

BIOGRAPHICAL SKETCH

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NAME: Lefkowitz, Elliot J.

eRA COMMONS USER NAME (credential, e.g., agency login): elliotl

POSITION TITLE: Full Professor of Microbiology

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE (if applicable)	Completion Date MM/YYYY	FIELD OF STUDY
Univ. of Maryland, College Park, MD	BS	05/1977	Microbiology
Univ. of Texas Medical Branch, Galveston, TX	PhD	06/1983	Microbiology
Univ. of Wisconsin, Madison, WI	Postdoctoral Fellow	02/1987	Microbiology
Univ. of Alabama at Birmingham, Birmingham, AL	Postdoctoral Fellow	05/1991	Microbiology

A. Personal Statement

As a faculty member at the University of Alabama at Birmingham (UAB), my research interests include contributing to the understanding of microbial genomics and evolution by developing and utilizing computational tools and bioinformatics techniques to mine sequence and other data for significant patterns characteristic of function and/or evolution. This includes research on the genomics and evolutionary history of many virus species, especially poxviruses, as well as work on the complete genomic sequencing and annotation of various bacterial species. I have been part of the teams that have sequenced the complete genomes of ectromelia virus, monkeypox virus, rabbitpox virus, *Ureaplasma urealyticum*, *Streptococcus pneumoniae* strain R6, and *Mycoplasma hyopneumoniae*. My work on basic bioinformatics tool development has included the development of new algorithms for the detection of virus regulatory motifs, tools for the identification of virus genes, the development and utilization of High-Performance Computing tools for bioinformatics analysis, and the development and use of tools for analyzing patterns of virus evolution. I was the first Principal Investigator of the Viral Bioinformatics Resource Center, an NIH/NIAID-sponsored effort to develop Bioinformatics Resource Centers (BRCs) for Biodefense and Emerging or Re-Emerging Infectious Diseases. And I continue to be involved in the BRC program, serving as the overall lead for virology and UAB site PI on a subaward from the University of Chicago for the ongoing Bacterial and Viral Bioinformatics Resource Center (BV-BRC). I also serve as Data Secretary for the International Committee on Taxonomy of Viruses (ICTV). In this role, I provide data management support; communicate the results of ICTV deliberations to the scientific community; extend and maintain the ICTV web site and taxonomic database; and interact with various international agencies such as the NIH National Center for Biotechnology Information to incorporate the official, ICTV virus taxonomy into their own taxonomic databases.

Since 2012, my research interests have also included a focus on the role that populations of microorganisms (the microbiota) play in health and disease by looking for associations between the populations of microbial genomes present in an environment or host (the microbiome) and phenotypic data describing that environment or host. Our work in this area encompasses both laboratory and clinical studies as well as the development of bioinformatics tools to support the analysis of the collected data. To better support the interdisciplinary nature of this work, I serve as a Co-Director of the UAB Microbiome Center. Given UAB's location in the middle of the deep south, many of the studies we support revolve around the identification of population disparities and diseases unique to our region that may be impacted by changes in human commensal or pathogenic microbial populations.

Since 1992 I have also played a leading role in developing and supporting the bioinformatics education, service, and research programs at the University of Alabama at Birmingham (UAB). I am Director of Bioinformatics for the UAB Center for Clinical and Translational Sciences (CCTS), an NIH/NCATS Clinical and Translational Science Award site and Director of the Bioinformatics Core for the UAB Microbiome Facility. I oversee a team of Bioinformaticians and Systems Analysts who work and collaborate with UAB investigators to provide them with the broad range of tools and expertise necessary to support their bioinformatics needs. My

team provides assistance in analyzing a wide range of data types including whole genome, epigenome, transcriptome, microbiome, and metagenomic sequence data. Our provision of bioinformatics support helps to ensure that each individual investigator and laboratory can maximize their ability to publish and obtain funding, and especially to derive biological knowledge and meaning from their data. Finally, I also serve as Co-Director of the UAB Undergraduate Bioinformatics Bachelor's-degree program that provides undergraduate students with an opportunity to obtain education and training in the computational and biological sciences.

