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Assigned Attorney:
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Jay W. Logsdon, Chief Deputy Public Defender, Bar Number: 8759
Elisa G. Massoth, Attorney at Law, Bar Number: 5647

IN THE DISTRICT COURT OF THE SECOND JUDICIAL DISTRICT OF THE STATE OF IDAHO, IN AND FOR THE COUNTY OF LATAH

STATE OF IDAHO **Plaintiff,** **V.** **BRYAN C. KOHBERGER,** **Defendant.**	**CASE NUMBER CR29-22-2805** **NOTICE OF FILING AFFIDAVIT OF LEAH LARKIN IN SUPPORT OF DEFENDANT'S THIRD MOTION TO COMPEL**

COMES NOW, Bryan C. Kohberger, by and through his attorney of record, Anne C. Taylor, Public Defender, and hereby files the attached Affidavit of Leah Larkin in support of the Defendant's Third Motion to Compel.

DATED this ___9____ day of August, 2023.

ANNE C. TAYLOR, PUBLIC DEFENDER
KOOTENAI COUNTY PUBLIC DEFENDER

BY: _____
ANNE TAYLOR
PUBLIC DEFENDER
ASSIGNED ATTORNEY

CERTIFICATE OF DELIVERY

I hereby certify that a true and correct copy of the foregoing was personally served as indicated below on the ___9____ day of August, 2023 addressed to:

Latah County Prosecuting Attorney –via Email: paservice@latahcountyid.gov
Elisa Massoth – via Email: legalassistant@kmrs.net

Anne C. Taylor, Public Defender
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Jay W. Logsdon, Chief Deputy Public Defender, Bar Number: 8759
Elisa G. Massoth, Bar Number: 5647

IN THE DISTRICT COURT OF THE SECOND JUDICIAL DISTRICT OF THE STATE OF IDAHO, IN AND FOR THE COUNTY OF LATAH

STATE OF IDAHO **Plaintiff,** **V.** **BRYAN C. KOHBERGER,** **Defendant.**	**CASE NUMBER CR29-22-2805** **AFFIDAVIT OF LEAH LARKIN**

STATE OF California
: ss.
County of Alameda)

1. I am an adult, over the age of 18, and I have personal knowledge of the facts set forth in this Affidavit;

2. I have been engaged as an expert in the above-entitled matter since July 27, 2023.

3. I am a genetic genealogist, having practiced genetic genealogy since 2014. My educational background is a bachelor's degree in Biology and a PhD in Botany. My curriculum vitae is

attached. As a genetic genealogist, I have a clear understanding of how genetic genealogy works. I have developed tools that are in widespread use by genealogy practitioners.

4. Genetic genealogy is best described as the use of DNA data to evaluate biological relationships. There are three categories of genealogical DNA test: Y-chromosome DNA (direct paternal line only), mitochondrial DNA (direct maternal line only), and autosomal DNA (all branches of a pedigree). A genetic genealogist integrates information from these DNA tests with genealogical documentation to reveal or corroborate relationships.

5. Genetic genealogy primarily uses autosomal DNA tests that were originally designed for biomedical research. Since 23andMe brought their health tests to the consumer market in late 2007, FamilyTreeDNA, AncestryDNA, MyHeritage, and a handful of smaller companies have launched their own genetic genealogy products. These companies all provide genealogy tools to their customers on their websites and also produce a "raw DNA data file" that the customer can download. The raw data file contains the genetic profile for that customer. This genetic profile is not the same as an STR profile that is commonly uploaded to CODIS in a forensic DNA analysis.

6. Most of the human genome is identical across all people. Only the DNA positions that vary between individuals are useful for genealogy. These variable positions are called "single nucleotide polymorphisms" (SNP, pronounced "snip"). The direct-to-consumer genealogy companies use a type of test called a microarray that samples roughly 600,000 of these DNA SNPs. Unlike the STR markers used for matching in CODIS, SNPs can convey information about medical and physical traits as well as biological relationships to close and distant cousins.

