with those steps to validate their software. However, Dr. Novroski testified that those steps provided by both SWGDAM and the Quality Assurance Program deal specifically with STR DNA analysis, and not SNP DNA analysis, which was used by Dr. Green.

Dr. Richard Green

Dr. Green testified that he is employed by the University of California in Santa Cruz as a professor of Biomolecular Engineering and is also the Scientific Director of the QB3 Program in their Quantitative Bioscience Institute. He teaches Genome Technology classes which is the technology used to extract DNA out of a sample and then sequence it. In addition, Dr. Green is on the senate faculty and has some appointments in the anthropology department. The QB3 program is a state-funded organization that is directed at the goal of helping to bring inventions and the science that is produced by the University into commercial enterprises. The research lab at the University focuses on ancient DNA and developing technologies for extracting DNA out of difficult samples. A difficult sample is often an older one or a small sample with not much DNA in it such as a rootless hair. Dr. Green also owns a company called Dovetail Genomics which makes a kit which allows people to take any sample with cells in it (ie. tissue, culture, etc.) and convert it into sequence data which can be placed into a DNA sequencer to reveal the three dimensional confirmation of DNA in the sample. Another company founded by Dr. Green is Claret Biosciences. Claret Biosciences also sells a kit where you place a sample with a small amount of fragmented DNA into it and then receive a library which can be placed into a DNA sequencer. Dr. Green has 16 patents in DNA technology issued in the United States. Another company owned by Dr. Green is Astrea Forensics, which was founded in 2018 after his lab at the University became involved in forensics when homeowners discovered the skeletal remains of a

small girl on their property while they were doing renovations. His lab was sent a lock of hair from the girl's head to see if they could determine the girl's identification. They wound up finding out that there was a great nephew of the little girl who was still alive, and after receiving a DNA sample from that living descendant, they were then able to ascertain the little girl's identity. They were also able to determine that she had died in 1876. After this project, Dr. Green became interested in forensic genetic genealogy or looking at DNA to find relatives to identify a person. Dr. Green was then asked by the FBI on several occasions to look at DNA from cold cases to help solve them, and, as a result, he started Astrea Forensics. Astrea Forensics is in the process of being accredited by ANAB (the National Accreditation Board). Astrea receives a lot of work from law enforcement agencies including the FBI, and deals with very difficult samples including rootless hairs, old bones, or any sample containing a small amount of fragmented DNA. Astrea Forensics has analyzed thousands of DNA samples for law enforcement since 2019. In addition, other labs including Othram, Bode, Parabon, and DNA Labs International have sent samples to Astrea Forensics to be analyzed. Dr. Green testified that he has analyzed hundreds of DNA samples.

While attending the University of Georgia, where he received a BS in Genetics, Dr. Green worked in a lab studying how genes are expressed differently in fruit flies. He then went on to teach math and physics in Africa while in the Peace Corps. Dr. Green received his post-doctoral degree in Molecular and Cell Biology with a designated emphasis in Computational Biology and Genetics from the University of California at Berkeley. As part of his thesis, he wrote several chapters on computational algorithms and computer programs to do DNA sequencing alignment and to evaluate the DNA sequencing alignment. He also wrote about alternative gene splicing, or where genes are put together in different ways depending on what cell type they are in. In addition, he has written hundreds of computer programs. After receiving his PhD in 2005, Dr. Green had a post-doctoral position at the Max Planck Institute, an independent research institute in Germany which studies ancient DNA. While he was there, Dr. Green researched the 454 data, a program created by Jonathan Rothberg, which sequenced DNA faster. His research involved looking into whether the 454 data could be used for DNA from old cave bear and mammoth bones. He then went on to research massive parallel sequencing on DNA recovered from Neanderthal bones. Massive parallel sequencing permitted the sequencing of hundreds of thousands of DNA fragments at once and generating data therefrom. This new technology permitted sequencing of even the smallest fragments of DNA by converting it into a library to be read by a machine. Using the Illumina sequencer, a person can sequence several billion pieces of DNA at the same time. In 2010, Dr. Green published a peer-reviewed paper on this research which won the Newcomb Cleveland prize as the best paper written in science that year. Dr. Green has published over 100 peer-reviewed articles about DNA technology or genomics or using whole genome sequencing to extract DNA, and dozens have been on the front covers of journals. He is also the editor of the Forensic Genomics Journal, and has testified as an expert in courts in Idaho and California.

As a computational biologist, Dr. Green uses a likelihood ratio which is a comparison of two numbers. Those numbers are the likelihood of some observation given some reality and a

likelihood of the observation given a different reality. Likelihood ratios have been used for over one hundred years and are widely accepted in the field of computational biology. Dr. Green has performed billions of likelihood calculations.

Dr. Green further testified that the 1,000 Genomes Project is a well known reference panel which is an adequate representation of worldwide variance and is well accepted within the scientific community as it can be used for any application in genomics, including forensics, where you want an actual catalog of actual people to understand human genetic variation.

Dr. Green testified that whole genome sequencing of SNP DNA has been studied by scientists for decades and is widely accepted in the scientific community. With the new technology for whole genome sequencing, thousands of genomes can be sequenced at one time. Thus, finding the places in the genome which are SNPs has become greatly accelerated as there are tens of millions of SNP locations in the human genome. Whole genome sequencing can be used to create a nuclear DNA profile, and this is done all of the time and is widely accepted within the scientific community. SNPs can be used in many ways, including in the field of genealogy. Dr. Green testified that SNP DNA testing is the best test to use when you have a challenging DNA sample (ie. rootless hairs). Rootless hairs contain only small amounts of DNA fragments in them. Dr. Green created a computer program–IBDGem–which places a statistical weight on a DNA sample when it is compared to another DNA sample. In order to develop a DNA profile from a unknown individual, and compare it to a DNA buccal swab sample of a known individual, certain steps must be followed. The steps of whole genome sequencing DNA extraction to library prep to sequencing are used by many labs and are generally accepted in the scientific community. After using the sequencer, Astrea Forensics uses IBDGem, the computer program that takes the data that's generated from the sequencer from each sample (rootless hair of unknown individual and buccal swab of known suspect) and compares the data. IBDGem asks the question, "How likely is it that the data I received from this hair comes from a person who has the genotype that I found in the buccal swab? And what is the likelihood that the DNA from the hair came from an unknown, unrelated individual?" The likelihood ratio tells you which one of those different scenarios is bigger and by how much. Dr. Green has tested the IBDGem software for accuracy. IBDGem was created because Dr. Green was dealing with special cases of genotyping inferences in that he was investigating DNA that is present in a rootless hair and wanted to infer a genotype directly out of that for investigative genetic genealogy purposes. The computer program has been tested and makes a genotype call that is consistent with the technology that 23AndMe (a genetic ancestry test) uses.

After conducting studies on the reliability of IBDGem, Dr. Green wrote a paper which is still in the process of being peer-reviewed. IBDGem has been available for public use for a few years. One quality assurance measure used to make sure the DNA did not come from multiple sources is another program created by Dr. Green called Tilda. Tilda is run before the samples are placed in IBDGem and runs an analysis of the evidence sample by itself to see if the nuclear DNA in the sample is consistent with coming from a single source. If there is no evidence that it is not from a single source, then they are confident that the DNA came from one single source.

Another quality assurance used by Astrea Forensics before samples are placed in IBDGem is MixENT. MixENT is a computer program which reads the library of the DNA which comes from the mitochondria, which is inherited from a person's mother. The mitochondrial DNA of the DNA sample should be the same type throughout. If the computer software shows different variants, then the sample comes from different mitochondrial versions which is evidence that the sample is a mixture of DNA samples and not just from one source. Dr. Green has published peer-reviewed articles on both Tilda and MixENT. Dr. Green testified that IBDGem calculates the probability of a DNA sample from a person of interest as compared to the sample he received by looking at each SNP read it sees from both samples. It can also calculate the probability of a DNA sample from a person of interest as compared to a panel of unknown, unrelated individuals using the 1,000 Genomes Project. Dr. Green testified that the 1,000 Genomes Project is used for statistical purposes in the denominator of the IBDGem formula to establish a likelihood ratio. Dr. Green testified that IBDGem never had a false positive outcome when he tested two samples of DNA from the same individual (i.e hair and saliva from same person). He explained that when he performs a negative control test, when he knows that the DNA is not coming from that exact person, IBDGem will show stronger evidence in support of what he knows to be the correct answer, and less evidence than when he performs a test where the DNA does come from that exact individual. Dr. Green testified that the IBDGem program is very conservative in that it overestimates the likelihood in the denominator of the equation which benefits the defense.