My overall career as detailed above, my scientific contributions as detailed below, and especially my current role as PI on the virus taxonomy knowledgebase grant, place me in an ideal position to serve as PI on this grant renewal application.

Citations relevant to this project include:

- a. Black EJ, Powell CS, Dempsey DM, Hendrickson RC, Mims LR, **Lefkowitz EJ**. Virus taxonomy: the database of the International Committee on Taxonomy of Viruses. *Nucleic Acids Res.* 2025 Volume 54, Issue D1, 6 January 2026, Pages D776–D789. PMID: 41296552. PMCID: PMC12807731.
- b. **Lefkowitz EJ**, Rutvisuttinunt W, Brister JR, Capria A, Click ES, Caravas J, Hatcher E, MacCannell D, Rota P, Singh I, Stewart L, St John A, Zmasek C, Brown LL. Report from the BV-BRC, CDC, NCBI, and NIAID Viral Sub-Species Classification Workshop. *J Virol.* 2026 Jul 21;100(7):e0021026. Epub 2026 Jun 12. PMID: 42283465; PMCID: PMC13386822.
- c. Adriaenssens EM, Roux S, Brister JR, Karsch-Mizrachi I, Kuhn JH, Varsani A, Yigang T, Reyes A, Lood C, **Lefkowitz EJ**, Sullivan MB, Edwards RA, Simmonds P, Rubino L, Sabanadzovic S, Krupovic M, Dutilh BE. Guidelines for public database submission of uncultivated virus genome sequences for taxonomic classification. 2023. *Nat Biotechnol.* Jul;41(7):898-902. PMID: 37430074. PMCID: PMC10526704.
- d. Siddell SG, Smith DB, Adriaenssens E, Alfenas-Zerbini P, Dutilh BE, Garcia ML, Junglen S, Krupovic M, Kuhn JH, Lambert AJ, **Lefkowitz EJ**, Łobocka M, Mushegian AR, Oksanen HM, Robertson DL, Rubino L, Sabanadzovic S, Simmonds P, Suzuki N, Van Doorslaer K, Vandamme AM, Varsani A, Zerbini FM. Virus taxonomy and the role of the International Committee on Taxonomy of Viruses (ICTV). 2023. *J Gen Virol.* May;104(5). PMID: 37141106. PMCID: PMC10227694.

B. Positions, Scientific Appointments, and Honors

Positions and Scientific Appointments

2021 – Present	Co-Director, UAB Microbiome Center
2021	Chair, NIH/NIAID Special Emphasis Panel IZAI1-FDS-W (M1) 1: “Emergency Awards: Rapid Investigation of SARS-CoV-2 and Coronavirus Disease 2019 (R21, R01)”
2020	Chair, NIH/NIAID Special Emphasis Panel ZAI1-ZL-W-S2: “Emergency Awards: Rapid Investigation of SARS-CoV-2 and Coronavirus Disease 2019”
2018 – Present	Co-Director, UAB Undergraduate Bioinformatics Program
2017 – Present	Member Editorial Board, PeerJ
2015 – Present	Member Editorial Board, Virology
2014 – Present	Data Secretary, International Committee on Taxonomy of Viruses
2013 – Present	Full Professor (with tenure), UAB Department of Microbiology
2011 – Present	Associate Editor, BMC Microbiology
2011 – Present	Director of Bioinformatics, UAB Center for Clinical and Translational Science
2010 – 2020	Member, Scientific Working Group, NIAID ViPR Virus Pathogen Resource Center
2010 – 2013	Associate Professor (with tenure), UAB Department of Microbiology
2009 – 2022	Member, Target Selection Board, NIAID Structural Genomics Centers for Infectious Diseases
2008 – Present	Member, Advisory Board, Archives of Virology
2008 – 2011	Co-Director, Biomedical Informatics, UAB Center for Clinical and Translational Science
2007 – 2014	Virus Data Subcommittee Chair, International Committee on Taxonomy of Viruses
2007 – Present	Secondary Faculty Appointment, UAB Department of Genetics