7. A microarray SNP profile is sometimes called a "kit." Once the lab test is complete, the genealogy company compares the new kit to those already in its database looking for long stretches of SNPs that are compatible. The company then presents these matches in a list, sorted by the amount of shared DNA measured in "centimorgans" (abbreviated cM).[1]

8. A standard DNA microarray requires approximately 200 ng of quality DNA.[2] That quality and quantity is often not available from crime scenes or degraded human remains. Instead, specialized laboratories can generate a SNP profile through a more complex process. First, they attempt to sequence the entire genome using "next-generation sequencing" (NGS) technology. This technology works a bit like skimming while reading a document. On the first pass, NGS technology will not capture all of the data, and it may make mistakes. NGS

[1] The default sorting at 23andMe is not by centimorgans but by "Strength of Relationship."

[2] Illumina, Infinium Global Screening Array (https://www.illumina.com/products/by-type/microarray-kits/infinium-global-screening.html : accessed 7 August 2023)

involves repeated passes (called "coverage") to get more accurate results. For human genome sequences, 30x to 50x coverage is recommended.[3]

9. Once the NGS file is obtained, it must be manipulated through bioinformatics to make it compatible with the genealogy databases. The extra data must be stripped out to just the SNPs that the genealogy companies test, and missing or ambiguous data must be inferred using statistical methods. The kit is then uploaded to a genealogy database and evaluated. A poor quality kit might have too few matches or it might have phantom matches that are not real measures of relationship. Often, the bioinformatics step must be repeated. This trial-and-error process can take several tries to produce a kit that works well in a genealogy database.

10. Only GEDmatch, FamilyTreeDNA, and some smaller entities allow crime scene and human remains samples to be uploaded. The Terms of Service at AncestryDNA, 23andMe, and MyHeritage prohibit forensic/investigative genetic genealogy in their databases.[4,5,6] However, in the absence of effective oversight, forensic genetic genealogists are on an "honor system" to obey the Terms of Service and the Department of Justice Interim Policy on forensic genetic genealogy.

11. Each of the genealogy databases compares the user's DNA data to all of the other data files in their database then presents a list of "DNA matches" who share meaningful amounts of DNA. The match list includes the match's name or alias, how much DNA they share in centimorgans, and occasionally a link to a family tree that the match has voluntarily provided.

12. The genetic genealogy databases are siloed from one another. If you test at AncestryDNA and your sibling tests at 23andMe, you will not be matched to one another because you are not in the same database. GEDmatch is a third-party site that functions as a genetic genealogy commons; a user can upload their raw DNA data file from their testing company and find matches to people who uploaded to GEDmatch from different companies. Like GEDmatch, FamilyTreeDNA and MyHeritage also allow uploads of raw data files; AncestryDNA and 23andMe do not.

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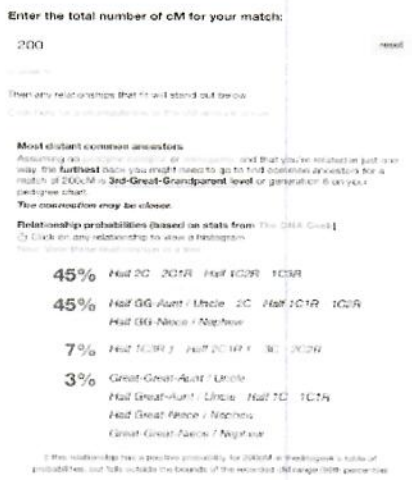
[3] Illumina, Coverage depth recommendations, (https://www.illumina.com/science/technology/next-generation-sequencing/plan-experiments/coverage.html : accessed 7 August 2023)

[4] AncestryDNA's Terms state, "You also agree: .... Not to use the information obtained from the DNA Services (including any downloaded DNA Data (defined in the Privacy Statement)) in whole, in part, and/or in combination with any other database, for any medical, diagnostic, or paternity testing purpose, in any judicial proceeding, or for any discriminatory purpose or illegal activity."