Dr. Green testified his peer-reviewed paper (published in early 2023), which detailed the use of IBDGem on rootless hairs, was written after a study was performed using DNA samples (rootless hairs and saliva) from 8 individuals. They conducted both positive (comparing saliva and hair from same person) and negative (comparing hair from one individual and saliva from a different individual) control tests. Each computation performed by IBDGem gave strong support for what Dr. Green knew to be the correct answer. Dr. Green showed all of the likelihood ratios IBDGem calculated in the form of graphs in his Power Point presentation (People's 3). The likelihood ratios are negative on the graphs when the DNA sample did not come from an unknown, unrelated individual. Dr. Green testified that there was always statistical support for what answer he knew to be true. Dr. Green testified that his IBDGem paper was cited 8 or 9 times, including by Dr. Bruce Budowle (a well-known leading figure in forensic science). Dr. Green noted that in his peer-reviewed paper, Dr. Budowle stated without any citation as if it was a true statement and obvious that, "[a] direct one-to-one comparison, with thousands to hundreds of thousands of SNPs likely would yield likelihood ratios far exceeding those routinely achieved with STRs" (People's 3E). Dr. Dan Krane (a defense witness in this hearing) and Dr. Edge wrote a preprint paper (Defendant's K), which was not published, criticizing IBDGem. Dr. Green was asked by the editor of the Genetics Journal to write a peer review of Dr. Krane and Dr. Edge's paper, and he did. In his peer review, Dr. Green testified that he wrote that Dr. Krane's paper tries to explain how IBDGem works after Dr. Krane used the program without actual human data. Dr. Green testified that he uses actual human data when using IBDGem. In addition, Dr. Krane also used much smaller reference panels than the 1,000 Genomes Project, did not calculate the likelihood ratio in the manner done using IBDGem, and did not conduct testing comparing a sample to a non-contributor. Dr. Green acknowledged that Dr. Harris, a peer reviewer of Dr.

Green's IBDGem paper, co-authored articles with Dr. Green once and his wife once, and acknowledged that they had all had dinner together.

Dr. Green further testified that he conducted another test to assure the accuracy of IBDGem using 50 individuals who donated saliva and a cut piece of head hair (30 of those individuals also donated a pubic hair). Dr. Green published the results from the 4,000 positive and negative control tests IBDGem completed on these samples on a website. IBDGem never got a positive likelihood ratio from a known non-contributor or a negative likelihood ratio from a known contributor. Dr. Green also tested IBDGem for when errors would occur by intentionally creating issues or problems (ie. sequencing error, DNA mixtures) to see how the computer program would work under those conditions. Even with errors, IBDGem still gave the correct answer. The more errors Dr. Green introduced into the program, the less positive the likelihood ratio was but it was still positive and gave the correct answer for what he knew to be true. Another way Dr. Green tested the accuracy of IBDGem was by using another company's computer program to take the DNA sequence data from a sample and infer a genotype with it. Normally, Astrea uses its own program, Astrea Impute 2, to perform this prior to using IBDGem. Here, Dr. Green used a program called GATK (Genome Analysis Tool Kit) and another program called GLIMPSE. The results with the negative control experiments produced a more negative likelihood ratio than the positive control experiments produce a positive ratio. This again showed that IBDGem is conservative as it is more confident when its making a negative comparison than when making a positive comparison. While the numbers were a bit different, Dr. Green received the same results he would have with IBDGem and Astrea Impute 2 as he did using IBDGem and these other programs. All the results show strong statistical support for the correct answer. Dr. Green testified that the use of Astrea Impute 2 is accepted in the scientific community as it calls genotypes from sequence data.

Dr. Green acknowledged that the FBI has published quality assurance standards for forensic DNA testing in laboratories (Defendant's E). Dr. Green testified that Astrea Forensics has a quality manager who wrote their quality manual as part of the application to become accredited, and it comports with the FBI quality assurance standards. Validation is one of the quality assurance standards in the FBI manual. However, Dr. Green testified that the FBI quality assurance standards apply to STR analyses and CODIS searching not SNP analyses, which are made by Astrea Forensics. He also testified that IBDGem has only been validated by the tests done by Astrea Forensics.

Dr. Green testified that he uses approximately six computer programs–none written by him–in addition to IBDGem when analyzing samples including BWA, BCFtools, and SAMStools. He testified that most of these programs are used by anyone sequencing DNA data. Dr. Green wrote a supplemental paper to his IBDGem paper (Defendant's F) and acknowledged that it was missing a binomial coefficient as part of the first equation which he claimed was a typographical error. In addition, the application for the patent (Defendant's G) for IBDGem which was submitted in September 2022 also had the same typo as the attorneys who filed the application for the patent copied the equation in the supplemental paper. Dr. Green testified that

while both have a typographical error, the software has no such error within it and he noted that Dr. Krane and Dr. Edge acknowledged in their second preprint paper (People's 4), which is also unpublished, that the missing binomial coefficient in Dr. Green's paper was a typographical error because it is appropriately included in the IBDGem code in the computer software.

Dr. Green testified that he added a feature (1d mode) to the IBDGem program after he wrote his paper about the program. The new feature can be seen in the patent application that was not in his paper. Astrea Forensics added the 1d mode to IBDGem to obtain a more accurate representation of the likelihood of the data under the model that they came from an unknown, unrelated individual. This feature enhanced the program. Astrea Forensics has also been asked by defense attorneys in other cases to test DNA samples.

Dr. Green further testified that prior to the creation of Astrea Forensics, he was asked to assist in the Zodiac killer cases which are all unsolved. He received some of the letters sent to a newspaper and a victim's father and was asked to extract DNA in order to identify who had sent the letters. Dr. Green was able to extract DNA from one of the letters and that person was identified, and confessed to writing the letters. Dr. Green testified that he was also asked to assist in the Bear Brook murders. The victims were all badly decomposed, and his lab received some hairs and biological tissue and was asked to generate DNA profiles. After generating DNA genotype files for the FBI, the FBI used investigative genetic genealogy on those files, and three of the victims were identified. He also created a DNA genotype file for a Jane Doe who had been murdered and after the FBI used investigative genetic genealogy, she too was identified. Dr. Green testified that the lab in Santa Cruz and Astrea Forensics only develop a genotype DNA file, they do not perform genetic genealogy tests. Dr. Green and Astrea Forensics have also done work for the National Center for Exploited and Missing Children (NCMEC). Dr. Green and Astrea Forensics were able to create a genotype file from DNA from a molar and eyelash of a woman who could not be identified because she had been beaten so badly when she was killed. The geneticists at the NCMEC were later able to identify the woman using the genotype file. Another case Astrea Forensics worked on involved multiple homicides in 1979 in California where a rootless hair was found next to one of the victims. Astrea Forensics extracted DNA from the hair, and developed a genotype file using whole genome sequencing. After using investigative genealogy tests, a suspect was named (Jurn Norris). A DNA sample from the suspect was sent to Astrea Forensics where they did an IBDGem comparison to the hair and sample they received from the Mr. Norris. The result was that it was more likely that the hair came from Mr. Norris than from an unknown, unrelated individual. Mr. Norris was found unfit to stand trial due to severe mental illness. Astrea Forensics was also asked to create a genotype file was from a woman who was wrapped in a rug and encased in concrete inside a club in New York City. She was found when remodeling of the building had commenced. Astrea Forensics received a piece of her bone, created a genotype file, and after investigative genealogy was used, she was identified. Astrea Forensics also worked on a case involving a missing girl where her backpack was found with hairs on it. They developed a genotype file from the hairs, and were later given comparison sample hairs from sisters of the missing girl to run IBDGem to see if those hairs matched the hairs from the backpack. IBDGem offered strong statistical support from

several of the hairs that it was one of multiple people that were all sisters of each other.