2006 – 2014	Chair, Virus Data Subcommittee, International Committee on Taxonomy of Viruses
2004 – 2010	Associate Professor, UAB Department of Microbiology
2001 – Present	Secondary Faculty Appointment, UAB Department of Computer and Information Sciences
1999 – 2004	Research Associate Professor, UAB Department of Microbiology
1992 – 2019	Director, Molecular and Genetic Bioinformatics Facility, UAB Center for AIDS Research
1991 – 1999	Research Assistant Professor, UAB Department of Microbiology

C. Contributions to Science

1. My initial scientific career introduced me to traditional bench-top research and involved research on viruses, viral immune defenses, and antiviral agents. I became increasingly involved in research related to viral genetics and evolution, areas of investigation that required I become proficient in the computational analysis (bioinformatics) of sequence data.
 - a. Coggins WB, **Lefkowitz EJ** & Sullender WM. Genetic variability among group A and group B respiratory syncytial viruses in a children's hospital. (1998) J Clin Microbiol. Dec;36(12):3552-7. PMID: 9817872; PMCID: PMC105239.
 - b. **Lefkowitz EJ**, Pattnaik AK & Ball LA. Complementation of a vesicular stomatitis virus glycoprotein G mutant with wild-type protein expressed from either a bovine papilloma virus or a vaccinia virus vector system. (1990) Virology. Oct;178(2):373-83. PMID: 2171187.
 - c. **Lefkowitz EJ** & Fleischmann WR Jr. An inhibitor of interferon action: I. Physical association of the inhibitor with interferon-gamma. (1985) J Interferon Res. Winter;5(1):85-99. PMID: 3921633.
 - d. **Lefkowitz E**, Worthington M, Conliffe MA, & Baron S. Comparative effectiveness of six antiviral agents in Herpes simplex type 1 infection of mice. (1976) Proc Soc Exp Biol Med. 152(3):337-42. PMID: 948482.
2. In the late 1990s, my work shifted from a combination of wet-bench and computational research, to solely bioinformatics-based research. This provided me with the opportunity to collaborate on a number of research projects involving the complete sequencing, annotation, and analysis of both bacterial and large viral genomes. I have been part of the teams that have sequenced the complete genomes of ectromelia virus, monkeypox virus, rabbitpox virus, *Ureaplasma urealyticum*, *Streptococcus pneumoniae* strain R6, and *Mycoplasma hyopneumoniae*. In addition to genome annotation, this work also included the reconstruction of the evolutionary histories of these organisms and the association of genomic features with mechanisms of pathogenesis.
 - a. Chen N, Li G, Liszewski MK, Atkinson JP, Jahrling PB, Feng Z, Schriewer J, Buck C, Wang C, **Lefkowitz, EJ**, Esposito JJ, Harms T, Damon IK, Roper RL, Upton C, & Buller, RM. Virulence differences between monkeypox virus isolates from West Africa and the Congo basin. Virology. (2005) Sep 15;340(1):46-63. PMID: 16023693; PMCID: PMC9534023.
 - b. Minion FC, **Lefkowitz EJ**, Madsen ML, Cleary BJ, Swartzell SM, & Mahairas GG. The genome sequence of *Mycoplasma hyopneumoniae* strain 232, the agent of swine mycoplasmosis. (2004) J Bacteriol. Nov;186(21):7123-33. PMID: 15489423; PMCID: PMC523201.
 - c. Hoskins J, Alborn Jr., WE, Arnold J, Blaszczyk LC, Burgett S, DeHoff BS, Estrem ST, Fritz L, Fu DJ, Fuller W, Geringer C, Gilmour R, Glass JS, Khoja H, Kraft AR, Lagace RE, LeBlanc DJ, Lee LN, **Lefkowitz EJ**, Lu J, Matsushima P, McAhern SM, McHenry M, McLeaster K, Mundy CW, Nicas TI, Norris FH, O'Gara M, Peery RB, Robertson, GT, Rockey P, Sun PM, Winkler ME, Yang Y, Young-Bellido, M, Zg-hao G, Zook CA, Baltz RH, Jaskunas SR, Rosteck PR, Skatrud PL, & Glass JI. Genome of the bacterium *Streptococcus pneumoniae* strain R6. (2001) J Bacteriol. Oct;183(19):5709-17. PMID: 11544234; PMCID: PMC95463.
 - d. Glass JI, **Lefkowitz EJ**, Glass, JS, Heiner CR, Chen EY, & Cassell GH. The complete sequence of the mucosal pathogen *Ureaplasma urealyticum*. (2000) Nature. Oct 12; 407:757-62. PMID: 11048724.
3. As my genomics collaborations progressed, my laboratory pursued interests in providing a better understanding of the evolutionary history of poxviruses and flaviviruses by investigating evolutionary patterns present in their genomic sequences. These patterns include those present in both coding