[5] 23andMe's Terms state: "You will not use the Services for any investigative forensic genealogy uses."

[6] MyHeritage's Terms state: "using the DNA Services for law enforcement purposes, forensic examinations, criminal investigations, "cold case" investigations, identification of unknown deceased people, location of relatives of deceased people using cadaver DNA, and/or all similar purposes, is **strictly prohibited**, unless a court order is obtained."

13. Broadly speaking, the more DNA two people share, the more closely they are related. The correlation is not perfect, though. Any given centimorgan amount can represent more than one possible relationship. The testing companies suggest probable relationships, but experienced genetic genealogists typically use the online "Shared cM Tool" (shown at right for a hypothetical match of 200 cM) to see mathematical probabilities of different relationships for a given centimorgan amount.[7] Note that there are nearly 20 possible relationships listed for a match of 200 cM, which is considered a fairly close match.



14. Adoptees have used genetic genealogy DNA tests to identify their biological families for roughly 15 years now. The same methods used for people with unknown parentage can be used to identify forensic samples from a crime scene or unidentified human remains. Unlike standard forensic STR tests which are used to identify individuals, genetic genealogy testing identifies possible relatives.

15. First, the genealogist attempts to build family trees for the DNA matches of the person of interest, starting with the closest matches. Relatively few users at GEDmatch and FamilyTreeDNA post their pedigrees there, so the genealogist must build trees for them. We attempt to identify the match using their screen name and email address. Then, we search public records, social media, obituaries, news articles, and genealogy websites to build out their tree through their parents, grandparents, and so on. Most genetic genealogists build these so-called research trees at Ancestry.com.

16. The goal of building trees is to figure out how two or more matches are related to one another. For example, if the person of interest matches two people who share a great-grandparent couple (making them 2nd cousins to one another), the genealogist now knows which branch of *their* tree is relevant to the search. The person of interest could be descended from that couple, or the connection could be one or more generations further back through either the husband or the wife in that couple.

17. Once several of the DNA matches have been connected to one another, the genealogist must figure out how the person of interest fits into the tree of those matches. We use age, sex, geographic location, and other circumstantial evidence alongside the DNA-based relationship predictions. A statistical tool called "What Are the Odds?" can analyze multiple DNA matches

[7] Jonny Perl, Blaine Bettinger, and Leah Larkin, 2020, The Shared cM Project 4.0 tool v4 (https://dnapainter.com/tools/sharedcmv4 : accessed 7 August 2023).

together to evaluate where the person of interest best fits into the tree based on the amounts of shared DNA.[8]

18. "What Are the Odds?" is not intended to give a definitive answer, rather it points the genealogist toward the most likely branches in the tree for further research. The tool is also not appropriate for all circumstances. For example, it is not intended for populations that married within themselves, for double cousins, or when most of the matches are below 40 cM.

19. The genealogist needs to do this for both the maternal and paternal sides of the person of interest's pedigree. Often, this involves building dozens of trees and performing several "What Are the Odds?" analyses. We are looking for instances where a descendant in one DNA family tree married a descendant in another DNA family tree, because those unions point to where the person of interest might fit into the tree. Often, the best we can do with the existing DNA matches is to focus on a set of cousins as candidates. Then, more DNA testing is required.

20. This process can vary in complexity depending on the individual starting point. In doing this type of research, the genetic genealogist will generate numerous documents to ensure an adequate paper trail. This paper trail can include: the list of DNA matches, the research tree with genealogical documentation, public record searches for members of the DNA family, correspondence with DNA matches, descendant diagrams showing how the DNA matches are related to one another, and "What Are the Odds?" analyses. This documentation is necessary and important for the following reasons: DNA matches sometimes hide their profiles, an error in the tree can mislead the genealogist, and the descendant diagrams and What Are the Odds? analyses are usually updated repeatedly during a search.