Dr. Green also testified in 2024 in the case of State of Idaho v David Dalrymple. That case involved a 1982 abduction of a young girl who was later found deceased. The FBI had recovered a few hairs from her underwear and on her sock. After identifying a suspect, the case went to trial, and the defendant was convicted. The original defendant who was convicted always maintained his innocence, and years later requested that the hairs be tested against his mitochondrial DNA as technology had advanced to the point that mitochondrial DNA could be extracted from samples. After testing found that the hairs did not contain the defendant's mitochondrial DNA, he was exonerated. Many years later, Dr. Green was asked to develop a genotype file from one of the remaining hairs while in his lab at Santa Cruz. Whole genome sequencing was used to create the genotype file. After receiving the genotype file, the FBI conducted a genealogy test and developed a suspect. The FBI then asked Dr. Green to compare a DNA sample from the suspect (David Dalrymple) and the suspect's brother with the hair. Dr. Green testified that this case led to the development of the IBDGem program. There was strong statistical data that the hair came from the suspect and not from his brother or an unknown, unrelated individual. Dr. Green testified in that case, and David Dalrymple was convicted. Dr. Green also worked on another case in California involving the abduction of a young girl in 1982 whose body was later found with a hair. While in his lab at Santa Cruz, Dr. Green developed a genotype file using whole genome sequencing from the hair which was used to conduct a genealogy test, and later led to a suspect. Dr. Green was then asked to compare the hair with the suspect's DNA (Robert Lanoue), and using IBDGem, Dr. Green concluded that the likelihood that the DNA from the hair came from the suspect was much higher than the likelihood that it came from an unknown, unrelated individual. Robert Lanoue later confessed and pleaded guilty.

Dr. Green also testified about several published peer-reviewed papers (People's 3D) that he did not write, which discussed extracting DNA using whole genome sequencing from rootless hairs and doing various analyses with the DNA from the rootless hairs. According to Dr. Green, one paper provided a "likelihood-ratio framework for comparing DNA from hair to known genotypes," much like what IBDGem does now. Some of the hairs were 4,000 years old, and two came from a person who lived in the 1700s as well as a person who lived in the 1800s. He also discussed a textbook published in 2012 regarding the extraction of ancient DNA, and how one could obtain DNA fragments from hairs. Dr. Green read from one of the peer-reviewed articles, published in 2024, entitled, "Prioritizing Privacy and Presentation of Supportable Hypothesis Testing in Forensic Genetic Genealogy [FGG] Investigations." The article stated, "[t]he value of FGG (forensic genetic genealogy) is not questioned, and over the next five to ten years it is anticipated that whole genome sequencing will become the primary method for generating forensic data." Additionally, the article stated, "[c]urrently in most FGG cases, victims and suspects are not sampled for SNP profiling. Instead, source attributions are confirmed or refuted by STR typing; however cases with highly degraded DNA and rootless hair, STR data cannot be generated." Dr. Green testified that whole genome sequencing is widely accepted in the scientific community. He further testified that while IBDGem is a new computer program, the principles used within it, which are behind the math used and data collected, are

accepted in the scientific community. IBDGem does a direct one-to-one comparison of data at thousands to hundreds of thousands of SNP positions which yields likelihood ratios far exceeding those routinely achieved with STRs.

The Defendant's Witnesses

Nathaniel Adams

Nathaniel Adams works as a systems engineer at Forensic Bioinformatic Services (FBS), in Dayton, Ohio. FBS is a forensic biology consulting company. Mr. Adams works with only defense attorneys on forensic DNA consultation where they review testing that has already been conducted in the case. Mr. Adams reviews the bench notes and laboratory notes generated during the DNA testing that had already been conducted. He also reviews the actual DNA testing, its protocols and validation studies as well as any computer software that was used. FBS does not perform any laboratory work on DNA samples. It only evaluates the DNA data it receives from defense attorneys after they are provided with it from prosecutors. Mr. Adams has designed hundreds of computer software programs and testified that no other entity oversees the work performed by FBS. Dr. Dan Krane is Mr. Adams' current boss at FBS and was also Mr. Adams' professor at Wright State University where he received his Bachelor's of Science Degree in 2014. Dr. Krane is also on Mr. Adams' Master's Degree thesis committee. Mr. Adam's started to attend Sinclair College in his junior or senior year of high school. He graduated high school in 2004 but did not receive his Associate's Degree in computer information systems until 2012 from Sinclair College. He testified that he believed he graduated summa cum laude from Wright State University with his Bachelor of Science because of his GPA but he was unsure. While obtaining his Bachelor's Degree, Mr. Adams completed a capstone project involving forensic DNA analysis software. Although Mr. Adams started a Master's Degree program and completed all of the course work necessary for a Master's Degree in computer science at Wright State University in early 2017, he has yet to complete the thesis portion. As a result, to this day, he has not received a Master's Degree. He testified that he did not complete his thesis, and has not received his Master's Degree because he lacked confidence to finalize his thesis and submit it. Mr. Adams testified that he knows that Wright State University has a time limit of 6-7 years for finishing a Master's Degree program. Mr. Adams said he filed an exemption asking for an extension with Wright State University so that he could remain in good standing.

Mr. Adams testified that he recently received a grant for research into probabilistic genotyping software. This grant was awarded to him in conjunction with a professor at Clarkson University and the Legal Aid Society. He has testified 30 times as an expert for the defense in forensic DNA analysis involving software systems including probabilistic genotyping software at both pre-trial suppression hearings as well as trials. He has always testified on behalf of the defense. Mr. Adams has reviewed 10 to 12 probabilistic genotyping software systems. He was a co-author in a peer review article regarding forensic DNA and probabilistic genotyping software, and he co-authored two other articles. He also wrote an article for a criminal defense lawyer magazine. None of his work has ever been cited by any prosecutors, and only one of his papers

was cited once. He has also given various lectures and presentations on probabilistic genotyping including a few at the American Academy of Forensic Science. However, most of his presentations have been in front of defense lawyers. He also participated in a conference which communicated concerns about the use of complex technologies by law enforcement in criminal investigations. He received a research grant to investigate modifications made to a probabilistic genotyping system called the Forensic Statistical Tool developed by the NYC Forensic DNA lab in the Office of the Chief Medical Examiner.

Mr. Adams testified that he is familiar with the IBDGem program as FBS was consulted on a criminal case a year ago that involved the use of that program. IBDGem is a probabilistic genotyping software which performs an analysis of biological data and performs statistical calculations on that data. He has examined the IBDGem program after he downloaded it from the internet. He put some of the data provided on the internet by Dr. Green and his team through the IBDGem program. He also testified for the defense in the state of Idaho in a criminal case where IBDGem was used. He testified that proper documentation of analyses is essential, and claimed that Astrea Forensics did not have proper documentation. But he also testified that he only took a few notes when he reviewed IBDGem as it was used in the specific case, and some of his notes were about the assistance he had provided the defense in understanding forensics and computer software, and some were about his general knowledge. Mr. Adams testified that out of 28 pages of notes (People's 16), only 7-8 pages were his analysis of the work of Astrea Forensics in this case even though he was provided with 28 terabytes of data from Astrea Forensics with respect to this case. For reference, one terabyte holds 850 million pages of Microsoft Word documents.

Mr. Adams quoted from SWGDAM and the American National Standard Institute (ANSI) in his Power Point presentation (Defendant's M) and testified that they both provide validations for probabilistic genotyping systems. However, Mr. Adams testified that SWGDAM as well as ANSI specifically stated that they only apply to STR testing and not whole genome sequencing or SNP to SNP testing as used in this case. Mr. Adams testified that the DNA Commission of the International Society for Forensic Genetics (DCISFG) recommends guidelines for validating software which performs biostatistical calculations with respect to forensic DNA. However, Mr. Adams noted that DCISGF does state that, "A rigorous validation study (both developmental and internal) should be sufficient to reveal shortcomings or errors in coding." Mr. Adams testified that he disagreed with that statement.

Mr. Adams testified with respect to the list of software programs used by Astrea Forensics for the analysis of data in this case but noted that there was no description of how the software programs interact or how any of them were specifically configured or how they were used. Some of the programs are widely used in computing, and some are for bioinformatics applications, and others were created by Dr. Green. However, Mr. Adams conceded that he never reviewed the pipeline of software provided by Astrea Forensics which was available in the District Attorney's Office or used the Snakemake program to trace that computational pipeline which would have described each program used and in what order, etc.

Mr. Adams testified that probabilistic genotyping is the use of biological modeling, statistical theory, computer algorithms and probability distributions to calculate likelihood ratios and/or infer genotypes for the DNA typing results of forensic samples. Probabilistic genotyping was first discussed in the late 1990s and has been used in casework for the past 16 years. There is an ongoing development of the methods of probabilistic genotyping. Often software can have bugs, defects, faults, and glitches, and sometimes these can lead to severe consequences. A computer program needs to be looked at from a multitude of perspectives in order for it to be considered dependable. The Institute of Electrical and Electronics Engineers (IEEE) states that all probabilistic genotyping software should be independently verified and validated. While he has created hundreds of software programs, including ones that assist in the analysis of DNA data that was already conducted, Mr. Adams testified that none of them were audited against IEEE's standards, and he acknowledged that compliance with the IEEE is optional. Mr. Adams testified that the calculation of likelihood ratios are of particular concern in probabilistic genotyping software. Likelihood ratios do not have true value and are highly dependent on the data and model, as well as the software which is being used.