sequences as well as regulatory sequences. The goals of our work included the provision of bioinformatics resources and analytical tools to the research community that could be used to support the development of environmental detectors, diagnostics, animal models, vaccines, and antimicrobial drugs, as well as provide a better understanding of the molecular biology, evolution, and epidemiology of these agents. Some of these efforts involved the development of the NIH-funded Bioinformatics Resource Center for Biodefense and Emerging or Re-Emerging Infectious Diseases directed at viral pathogens (Bacterial and Viral Bioinformatics Resource Center; BV-BRC). I also serve as Data Secretary for the International Committee on Taxonomy of Viruses (ICTV). In this role I provide support to the ICTV for handling of viral taxonomy proposals; communicate the results of ICTV deliberations to the scientific community; and interact with various international agencies such as the NIH National Center for Biotechnology Information to incorporate the official, ICTV virus taxonomy into their own taxonomic databases.

- a. Olson RD, Assaf R, Brettin T, Conrad N, Cucinell C, Davis JJ, Dempsey DM, Dickerman A, Dietrich EM, Kenyon RW, Kuscuoglu M, **Lefkowitz EJ**, Lu J, Machi D, Macken C, Mao C, Niewiadomska A, Nguyen M, Olsen GJ, Overbeek JC, Parrello B, Parrello V, Porter JS, Pusch GD, Shukla M, Singh I, Stewart L, Tan G, Thomas C, VanOeffelen M, Vonstein V, Wallace ZS, Warren AS, Wattam AR, Xia F, Yoo H, Zhang Y, Zmasek CM, Scheuermann RH, Stevens RL. Introducing the Bacterial and Viral Bioinformatics Resource Center (BV-BRC): a resource combining PATRIC, IRD and ViPR. *Nucleic Acids Res.* 2023 Jan 6;51(D1):D678-D689. PMID: 36350631; PMCID: PMC9825582.
 - b. Dutilh BE, Varsani A, Tong Y, Simmonds P, Sabanadzovic S, Rubino L, Roux S, Muñoz AR, Lood C, **Lefkowitz EJ**, Kuhn JH, Krupovic M, Edwards RA, Brister JR, Adriaenssens EM, Sullivan MB. Perspective on taxonomic classification of uncultivated viruses. *Curr Opin Virol.* 2021 Nov 12;51:207-215. PMID: 34781105.
 - c. Hatcher EL, **Hendrickson RC**, & **Lefkowitz EJ**. Identification of nucleotide-level changes impacting gene content and genome evolution in orthopoxviruses (2014). *J Virol.* Dec;88(23):13651-68. PMID: 25231308; PMCID: PMC4248964.
 - d. Virus taxonomy: classification and nomenclature of viruses: Ninth Report of the International Committee on Taxonomy of Viruses. (2012) Ed: King, AMQ, Adams, MJ, Carstens, EB & **Lefkowitz, EJ** San Diego: Elsevier.
4. My research interests as described above, have always started with a biological question for which our collaborators generated research data in the laboratory, and my group analyzed that data using bioinformatics tools and databases. Frequently my group has been involved in the development and use of novel bioinformatics algorithms and tools to assist in helping us understand the biological data that was the focus of a particular study. The citations below provide examples of some of the bioinformatics tools and bioinformatics analyses we have developed and supported. More recently, we have been developing and utilizing tools for the analysis of microbiome and metagenomic next generation sequence data. These efforts and citations were discussed above under my personal statement.
- a. Van Der Pol, WJ, Kumar, R., Morrow CD, Blanchard, EE, Taylor, CM, Martin, DH, **Lefkowitz EJ**, Muzny, CA. (2018) In Silico and Experimental Evaluation of Primer Sets for Species Level Resolution of the Vaginal Microbiota using 16S rRNA Gene Sequencing. *The Journal of Infectious Diseases.* Aug 14;218(6):966-978. PMID: 29718358; PMCID: PMC6093354.
 - b. Xiao L, Ptacek T, **Osborne JD**, Crabb DM, Simmons WL, **Lefkowitz EJ**, Waites KB, Atkinson TP, Dybvig K. Comparative genome analysis of *Mycoplasma pneumoniae*. (2015) *BMC Genomics.* Aug 16;16(1):610. PMID: 26275904; PMCID: PMC4537597.
 - c. Wang C & **Lefkowitz EJ**. Genomic multiple sequence alignments: refinement using a genetic algorithm. (2005) *BMC Bioinformatics.* Aug 8;6:200. PMID: 16086841; PMCID: PMC1208854.
 - d. **Lefkowitz EJ**, Upton C, Changayil SS, Buck C, Traktman P, & Buller RM. Poxvirus Bioinformatics Resource Center: a comprehensive Poxviridae informational and analytical resource. (2005) *Nucleic Acids Res.* Jan 1;33(Database issue):D311-6. PMID: 15608205; PMCID: PMC540064.
5. In recent years, as biomedical research has begun to appreciate the role that both commensal and pathogenetic microorganisms play in human health, my role as Director of Bioinformatics for the UAB Microbiome Facility has involved myself and my bioinformatics staff in collaborations studying the role of the microbiome in a wide variety of biological systems. The facility has supported research that has