21. As a Genetic Genealogist I have learned about the power and the privacy implications of genetic genealogy. The tests themselves were designed to reveal biomedical information and can also reveal "family secrets" about the tester. In many cases, private information can be inferred about the DNA relatives of the tester as well.[9] For those reasons, leaders in the genetic genealogy community developed standards that emphasize consent and privacy.[10]

22. I am aware of the Department of Justice Interim Policy to limit when Forensic Genetic Genealogy can be used and which databases are accessible to law enforcement.[11] It is possible

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[8] Jonny Perl, Leah Larkin, and Andrew Millard, 2018, What Are the Odds? (https://dnapainter.com/tools/probability : accessed 4 August, 2023).

[9] Leah Larkin, 2017, Cystic fibrosis: A case study in genetic privacy, The DNA Geek Blog (https://thednageek.com/cystic-fibrosis-a-case-study-in-genetic-privacy/ : accessed 2 August 2023)

[10] Leah Larkin, 2017, Cystic fibrosis: A case study in genetic privacy, The DNA Geek Blog (https://thednageek.com/cystic-fibrosis-a-case-study-in-genetic-privacy/ : accessed 2 August 2023)

[11] United States Department of Justice, 2019, Interim Policy: Forensic Genetic Genealogical DNA Analysis and Searching (https://www.justice.gov/olp/page/file/1204386/download : accessed 7 August 2023)

for the databases to be utilized in a way that circumvents these core principles. Notably, I am aware of:

a. A case in which the chain of custody failed and the wrong SNP profile was sent to the wrong client.
b. Investigative genetic genealogists uploading SNP profiles to a forbidden database in violation of that company's Terms of Service and the Department of Justice Interim Policy.
c. Forensic genetic genealogy being used for a case that did not meet the Department of Justice threshold.
d. Investigative genetic genealogists using security loopholes to see DNA kits who are opted out of forensic matching at GEDmatch and FamilyTreeDNA.
e. A case in which a SNP profile was performed on an innocent woman, a potential Fourth Amendment violation of her right to privacy, and uploaded to GEDmatch without her knowledge or consent.

23. Having access to the data and methods used to identify someone will provide answers to:
    a. compliance with Department of Justice Policies;
    b. how a DNA sample was handled from the time of collection through its forensic genetic genealogy testing;
    c. the process of SNP creation;
    d. the use of the SNP profile;
    e. the use (or lack thereof) of loopholes and violations of terms of service to the various genetic genealogy databases.

FURTHER YOUR AFFIANT SAYETH NAUGHT.

DATED this 8th day of August, 2023.

LEAH LARKIN

SUBSCRIBED AND SWORN to before me this _____ day of August, 2023.

see CA Attached

Notary Public in and for the State of _____
Commission Expires:

CALIFORNIA JURAT WITH AFFIANT STATEMENT **GOVERNMENT CODE § 8202**

☑ See Attached Document (Notary to cross out lines 1–6 below)
☐ See Statement Below (Lines 1–6 to be completed only by document signer[s], *not* Notary)

1
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Signature of Document Signer No. 1 *Signature of Document Signer No. 2 (if any)*

A notary public or other officer completing this certificate verifies only the identity of the individual who signed the document to which this certificate is attached, and not the truthfulness, accuracy, or validity of that document.

State of California
County of Alameda

Subscribed and sworn to (or affirmed) before me on this 8th day of August, 2023,
Date *Month* *Year*
by
(1) Leah Laperle Larkin
(and (2)_____),
Name(s) of Signer(s)

proved to me on the basis of satisfactory evidence to be the person(s) who appeared before me.

JONATHAN SALVADOR ROMAN
Notary Public - California
Alameda County
Commission # 2422872
My Comm. Expires Oct 23, 2026

Signature Jonathan Roman
Signature of Notary Public

Seal
Place Notary Seal Above

OPTIONAL

Though this section is optional, completing this information can deter alteration of the document or fraudulent reattachment of this form to an unintended document.