Mr. Adams testified that he reviewed a validation folder from Astrea Forensics which was a review of the validation of IBDGem. In his opinion, the validation folder did not satisfy the validation requirements listed by IEEE. When examining bench notes provided by Astrea Forensics about IBDGem from a hair sample in 2021, Mr. Adams was concerned when he read the following: "The shift on the HWE plot, where low population frequency SNPs have systematically lower HET calls, and high population frequency SNPs have systematically higher heterozygosity." Mr. Adams testified that this could be caused by a mixture of DNA from multiple individuals. While Dr. Green writes in the bench notes that the sample is not necessarily a mixed sample of DNA from multiple individuals, but could be an individual with mixed ancestry, Mr. Adams testified that Dr. Green's response is a research and development response to a circumstance. It is not an operationalized formal process where the concern is addressed using casework. In his opinion, based on those bench notes, Astrea Forensics' method for asserting a sample is not a mixture is questionable. Mr. Adams conceded that he did not know if that 2021 sample was from this specific case. Mr. Adam's testified that in another lengthy bench note, Dr. Green's team discussed where there were undetermined or unknown reads in sequencing data, one of his team members wrote "QC'd." Mr. Adams testified that this stands for quality control which happens in the development stage of a computer program, and testified that they have no quality assurance framework at this point. Mr. Adams further testified that Astrea Forensics does not have an integration test plan procedure or the results from executing a test plan. Without these items, a computer program cannot be verified and validated, and is unreliable. Mr. Adams testified that an unreliable computer program is not generally accepted in the computer software and engineering scientific community. Mr. Adams testified that there have been 15 "commits" or modifications to IBDGem since 2023 but later admitted they were made during the developmental stage of the computer program. Mr. Adams testified that he did not know if these commits only involved changes to the README file or the file that the developers write to help people to understand and read the program. In addition, several bugs have been fixed in the program since its release. One of the bugs involved a reading error with

input and output of data from IBDGem. Mr. Adams acknowledged that one of the bugs fixed did not relate to IBDGem or this case because it was genetic testing of animals in Astrea Forensics used for animal conservation. Another bug fixed was to VCF Parser but Mr. Adams did not know if the VCF Parser was used in this case. Mr. Adams also testified that a variety of phases of the development cycle of IBDGem are missing materials including documentation that would be expected for this type of software. But, Mr. Adams admitted that he did not download any underlying data pertaining to IBDGem.

Dr. Dan Krane

Dr. Krane is a professor of Biological Sciences at Wright State University, and the president and CEO of Forensic Bioinformatics (FBS). He has taught many courses over the years, including some in population genetics and molecular biology. He is also the chair of his departments's faculty development committee. FBS was incorporated in April 2002, and reviews DNA test results typically generated by crime laboratories to help other individuals get a better understanding of the significance of those results and identify some errors or alternative interpretations of those test results. Nathaniel Adams was a student of his and is now one of his employees at FBS. Dr. Krane is also a member of Mr. Adams' graduate Master's Degree thesis committee.

After receiving a Bachelor's Degree in biology and chemistry from John Carroll University, Dr. Krane earned his PhD from Pennsylvania State University in biochemistry. He also did some post-doctoral studies in the genetics department of the medical school at Washington University as well as in the organismic and evolutionary biology department at Harvard University. He has received grants for funding for research projects pertaining to measures of genetic diversity as well as education related to bioinformatics. He authored Wright State University's laboratory manual and is also the author of a textbook called Fundamental Concepts of Bioinformatics. Recently, he co-authored a chapter on the validation of probabilistic genotyping algorithms. He has been an author or co-author of 50 peer-reviewed articles relating to molecular biology and/or population genetics. In the past 15 years, most of his articles pertained to forensic DNA profiling. He published an article entitled, "Empirical Analysis of the STR Profiles Resulting in Conceptual Mixtures." Dr. Krane testified this was the first published article to draw attention to problems associated with attaching statistical weights to DNA profiles. Another paper he wrote entitled, "Sequential Unmasking: A Means of Minimizing Observer Effects in Forensic DNA Interpretation," stated that it would be essential for forensic scientists to adopt a practice of interpreting test results in a blind fashion. His most cited paper entitled, "Context Management Toolbox: A Linear Sequential Unmasking (LSU) Approach for Minimizing Cognitive Bias in Forensic Decision-Making," deals with a rigorous approach for blind testing to reduce the risks associated with examiner bias and the interpretation of DNA results. He has given many presentations on forensic DNA profiling since the 1990s. Dr. Krane acknowledged that he has never worked in a forensic crime lab or taken a crime scene sample and generated a DNA profile from it for the purposes of comparison in a criminal investigation. He also participated in a study of forensic algorithms with other experts, and testified

approximately 35 times in court as an expert in forensic DNA profiling. In one case he testified with respect to RFLP DNA testing and in another case, he testified with respect to PCR testing. He referred to PCR testing as a "paradigm shift" during that time since it involved the amplification step of PCR and looking at polymorphic markers. Dr. Krane stated that every time he testified regarding the admissibility of RFLP, PCR, STR, mitochondrial, YSTR, and low copy carbon DNA testing, he testified that the DNA test results using those types of tests should be suppressed. Dr. Krane testified that he now believes that STR testing is accepted in the scientific community because of the widespread use of it as well as the many peer-reviewed articles that have been published about it. He believes that after 10 to 20 peer review articles have been published regarding a type of DNA test or software, it is generally accepted in the scientific community. He did acknowledge that there is literature by Dr. Green and Dr. Novroski regarding SNPs, which was used in this case, that dates back to 2011. Dr. Krane also testified in cases regarding probabilistic genotyping software including TrueAllele, STRmix, and Forensic Statistic Tool. In those cases, he also testified against the admissibility of the DNA test results using those software programs. Recently, he testified in the State of Idaho in a criminal case (State of Idaho v David Dalrymple) where SNP analysis and IBDGem software were used, and he testified against the admissibility of the DNA test results. While Dr. Krane testified that he is an expert in SNP analysis, he stated that he has never performed wet lab work on a SNP sample. He testified that with respect to the case at hand, he is not raising any issues with respect to the wet lab procedures which were used by Astrea Forensics except that the techniques they used were different from STR testing. He was unaware that Astrea Forensic's whole genome sequencing kit has been purchased by DNA Labs International. An advertisement for DNA Labs International (People's 27) was introduced into evidence and Dr. Krane testified that it showed they were advertising for potential clients to use the kit for genealogical testing in the criminal context. Dr. Krane also acknowledged that SWGDAM published guidelines for SNP analysis by forensic DNA testing laboratories (People's 28). SWGDAM listed one of the population databases as the 1,000 Genomes Project and also listed it as a resource under SNP resources for genealogical testing.

He was also asked by a judge, who was sitting on a federal case in Michigan, for assistance in helping her to understand the issues as an independent expert. That case involved the admissibility of a probabilistic genotyping program. In that case, Nathan Adams testified for the defense. He informed the judge that it might have been a conflict of interest but she assured him that he should not be concerned about that, and she called in Dr. Michael Coble as another independent expert for assistance to explain the prosecution's position. He also testified that he had been reviewing emails and speaking with Mr. Adams about the case before the judge asked him for his help. Dr. Krane testified that it would help FBS, his company, if the defense was successful in that case. Dr. Krane further testified that FBS has been compensated every time he has testified since 2002. Dr. Travis Doom, the chair of Mr. Adams' Master's Degree thesis committee, has an affiliation with FBS and is also a shareholder. When asked if he saw a conflict of interest as to he and Dr. Doom being on Mr. Adams' Master's Degree thesis committee, Dr. Krane answered in the negative. In addition, when asked if it is within FBS' best interest to have Mr. Adams listed as a Master's Degree student in good standing, Dr. Krane

responded, "I suppose." Dr. Krane testified that he wrote a chapter in a book about DNA (People's 29) and with respect to defense lawyers' cross examination of a DNA expert challenging the expert's credentials, Dr. Krane wrote, "If the witness does not have at least a Master's Degree, you may be in a position not only to hammer on the witness's lack of credentials, but also to strike a damaging blow based upon the lack of sophisticated knowledge." Dr. Krane then acknowledged that it could be perceived that his and Dr. Doom's academic relationship with Mr. Adams is a conflict of interest.