resulted in over 200 publications related to the microbiome. Publications in which the bioinformatics core has played an integral role in analyzing microbiome data include:

- a. Meza-Perez S, Liu M, Silva-Sanchez A, Morrow CD, Eipers PG, **Lefkowitz EJ**, Ptacek T, Scharer CD, Rosenberg AF, Hill DD, Arend RC, Gray MJ, Randall TD. Proteobacteria impair anti-tumor immunity in the omentum by consuming arginine. *Cell Host Microbe*. 2024 Jul 10;32(7):1177-1191.e7. PMID: 38942027; PMCID: PMC11245731.
- b. Carson TL, Byrd DA, Smith KS, Carter D, Gomez M, Abaskaron M, Little RB, Holmes ST, van Der Pol WJ, **Lefkowitz EJ**, Morrow CD, Fruge AD. A case-control study of the association between the gut microbiota and colorectal cancer: exploring the roles of diet, stress, and race. 2024. *Gut Pathogens*. March 11; 16(13). PMID: 36711747; PMCID: PMC9882682.
- c. Subramaniam A, Van Der Pol WJ, Ptacek T, Lobashevsky E, Neely C, Biggio JR Jr, **Lefkowitz EJ**, Morrow CD, Edwards RK. Midtrimester microbial DNA variations in maternal serum of women who experience spontaneous preterm birth. (2020) *J Matern Fetal Neonatal Med*. Feb;33(3):359-367. PMID: 29909752; PMCID: PMC6342669.
- d. Paulsen JA, Ptacek TS, Carter SJ, Liu N, Kumar R, Hyndman L, **Lefkowitz EJ**, Morrow CD, Rogers LQ. (2017) Gut microbiota composition associated with alterations in cardiorespiratory fitness and psychosocial outcomes among breast cancer survivors. (2017) *Support Care Cancer*. 25(5):1563-1570. PMID: 28064384; PMCID: PMC5380600.

Complete List of Published Work in MyBibliography:

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