Description of Attached Document

Title or Type of Document: Affidavit of Leah Larkin **Document Date:** August 8th, 2023

Number of Pages: 6 **Signer(s) Other Than Named Above:** _____

Leah LaPerle Larkin, Ph.D.

Genetic Genealogy Expert
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OVERVIEW

Professional genetic genealogist, educator, and innovator

EDUCATION

Ph.D. in Botany, 2002	University of Texas at Austin	Austin, TX
B.A. in Biology, 1991	Swarthmore College	Swarthmore, PA

PROFESSIONAL EXPERIENCE

Genetic Genealogy

2016– Founder and Lead Genealogist at *The DNA Geek* — Livermore, CA
Consulting services for unknown parentage searches, genealogy speaker and educator

2016– Author of The DNA Geek Blog (253 posts as of 24 July 2023)
Highlighting the science, methods, and ethics of genetic genealogy

2023 Co-developer of BanyanDNA, an online tool for advanced genetic genealogy analyses

2018 Co-developer of the What Are the Odds? tool (WATO), a revolutionary tool for statistical analyses of autosomal DNA matches

2018 Genealogist for the TLC television show *Taken at Birth*

2017 Genealogy consultant for the TLC television show *I Should Have Known*

2016–2018 Editor, *Journal of Genetic Genealogy*
Solicited manuscripts, coordinated peer reviews, edited papers for publication

Scientific Editing and Grant Writing

2011–2015 Scientific Editor, Edanz Group — Hong Kong
Provided English-language scientific editing and publication-related services to clients globally

2011–2015 Scientific Editor, ISIS Group — Cambridge, MA
Revise and refine grant proposals to US funding agencies for primarily biomedical research scientists

Teaching and Assessment

2014 Freelance Pedagogy Writer (HS Biology), Pearson White Plains, NY
Wrote instructional materials for 10-day professional development workshop for teachers

2013–2015 Freelance Content Specialist (K–12 Math), Symmetry Barrington, IL
Wrote and edited standardized test items, workbooks, and digital interactive learning materials

2014 Freelance Assessment Writer (G5 and G7 Biology), Questar Assessment Brewster, NY

2014 Freelance Course Evaluator (HS Health Course), CompassLearning Austin, TX

2013 Freelance Lesson Writer (G8 Life Science), SureScore Austin, TX

2013 Adjunct Lecturer, San Francisco State University (Evolution) San Francisco, CA

2008–2010 Assistant Professor of Biological Sciences, University of the Pacific Stockton, CA
Courses: Principles of Biology I & II, Evolution, Biology of Insects, Evolutionary Medicine, Undergraduate Research

2006–2008 Adjunct , University of New Mexico Albuquerque, NM
Courses: Plant–Insect Interactions, Biology for Non-Majors, Systematics Seminar

2003, Fall Instructor, TVI (now CNM) Community College Albuquerque, NM
Courses: Introductory Biology for Majors, Biology for Non-Majors

1992–2000 Teaching Assistant, The University of Texas Austin, TX
Courses: General Botany, Native Plants, Field Biology, Ecology and Evolution, Laboratory in Cell & Molecular Biology, Laboratory in Structure & Function of Organisms.

Scientific Research

2004–2008 Research Assistant Professor of Biology, University of New Mexico Albuquerque, NM
Conducted independent research on insect taxonomy; supervised undergraduate research students

2007–2009 National Science Foundation grant-review panel member, *ad hoc* grant reviewer for the NSF, the National Geographic Society, and the University of New Mexico Department of Biology

2005–2010 *Ad hoc* manuscript reviewer for scientific journals

2000–2001 Assistant editor, *Lundellia: Journal of the Plant Resources Center of UT-Austin*

1998–1999 Botany Research Assistant, The University of Texas at Austin Austin, TX