Dr. Krane testified that he co-authored a paper on forensic likelihood ratios from low-coverage sequencing which focused on Dr. Green's IBDGem computer program which he claims is a "paradigm shift" (Defendant's O). The paper was first submitted in May 2024. After Dr. Green's peer review of this paper, the journal did not want to publish Dr. Krane's paper. In November 2023, Dr. Krane and his colleagues submitted a much longer, substantive and detailed analysis. The paper was peer-reviewed again, ultimately accepted for publication on May 11, 2025, and was published in the Journal of Forensic Science International: Genetics. Dr. Krane also submitted his paper for publication to the Journal of Heredity. However, the Journal of Heredity declined to consider it for publication. Their paper focuses on the fact that IBDGem tests the hypothesis that the sample comes from an individual who is included in the reference panel, and that this hypothesis is generally not of forensic interest because the defense hypothesis is not typically that evidence comes from an individual included in a reference database. In addition, their paper addressed that the likelihood ratios generated by IBDGem can be much larger–often by many orders of magnitude than those computed for the more standard forensic null hypothesis–creating the impression of stronger evidence for identity than is warranted. For example, if the likelihood ratio is 837, using Dr. Krane's calculation, IBDGem delivers an answer of 690 million. Dr. Krane testified that IBDGem's likelihood ratio is very prejudicial to the person of interest. Dr. Krane testified that the data he used for his likelihood ratio came from a haploid (single set of unpaired chromosome) model but humans are diploids (receiving one set of chromosomes from mother and one set from father), and IBDGem uses diploid data. IBDGem uses DNA profiles from humans in the 1,000 Genomes Project. Dr. Krane testified that he started with a haploid because it is a simplified example to see if IBDGem failed with respect to something simple at first. Thereafter, he performed a test using diploids. In addition, Dr. Krane only used a sample size of 5 simulated DNA profiles yet he testified that the 2,504 sample size in the 1,000 Genomes Project was not large enough. In addition, Dr. Krane's data was run using linkage equilibrium but Dr. Krane testified that humans are in linkage disequilibrium. In another test run by Dr. Krane, he used a sample size of 100 and used diploids. However, the DNA was simulated for the diploids he used. Dr. Krane further testified that while IBDGem looks at 100 SNP windows at a time, the data he used looked at much more than 100 sites and produced information on hundreds of thousands of sites.

In preparing for his testimony, Dr. Krane received 28 terabytes of data from the prosecution but he testified he only "superficially" reviewed the bench notes therein and only glanced at the raw data provided. He testified that he did not review the slack messages, JIRA tickets, and Laboratory Information Management System (LIMS). While Dr. Krane reviewed the

source code for IBDGem, he did not take any notes with respect to it and he only "very superficially" reviewed the internal and external emails from Astrea Forensics labs and Dr. Green. He also received photographs of the evidence as well as photographs of the packaging of the evidence in this case but did not review them. In addition, he received all of the underlying data for the individual likelihoods but did not look at it, and he also received validation data for IBDGem but only looked at it "[t]o the extent to which it's been published." Dr. Krane testified that he prepared a 14 page affidavit to the Court stating that all of this information was vital to him to help him assist in the analysis of this case. However, he testified that he did not perform a comprehensive review.

Dr. Krane's biggest critique of Dr. Green's IBDGem program is that it uses the 1,000 Genomes Project as an alternate suspect pool since it has never been used as an alternative suspect pool. One peer reviewer of Dr. Krane's paper wrote that the IBDGem program should be discouraged and also stated, "the low citation rate for [Dr. Green's] paper suggests it is not being adopted by forensic scientists" (Defense Q). Dr. Krane acknowledged that when he submitted his paper for publication, he submitted a list of proposed peer reviewers. The peer reviewers ultimately chosen by the editor of the journal are unanimous and Dr. Krane admitted that he did not know anything about their background qualifications. In addition, the comments by the peer reviewer were written on April 14, 2025, after the defendant in this case was indicted, and after Dr. Krane knew that he would be involved in this case. In addition, Dr. Krane provided the peer reviewers with all of the data he generated with his paper but acknowledged that he did not provide the prosecution in this case with this data.

Dr. Krane testified that Dr. Green's IBDGem program is very novel and radically different than anything that has been done before. Dr. Krane testified that the first generation of DNA testing called restriction fragment length polymorphism test (RFLP) was invented in the 1980s and became the norm testing for DNA in laboratories in the early 1990s. At that time, it was scientifically accepted because it was being widely used and by that time, there were many peer-reviewed articles written about it. The next form of DNA testing was called the polymerase chain reaction (PCR). It was not scientifically accepted until it started to become widely used in the mid-1990s, and also after many publications had been written about it. Finally, after STR testing of DNA was invented, it became widely accepted by the end of the 1990s after laboratories invested money in equipment and infrastructure to perform this testing. In addition, protocols and validation studies were done to make sure this testing obtained reliable results.

Dr. Krane testified that IBDGem generates a likelihood ratio asking a fundamentally different question. Normally, a program would ask what is the chance that someone else might be the source of this DNA. However, IBDGem asks what is the chance that the DNA sample is from one of the 2,504 people from the reference panel for whom we have whole genome sequence information. Dr. Krane also testified that the library preparation and the process of DNA sequencing done by Dr. Krane is done on completely different instruments and using different protocols than have been used before. In reviewing Dr. Green's PowerPoint presentation on IBDGem, Dr. Krane notes that one half of the graph is a representation of how

much weight can be given to a prosecution theory of the case and the other half is a representation of how much weight can be given to a defense theory of the case. In the lower left corner, it states "unrelated individual as modeled by the panel." Dr. Krane testified that it would be much clearer and much better understood if instead of an "unknown, unrelated individual as modeled by the panel," it said instead, "an unknown, unrelated individual who is represented or whose whole genome sequence has been included in the panel." In his opinion, the question IBDGem asks is answered by IBDGem but not in a way that is useful or helpful. IBDGem rests entirely on the proposition that the markers are in what geneticists call linkage equilibrium. Dr. Krane testified that he does not think that anyone believes that SNP data from whole genome sequencing results are in linkage equilibrium. Dr. Krane testified that Dr. Green states in his IBDGem paper that it would be foolish to suggest that they are. In addition, Dr. Krane testified that Dr. Green used the LD mode to evaluate test results but a slide in his PowerPoint demonstrates he is using the non-LD mode. With respect to another slide in Dr. Green's PowerPoint presentation, Dr. Krane testified that it states that IBDGem looks at windows containing 100 observed genetic variants but Dr. Green's paper states that it looks at windows containing 200 observed genetic variants. Dr. Krane testified that since the 1980s, the question that has been asked when doing DNA testing is what is the chance that a randomly chosen, unrelated person from a given reference population might also be confused as being the source of DNA found in common between a suspect and an evidence sample. That is a completely different question than what is the chance that the source of this evidence is one of 2,504 people whose genomes have been sequenced. While Dr. Krane testified that the trier of fact should decide who is in the alternate suspect pool, he acknowledged that he could foresee some practical problems with that. In his opinion, Dr. Krane testified that IBDGem is not generally accepted in the scientific community as it has only been used by Dr. Green and his team, and there is only one peer review article which talks about IBDGem as well as his paper which criticizes it.

Conclusions of Law

This Court notes at the outset that "the modern trend in the law of evidence has been away from imposing a special test on scientific evidence and toward using the traditional standards of relevancy and the need for expertise . . . " (People v Wesley, 83 NY2d 417, 426 [1994] [internal quotation marks and citation omitted]). Thus, novel scientific evidence can be admitted without any hearing (id.).

However, the long-established test used to determine the admissibility of novel scientific evidence is set forth in Frye v United States (293 F 1013 [DC 1923]). That is, "whether the accepted techniques, when properly performed, generate results accepted as reliable within the scientific community generally" (Wesley at 422). "The particular procedure need not be 'unanimously indorsed by the scientific community but must be generally acceptable as reliable'" (id. at 423 quoting People v Middleton, 54 NY2d 42, 29 [1981]). The relevant scientific community are those "scientists who would be expected to be familiar with the particular use of the evidence at issue" (Wesley at 439).

The Frye test should not be based on counting scientists votes to determine how many disagree or oppose the new scientific evidence, but rather, "[t]he more exact inquiry should be whether the dissenting voices are from scientists who have empirical proof to refute the validated empirical evidence and thus substantiate their competing hypotheses" (People v Williams, 35 NY3d 24, 54 n 6 [2020]).

Furthermore, it has been held that "the mere fact that a court is the first to evaluate novel scientific evidence does not mean that the evidence is unreliable" (Wesley at 437). Whereas here, the People are the proponent of the novel scientific evidence, the burden rests with the People to establish its general acceptance in the relevant scientific community (*see* Williams at 40).

General acceptance of reliability in the scientific community has been shown through the admission of peer-reviewed articles or scientific literature demonstrating the new scientific evidence is reliable (*see* People v Wakefield, 38 NY3d 367 [2022]; Williams, 35 NY3d 24) as well as through legal precedent or expert testimony (*see* People v Vaughn, 43 NY3d 190 [2024]; Williams, 35 NY3d 24). Even where a new scientific methodology was not being used in many forensic crime laboratories at the time of the Frye hearing, it was still found reliable and generally accepted by the scientific community based on "the empirical evidence of its validity, as demonstrated by multiple validation studies, including collaborative studies, peer-reviewed publications in scientific journals and its use in other jurisdictions" (Wakefield at 381).

Here, this Court is asked to determine whether Astrea Forensics use of whole genome sequencing, to extract DNA from rootless hairs in order to generate SNP data and create a DNA profile therefrom, as well as the use of IBDGem–their probabilistic genotyping software program used to compare the DNA profile generated by them with the DNA profile of a known suspect–is generally accepted in the relevant scientific community.

The Court finds that Astrea's method of using whole genome sequencing to extract DNA from rootless hairs in order to generate SNP data and create a DNA profile is generally accepted as reliable within the scientific community based not only on the expert testimony of Dr. Harris, Dr. Novroski, and Dr. Green, but also on the numerous peer-reviewed articles submitted by the People into evidence regarding whole genome sequencing and the use of SNP data to create a DNA profile, and also based on its use in other jurisdictions including Idaho and California (*see* Vaughn, 43 NY3d 190; Wakefield, 38 NY3d 367; Williams, 35 NY3d 24). Dr. Harris, an expert in population genetics and bioinformatics (biology and computer science), testified that she wrote 40 peer-reviewed articles with most of them concentrating on whole genome sequencing. According to Dr. Harris, the best method to develop a DNA profile when you are dealing with a short fragment of DNA–where the sample collected only contains a small amount of DNA (ie. rootless hairs)– is whole genome sequencing. She testified that the use of whole genome sequencing to create a nuclear DNA profile is generally accepted as reliable in the scientific community. Dr. Harris also testified that SNP DNA has been used in many scientific fields including forensic identification and medical genetics. Dr. Harris further testified that, like

Astrea Forensics, she herself has library prepped a small amount of DNA, and then placed it into an Ilumina sequencer–the dominant technology on the market that has been generally accepted by the scientific community as reliable–to receive an output of pieces of DNA. Thereafter, she has also taken those pieces of DNA and has stitched them together to create a DNA profile. Dr. Harris also peer-reviewed Dr. Green's paper discussing whole genome sequencing of rootless hairs which included the studies he performed and his results, and in her opinion, Dr. Green's method using whole genome sequencing and SNP data to create a DNA profile was "suitable for forensic use" and "generally accepted in the scientific community."

Similarly, Dr. Novroski, an expert in forensic science and DNA sequencing, who has processed thousands of DNA extractions to develop DNA profiles therefrom, and also written two chapters in two textbooks about SNPs and advanced technologies with focus on challenged DNA samples including rootless hairs, testified that whole genome sequencing and the use of SNPs have been used by scientists for decades. She further testified that whole genome sequencing has been used in the field of forensic science for the past 5-7 years, and that both the use of whole genome sequencing and SNP data to create a nuclear DNA profile is generally accepted as reliable by the scientific community. Dr. Novroski testified that SNP information is often used where a scientist is dealing with a degraded or challenged sample (ie. rootless hair) to uncover the information necessary to make an identity determination for ancestry or genealogy due to the fact that there is no large fragment of DNA so STRs cannot be used. Dr. Novroski then explained that steps used by scientists in analyzing SNP DNA which include extraction of DNA from the sample, quantifying how much DNA is present from the extraction, using a library preparation kit on the sample, and then sequencing the entire genome by placing it in a sequencer machine. After the sequencer generates information in the form of DNA reads, the DNA can be compared to other SNP DNA profiles (ie. GEDmatch or FamilyTree DNA) and statistics are performed on both DNA profiles. The Court notes that the steps used by scientists in analyzing SNP DNA, as testified to by Dr. Novroski, mirror the steps taken by Astrea Forensics when extracting DNA and creating a DNA profile. Dr. Novroski testified that targeted SNP testing of data observed from a DNA sample is generally accepted as reliable within the scientific community, and that Astrea Forensic's method of extracting the DNA and using the Illumina sequencer is generally accepted within the scientific community as reliable. Dr. Novroski testified that SNP DNA has even been used in courtrooms including a case in Kern County California as well as in an Innocence Project case in Idaho. She also testified that there have been hundreds of cases where SNP DNA was used to identify previously unidentified human remains or a perpetrator in a criminal case using the genetic genealogical landscape in forensic science.

Finally, Dr. Green, an expert in computational biology, populations genetics, forensic science, and the owner of Astrea Forensics, testified with respect to whole genome sequencing and the use of SNP data to create a DNA profile. Dr. Green is a professor of Biomolecular Engineering at the University of California in Santa Cruz where he teaches classes about the technology used to extract DNA out of a sample and the process of sequencing the DNA. He has also written over one hundred peer-reviewed articles with respect to DNA technology, genomics,

and the use of whole genome sequencing, and is the editor of the Forensic Genomics Journal. Dr. Green testified that the research lab at the University focuses on ancient DNA and developing technologies for extracting DNA out of difficult samples or those with little DNA within them (ie. rootless hairs). According to Dr. Green, whole genome sequencing of SNP DNA to create a nuclear DNA profile has been studied by scientists for decades and is widely accepted by the scientific community as reliable. Dr. Green testified that the steps of whole genome sequencing DNA extraction including library preparation and sequencing are used by many labs and are generally accepted as reliable in the scientific community. In addition, Dr. Green testified that the use of SNPs is the best test to use when dealing with a challenging sample with little DNA (ie. rootless hairs). As a result of all of his work with the FBI in helping them to solve cold cases, Dr. Green started Astrea Forensics in 2018. Dr. Green testified that Astrea Forensics receives much of its work from law enforcement, including the FBI, and deals with any sample containing a small amount of fragmented DNA including rootless hairs and old bones. According to Dr. Green, Astrea Forensics has analyzed thousands of DNA samples for law enforcement since 2019. In addition, Dr. Green testified that Astrea Forensics has received DNA samples to analyze from other DNA labs including Othram, Bode, Parabon, and DNA Labs International. Dr. Green has also testified as an expert in courts in Idaho and California. Notably, in 2024, he testified in the criminal case of State of Idaho v David Dalrymple, who was convicted based on Astrea Forensics' use of whole genome sequencing to extract DNA from rootless hairs found on the victim in order to generate SNP data, and created a DNA profile therefrom. In that case, Astrea Forensics also utilized IBDGem to compare the DNA profile generated by Astrea with the DNA profile of a known suspect (David Dalrymple), and the court admitted this novel scientific evidence at trial. While this Court is cognizant of the fact that the State of Idaho does not adopt the Frye test as the State of New York does, but rather focuses on the reliability and relevance of the expert testimony and evidence (*see* Idaho Rules of Evidence 702), novel scientific evidence has been found to be generally accepted as reliable within the scientific community even where "courts in [other jurisdictions] did not use the Frye standard, based on expert testimony, [but] found that the [novel scientific evidence] w[as] sufficiently reliable to be submitted to the jury" (People v Palumbo (162 Misc 2d 650, 656 [Sup Ct, Kings County 1994] [denying defendant's motion for a Frye hearing with respect to the admissibility of PCR test results on the ground that it had been accepted in other jurisdictions and therefore, was generally accepted as reliable]).