1991–1992 McHenry Research Fellow, Academy of Natural Sciences Philadelphia, PA

1989–1990 Biochemistry Research Technician, Swarthmore College Swarthmore, PA

GENETIC GENEALOGY PRESENTATIONS

2023	Applied Genetic Genealogy (4-week course)	Applied Genealogy Institute
	Autosomal and X-DNA Analysis	Salt Lake Institute of Genealogy
	From Madness to Method: Making Sense of Your DNA Results	Eventbrite
	LucidChart for Genetic Genealogy	DNAngels
		Eventbrite
	No One Told Me There Would Be Math! DNA Numbers Made Easy	
		Eventbrite
	Relationship Predictors	Eventbrite
	SOLVED! Case Studies in Genetic Genealogy	Eventbrite
	Third Party Tools	Salt Lake Institute of Genealogy
	What's Next? Your Future in Genetic Genealogy	
		Salt Lake Institute of Genealogy
	When Your Tree Is a Banyan: Untangling Endogamy	Eventbrite
	Working With WATO (What Are the Odds?)	Eventbrite
		Pima County (AZ) Genealogical Society
		Texas Institute of Genealogical Research
2022	Applied Genetic Genealogy (4-week course)	Applied Genealogy Institute
	DNA Directions (3-part workshop)	Family History Academy
	From Madness to Method: Making Sense of Your DNA Results	Eventbrite
	The Hicks Babies: Research Strategies for Adoptees	Eventbrite
		Connecticut Society of Genealogists
		South King County (WA) Genealogical Society
	Panel on Human Chimerism: Developmental Biology	
		Association of Professional Genealogists Forensic Genealogy Group
	SOLVED! Case Studies in Genetic Genealogy	Eventbrite
	What Are the Odds? Workshop (2-part workshop)	Family History Academy
	When Your Tree Is a Banyan: Untangling Endogamy	Eventbrite
	Working With WATO (What Are the Odds?)	Eventbrite
		Ventura County (CA) Genealogical Society
2021	Evaluating Shared Autosomal and X-DNA	Salt Lake Institute of Genealogy
	From Madness to Method: A Step by Step Guide to DNA	SCGS Jamboree
	From Madness to Method: Making Sense of Your DNA Results	Eventbrite
	Introduction to WATO (What Are the Odds?)	
		Auckland & Christchurch (New Zealand) Family History Expos
	What's Next? Your Future in Genetic Genealogy	
		Salt Lake Institute of Genealogy
	When Your Tree Is a Banyan: Untangling Endogamy	RootsTech
		Auckland & Christchurch (New Zealand) Family History Expos
		Ventura County (CA) Genealogical Society
	Working With WATO (What Are the Odds?)	SCGS Jamboree

2020 The Hicks Babies: Research Strategies for Adoptees
Austin (TX) Genealogical Society
Introduction to What Are the Odds? (WATO) RootsTech, Salt Lake City, UT
What Are the Odds? (WATO) Right to Know
What Are the Odds? (WATO) Workshop RootsTech, Salt Lake City, UT
2019 The Hicks Babies: Research Strategies for Adoptees
SCGS Jamboree, Burbank, CA
The Uses and Misuses of Segment Data SCGS Jamboree, Burbank, CA
What Are the Odds? (WATO): A Workshop SCGS Jamboree, Burbank, CA
What Are the Odds? Getting the Most Out of AutoClusters, Theory of Family Relativity™, and DNA Matches MyHeritage Live, Amsterdam, Netherlands
When Your Tree Is a Banyan: Untangling Endogamy in your Family History
Family History Fanatics
2018 Beyond Centimorgans: Segment Size and Number Can Distinguish Relationships SCGS Jamboree, Burbank, CA
Genome Mate Pro workshop SCGS Jamboree, Burbank, CA
When Your Tree Is a Banyan: Untangling Endogamy in your Family History
SCGS Jamboree, Burbank, CA
2017 Science the Heck Out of Your DNA: Using Hypotheses and Probability to Solve Genealogical Problems i4GG conference, San Diego, CA
2016 When Your Tree Is a Banyan: Coping with Endogamy in Genetic Genealogy
i4GG conference, San Diego, CA

SCIENTIFIC PUBLICATIONS

Geurts, P., L. Zhao, Y. Hsia, E. Gnesa, S. Tang, F. Jeffery, C. La Mattina, A. Franz, **L. Larkin**, and C. Vierra. 2010. Synthetic spider silk fibers spun from pyriform spidroin 2, A glue silk protein discovered in orb-weaving spider attachment discs. *Biomacromolecules* 11: 3495–3503.