Based on the foregoing testimony and evidence admitted at the hearing, and the fact that neither of defendant's expert witnesses controverted Astrea Forensics' use of whole genome sequencing, to extract DNA from rootless hairs to generate SNP data and create a DNA profile therefrom, this Court finds that Astrea Forensic's use of whole genome sequencing to generate SNP data and create a DNA profile therefrom is generally accepted as reliable within the scientific community (*see* Wesley, 83 NY2d 417; Vaughn, 43 NY3d 190; Wakefield, 38 NY3d 367; Williams, 35 NY3d 24; Palumbo, 162 Misc 2d 650).

Turning to Astrea Forensic's use of IBDGem–their probabilistic genotyping software program used to compare the DNA profile generated by them with the DNA profile of a known

suspect–the Court finds it is generally accepted as reliable within the scientific community. This Court bases its finding upon the expert testimony of Dr. Harris and Dr. Green, as well as the peer- reviewed article co-authored by Dr. Green with respect to Astrea Forensic's use of whole genome sequencing and IBDGem (Defendant's B), the numerous peer-reviewed articles which discuss the underlying methodologies used by IBDGem including likelihood ratios, linkage disequilibrium, and the 1,000 Genomes Project as a reference panel (People's 1B, 1E, 2B, 3D), the voluminous validation studies of IBDGem performed by Astrea Forensics, and its use in other jurisdictions (*see* Vaughn, 43 NY3d 190; Wakefield, 38 NY2d 367; Williams, 35 NY3d 24; Palumbo, 162 Misc 2d 650).

Dr. Green testified that IBDGem does a direct one-to-one comparison of data at thousands to hundreds of thousands of SNP positions which yields likelihood ratios far exceeding those routinely achieved with STRs. IBDGem uses a likelihood ratio, which is a comparison of two numbers. Those numbers are the likelihood of some observation given some reality, and a likelihood of the observation given a different reality. He testified that likelihood ratios have been used for over one hundred years, are widely accepted in the field of computational biology, and that he has calculated billions of them. He even discussed peer-reviewed articles (People's 3D) in support of the use of likelihood ratios showing that they are acceptable as reliable in the scientific community. In further support of this, Dr. Harris also testified that she has also used likelihood ratios to calculate how likely some observations were that she made under different scenarios to confirm or disprove her hypotheses, and that the use of a computer program to calculate a likelihood ratio of the statistical significance in whole genome sequencing DNA profiles is widely accepted in the scientific community.

Dr. Green testified that IBDGem places a statistical weight on a DNA sample when it is compared to another DNA sample. IBDGem takes the data that is generated from the sequencer from each sample (rootless hair of unknown individual and buccal swab of known suspect) and compares the data. IBDGem asks the question, "How likely is it that the data I received from this hair comes from a person who has the genotype that I found in the buccal swab? And what is the likelihood that the DNA from the hair came from an unknown, unrelated individual?" The likelihood ratio tells you which one of those different scenarios is bigger and by how much. It can also calculate the probability of a DNA sample from a person of interest as compared to a panel of unknown, unrelated individuals using the 1,000 Genomes Project.

Dr. Green testified that the 1,000 Genomes Project is a well known reference panel which is an adequate representation of worldwide variance and is well accepted within the scientific community as it can be used for any application in genomics, including forensics, where you want an actual catalog of actual people to understand human genetic variation. In further support of this, Dr. Harris testified that the 1,000 Genomes Project is the best public reference panel to use when calculating likelihood ratios in population genetics, and that Dr. Green's IBDGem software's use of the 1,000 Genomes Project is not the only time that the 1,000 Genomes Project has been used by scientists to calibrate statistical significance of SNP DNA testing and comparisons. Dr. Harris testified that in the scientific field, there have been many peer-reviewed

articles (People's 1E) using the data from the 1,000 Genomes Project. Similarly, Dr. Novroski testified that the use of the 1,000 Genomes Project is accepted in the general scientific forensic community as being a sufficient reference panel and is best suited to capture global genetic variation. She also testified that there are labs across the country which utilize the 1,000 Genomes Project to solve cases as well as peer-reviewed articles supporting the use of the 1,000 Genomes Project (People's 2B). Dr. Novroski also testified that comparing a SNP DNA sample to a sample from a reference panel (such as the 1,000 Genomes Project) as well as attaching a statistical significance to that comparison is generally accepted by the forensic scientific community.

Dr. Green testified that in all of the numerous validation studies he performed, IBDGem never had a false positive or false negative outcome when he tested two samples of DNA from the same individual (i.e hair and saliva from same person). He explained that when he performed a negative control test, when he knew that the DNA was not coming from that exact person, IBDGem showed stronger evidence in support of what he knew to be the correct answer, and less evidence than when he performed a test where the DNA did come from that exact individual. Dr. Green testified that the IBDGem program is very conservative in that it overestimates the likelihood in the denominator of the equation which benefits the defense. After reviewing all of the results of the tests conducted by Dr. Green set forth in his paper, Dr. Harris concluded that the IBDGem method using its likelihood ratio was confident about both outcomes, and was accurate.

Dr. Green testified that his peer-reviewed paper (Defendant's B), which detailed the use of IBDGem on rootless hairs was written after a study was performed using DNA samples (rootless hairs and saliva) from 8 individuals. They conducted both positive (comparing saliva and hair from same person) and negative (comparing hair from one individual and saliva from a different individual) control tests. Each computation performed by IBDGem gave strong support for what Dr. Green knew to be the correct answer. Dr. Green showed all of the likelihood ratios IBDGem calculated in the form of graphs in his Power Point presentation (People's 3). The likelihood ratios are negative on the graphs when the DNA sample did not come from an unknown, unrelated individual. Dr. Green testified that there was always statistical support for what answer he knew to be true. Dr. Harris testified that while peer reviewing Dr. Green's paper, she studied the equations used by Dr. Green in his IBDGem computer software program, his studies, and his results, and found that IBDGem was reliable. In her opinion, IBDGem is "suitable for forensic use" and "generally accepted in the scientific community."

With respect to the accuracy of IBDGem, Dr. Green has tested the IBDGem software for accuracy, and after conducting studies on the reliability of IBDGem, Dr. Green wrote a paper which is still in the process of being peer-reviewed. One quality assurance measure used to make sure the DNA did not come from multiple sources is another program created by Dr. Green called Tilda. Dr. Green explained how Tilda is run before the samples are placed in IBDGem and runs an analysis of the evidence sample by itself to see if the nuclear DNA in the sample is consistent with coming from a single source. He testified about a second quality assurance used

by Astrea Forensics before samples are placed in IBDGem called MixENT. He explained that MixENT is a computer program which reads the library of the DNA which comes from the mitochondria, which is inherited from a person's mother. The mitochondrial DNA of the DNA sample should be the same type throughout. If the computer software shows different variants, then the sample comes from different mitochondrial versions which is evidence that the sample is a mixture of DNA samples and not just from one source. Dr. Green has published peer-reviewed articles on both Tilda and MixENT.

Dr. Green further testified that he conducted another test to ensure the accuracy of IBDGem using 50 individuals who donated saliva and a cut piece of head hair (30 of those individuals also donated a pubic hair). Dr. Green published the results from the 4,000 positive and negative control tests IBDGem completed on these samples on a website. IBDGem never got a positive likelihood ratio from a known non-contributor or a negative likelihood ratio from a known contributor. Dr. Green also tested IBDGem for when errors would occur by intentionally creating issues or problems (ie. sequencing error, DNA mixtures) to see how the computer program would work under those conditions. Even with errors, IBDGem still gave the correct answer. The more errors Dr. Green introduced into the program, the less positive the likelihood ratio was but it was still positive and gave the correct answer for what he knew to be true. Another way Dr. Green tested the accuracy of IBDGem, was by using another company's computer program to take the DNA sequence data from a sample and infer a genotype with it. Normally, Astrea uses its own program, Astrea Impute 2, to perform this prior to using IBDGem. Here, Dr. Green used a program called GATK (Genome Analysis Tool Kit) and another program called GLIMPSE. The results with the negative control experiments produced a more negative likelihood ratio than the positive control experiments produced a positive ratio. This again showed that IBDGem is conservative as it is more confident when its making a negative comparison than when making a positive comparison. While the numbers were a bit different, Dr. Green received the same results he would have with IBDGem and Astrea Impute 2 as he did using IBDGem and these other programs. All the results show strong statistical support for the correct answer. Dr. Green testified that the use of Astrea Impute 2 is accepted in the scientific community as it calls genotypes from sequence data.

While the defense takes issue with the fact that all of the validation studies done of IBDGem were performed by Dr. Green, who is the creator of IBDGem, it has been held that the fact that a developer of a computer software program was involved "in many of the validation studies does not preclude a determination of general acceptance as a matter of law (Wakefield at 382). In Wakefield, the court noted, as defense counsel notes in this case, their concern that not only was the creator of the computer software involved in the validation studies performed, but that the technology was proprietary. Despite this, the court found that "[t]his skepticism, however, must be tempered by the import of the empirical evidence of reliability demonstrated here and the acceptance of the methodology by the relevant scientific community" (Wakefield at 381).

In addition to co-authoring a peer-reviewed paper on IBDGem showing all of his tests

and results using IBDGem were accurate and reliable, Dr. Green testified that IBDGem has been available for public use for a few years. It has been held that where, as here, "[t]he mathematical and scientific principles underlying the [software] system . . . are well-established and independent validation of the reliability of the software is available in the form of a free trial that can be used to verify a known sample," this is further proof that it is generally accepted as reliable in the scientific community (Wakefield at 376).

As noted earlier, IBDGem was accepted as reliable by the State of Idaho in the case of State of Idaho v David Dalrymple. Again, this Court notes that the State of Idaho does not adopt the Frye test. However, novel scientific evidence has been found to be generally accepted as reliable within the scientific community even where "courts in [other jurisdictions] did not use the Frye standard, based on expert testimony, [but] found that the [novel scientific evidence] w[as] sufficiently reliable to be submitted to the jury" (Palumbo at 656). The Court further notes that Dr. Krane and Nathaniel Adams– the defense witnesses in this hearing–testified in the Dalrymple case, that IBDGem was not generally accepted as reliable in the scientific community, and the Court nevertheless found that it was, and admitted the DNA evidence obtained using IBDGem. The Court notes that there were also other criminal cases in California where IBDGem was used. While those cases never went to trial as one defendant pleaded guilty and the other was found unfit to stand trial due to severe mental illness, IBDGem was able to create a DNA profile for both suspects (Robert Lanoue and Jurn Norris) from rootless hairs left at crime scenes in 1979 and 1982.

The Court notes that while there has yet to be another peer-reviewed article written specifically in support of IBDGem, Dr. Green's paper has been cited at least 8 or 9 times. In addition, there have been many peer-reviewed articles discussing and accepting as reliable the underlying methodologies used by IBDGem including likelihood ratios, the use of the 1,000 Genomes Project as a reference panel as well as the use of linkage disequilibrium (People's 1B, 1E, 2B, 3D). To date, the only peer-reviewed paper criticizing IBDGem was written by Dr. Krane (Defendant's O), an expert in forensic DNA profiling, molecular biology, bioinformatics and population genetics, who was also one of the witnesses for the defense in this case. At the outset, the Court notes that Dr. Krane has always testified on behalf of the defense and against the admissibility of novel scientific evidence. In addition, Dr. Krane testified that he has never worked in a forensic crime lab or generated a DNA profile from a crime scene sample. The Court also notes that the first draft of Dr. Krane's paper criticizing Dr. Green's paper was rejected by the Journal of Forensic Science International: Genetics as well as the Journal of Heredity, and was only published in May 11, 2025, by the Journal of Forensic Science International: Genetics after he submitted a second draft. Notably, Dr. Green was asked by that journal to write a peer review of Dr. Krane's paper. Dr. Green testified that he explained in his peer review that Dr. Krane's paper tried to explain how IBDGem worked after Dr. Krane used the program without any actual human data. Dr. Green testified that he uses actual human data when using IBDGem. In addition, Dr. Green noted that Dr. Krane used much smaller reference panels than the 1,000 Genomes Project, did not calculate the likelihood ratio in the manner done using IBDGem, and did not conduct testing comparing a sample to a non-contributor. In fact, Dr.

Krane testified that the data he used was from a haploid, and that IBDGem uses diploid data since humans are diploids. He also testified that he used a sample size of 5 simulated DNA profiles, yet he testified that the 2,504 sample size in the 1,000 Genomes Project was not large enough. In addition, Dr. Krane's data was run using linkage equilibrium but Dr. Krane testified that humans are in linkage disequilibrium, and that IBDGem uses linkage disequilibrium. In another test run by Dr. Krane, he used a sample size of 100 and used diploids. However, the DNA was simulated for the diploids, and was not real.

Although Dr. Krane also testified that the likelihood ratios generated by IBDGem were much larger than those computed for more standard forensic null hypothesis and creates the impression of stronger evidence for identity than is warranted, Dr. Krane did not testify that IBDGem reached the incorrect answer (produced a false positive or false negative answer) but only overinflated the likelihood ratio of the answer. He also testified that IBDGem generates a likelihood ratio asking a fundamentally different question, to wit, "what is the chance that this DNA sample is from one of the 2,504 people from the 1,000 Genomes reference panel for whom we have whole genome sequence information?" In his opinion, the better question is what has been asked for years which is, "what is the chance that a randomly chosen, unrelated person from a given reference population might also be confused as being the source of DNA found in common between a suspect and an evidence sample?" The Court notes that while the question IBDGem asks may be different, this does not make it incorrect.

Additionally, Dr. Krane's biggest critique of the IBDGem program was its use of the 1,000 Genomes Project as an alternate suspect pool as he believes IBDGem looks to see if the DNA sample actually came from someone in the 1,000 Genomes Project. However, Dr. Green testified that the 1,000 Genomes Project is used for statistical purposes in the denominator of the IBDGem formula to establish a likelihood ratio. Thus, this critique is flawed.

Turning to the testimony of the second witness proffered by the defense, Nathaniel Adams, while Mr. Adams purports to be an expert in software development and probabilistic genotyping software, and has been found in other courts to be considered an expert, this Court disagrees. Mr. Adams only obtained his Bachelor's Degree from Wright University ten years after starting his collegiate career. In addition, while he started his Master's Degree program at Wright University, and completed all of the course work therefor in 2017, he still has not obtained a Master's Degree as he never completed his Master's Degree thesis. In addition, Mr. Adams has not published one peer-reviewed article. The Court also notes that Dr. Krane, the other witness for the defense in this hearing, was Mr. Adams' professor at Wright State University where he received his Bachelor's of Science in 2014, is on his Master's Degree thesis committee, and is his current boss. Interestingly, the Court notes that Dr. Krane testified that he wrote a chapter in a book about DNA (People's 29) which contains a section with respect to defense lawyers' cross examination of DNA experts and how to challenge the expert's credentials. In that section, Dr. Krane wrote, "If the witness does not have at least a Master's Degree, you may be in a position not only to hammer on the witness's lack of credentials, but also to strike a damaging blow based upon the lack of sophisticated knowledge." Based upon the

foregoing, this Court does not find Mr. Adams to be a sufficient expert in software development and probabilistic genotyping software. The Court also notes that Mr. Adams has only testified on behalf of defendants and has always testified against the admissibility of new scientific computer software. In any event, Mr. Adams' critique of IBDGem was flawed. Mr. Adams testified that IBDGem did not adhere to IEEE standards but then conceded that adherence to IEEE standards is not mandatory but voluntary (*see* People v Burrus, 81 Misc3d 550 [Sup Ct, Kings County 2023]). Mr. Adams also testified with respect to the computer software programs used by IBDGem, and stated that there was no description of how the software programs interacted with one another or how any of them were specifically configured or used. However, Mr. Adams admitted that he never reviewed the pipeline software provided by Astrea Forensics with respect to IBDGem which would have described each program, how they were used, in what order they were used, and how they interacted with each other.

In conclusion, neither Dr. Krane nor Mr. Adams provided "empirical proof to refute the validated empirical evidence" presented by Dr. Green with respect to the validity and reliability of IBDGem (Williams at 54 n 6). Furthermore, Dr. Green testified, and this Court agrees, that while IBDGem is a relatively new software system, the principles used within it, which are behind the math used and data collected, are accepted as reliable in the scientific community based on the numerous peer review articles written with respect to the use of likelihood ratios as well as the use of the 1,000 Genomes Project as a reference panel and the use of linkage disequilibrium, all of which are implemented by IBDGem.

Therefore, it is

ORDERED that nuclear DNA results as well as expert testimony pertaining to said nuclear DNA results obtained from rootless hairs recovered from the person and/or crime scene of Maureen Brainard Barnes, Megan Waterman, Amber Costello, Sandra Costilla, Jessica Taylor and Valerie Mack, are admissible at trial.

Dated: September 3, 2025

HON. TIMOTHY P. MAZZEI, J.S.C.