Marshall, D. L., A. P. Tyler, M. G. Shaner, N. J. Abrahamson, J. J. Avritt, M. G. Barnes, **L. L. Larkin**, J. S. Medeiros, J. Reynolds, H. L. Simpson, and S. Maliakal-Witt. 2010. Pollen performance of *Raphanus sativus* (Brassicaceae) declines over time in response to elevated [CO_2] *Plant Sexual Reproduction* 23: 325–336.

Blasingame, E., T. Tuton-Blasingame, **L. Larkin**, A. M. Falick, P. Geurts, X. Hu, V. Vaidyanathan, A. Visperas, C. La Mattina, and C. Vierra. 2009. Pyriform spidroin 1, a novel member of the silk gene family that anchors dragline silk fibers in attachment discs of the black widow spider, *Latrodectus hesperus. Journal of Biological Chemistry* 284 (42): 29097–29108.

Brady, S. G., **L. L. Larkin**, and B. N. Danforth. 2009. The timeline of aculeate evolution. *Invited chapter to* The TimeTree of Life, ed. Blair Hedges & Sudhir Kumar, Oxford University Press.

Larkin, L. L., J. L. Neff & B. B. Simpson. 2008. The evolution of a pollen diet: Host choice and diet breadth of Andrena bees (Hymenoptera: Andrenidae). *Apidologie* 39: 133–145.

Larkin, L. L., S. Droege, R. Andrus and T. Griswold. 2006. An interactive web-based key to the *Andrena* species of the eastern United States. *Online at:* http://pick5.pick.uga.edu/mp/20q?guide=Andrena_female and guide=Andrena_male.

Simpson, B. B., **L. L. Larkin**, A. Weeks, & J. McDill. 2006. Phylogeny and biogeography of *Pomaria* (Caesalpinioideae: Leguminosae). *Systematic Botany* 31(4): 792–804.

Pohl, T. & **L. L. Larkin**. 2006. A new species of *Andrena* (Hymenoptera: Andrenidae) from Mexico. *Journal of the Kansas Entomological Society* 79(1): 104–109.

Larkin, L. L., J. L. Neff & B. B. Simpson. 2006. Phylogeny of the *Callandrena* subgenus of *Andrena* (Hymenoptera: Andrenidae) based on mitochondrial and nuclear DNA data: Polyphyly and convergent evolution. *Molecular Phylogenetics and Evolution* 38(2): 330–343.

Larkin, L. L. 2004. Four new species of fall *Andrena* from the southwestern United States. *Journal of the Kansas Entomological Society* 77(3): 254–268.

Simpson, B. B., A. Weeks, D. M. Helfgott & **L. L. Larkin**. 2004. Species relationships in *Krameria* (Krameriaceae) based on ITS sequences and morphology: Implications for character evolution and biogeography. *Systematic Botany* 29(1): 97–108 + cover photo.

Simpson, B. B., **L. L. Larkin**, & A. Weeks. 2003. Progress towards resolving the relationships of the *Caesalpinia* group (Caesalpinieae: Caesalpinioideae: Fabaceae). pp. 123–148 *In* B. Klitgaard & A. Bruneau (editors). *Advances in Legume Systematics X. Higher-Level Systematics and Biogeography*. Royal Botanic Gardens, Kew, Richmond.

Neff, J. L. & **L. L. Larkin**. 2002. *Andrena chaparralensis* new species, a new vernal bee associated with Asteraceae on the South Texas Plains (Hymenoptera, Apoidea, Andrenidae). *Journal of the Kansas Entomological Society* 75(4): 268–273.