Thomas Christiaan Friedrich

Curriculum vitae

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formal education

2003–2004 **postdoc**	David I. Watkins, University of Wisconsin–Madison Co-evolution of SIV and host cellular immune responses
1998–2003 **Ph.D.**	University of Wisconsin–Madison
thesis title	The functional significance of AIDS virus escape from cytotoxic T-lymphocyte responses
mentor	David I. Watkins
1992–1997 **B.S. (Honors)**	University of Wisconsin–Madison
major	Cellular & Molecular Biology

positions held

since 2019	Professor, University of Wisconsin–Madison
2013–2019	Associate Professor, University of Wisconsin–Madison
2008–2013	Assistant Professor, University of Wisconsin–Madison
since 2008	Affiliate Scientist, Wisconsin National Primate Research Center (WNPRC)
since 2004	Head, Virology Services Unit, WNPRC
2004–2008	Assistant Scientist, WNPRC
1998	Visiting Researcher, Institute for Virology, University of Glasgow, UK

honors and awards

2022	UW–Madison Kellett Mid-Career Award
2021	Zoetis Award for Veterinary Research Excellence
2012	UW–Madison University Housing Honored Instructor Award
2010–2011	UW–Madison Vilas Trustees Associate
2005	Keystone Symposia: HIV Vaccines NIAID Scholarship
2004	International AIDS Society Young Investigator Award
2004	XV International AIDS Conference Travel Scholarship
2004	Keystone Symposia: HIV Vaccines Young Investigator Scholarship
2003	Keystone Symposia: HIV Vaccines Young Investigator Scholarship
1997	Bachelor of Science with Honors

professional societies

since 2007	American Society for Microbiology
since 2013	American Association for the Advancement of Science
since 2016	International Society for Influenza and Other Respiratory Viruses (ISIRV)
since 2017	American Society for Virology
since 2019	American Society for Tropical Medicine and Hygiene

I. Research accomplishments

I.A. Publications

Members of my laboratory indicated in **bold**

* indicates equal contribution by two or more authors

I.A.1. Peer-reviewed publications

1. **Machkovech HM**, Hahn AM, Garonzik Wang J, Grubaugh ND, Halfmann PJ, Johnson MC, Lemieux JE, O'Connor DH, Piantadosi A, **Wei W**, **Friedrich TC**. Persistent SARS-CoV-2 infection: significance and implications. ***Lancet Infect Dis.*** 2024. PMID: 38340735

2. Shafer MM, Bobholz MJ, Vuyk WC, Gregory DA, Roguet A, Haddock Soto LA, Rushford C, Janssen KH, Emmen IE, **Ries H**J, Pilch HE, Mullen PA, Fahney RB, **Wei W**, Lambert M, Wenzel J, Halfmann P, Kawaoka Y, Wilson NA, **Friedrich TC**, Pray IW, Westergaard R, O'Connor DH, Johnson MC. Tracing the origin of SARS-CoV-2 omicron-like spike sequences detected in an urban sewershed: a targeted, longitudinal surveillance study of a cryptic wastewater lineage. ***Lancet Microbe.*** 2024. PMID: 38484748

3. Singh T, Miller IG, Venkatayogi S, Webster H, Heimsath HJ, Eudailey JA, Dudley DM, Kumar A, Mangan RJ, Thein A, Aliota MT, Newman CM, Mohns MS, Breitbach ME, Berry M, **Friedrich TC**, Wiehe K, O'Connor DH, Permar SR. Prior dengue virus serotype 3 infection modulates subsequent plasmablast responses to Zika virus infection in rhesus macaques. ***MBio.*** 2024. e0316023. PMID: 38349142

4. Grunst MW, Gil HM, Grandea AG 3rd, Snow BJ, Andrabi R, Nedellec R, Burton I, Clark NM, Janaka SK, Keles NK, Moriarty RV, **Weiler AM**, Capuano S 3rd, Fennessey CM, **Friedrich TC**, O'Connor SL, O'Connor DH, Broman AT, Keele BF, Lifson JD, Hangartner L, Burton DR, Evans DT. Potent antibody-dependent cellular cytotoxicity of a V2-specific antibody is not sufficient for protection of macaques against SIV challenge. ***PLoS Pathog.*** 2024. n20(1):e1011819. PMID: 38252675

5. Wang H, Solomon J, Reza SMS, Yang HJ, Chu WT, Crozier I, Sayre PJ, Lee BY, Mani V, **Friedrich TC**, O'Connor DH, Worwa G, Kuhn JH, Calcagno C, Castro MA. Repeatability of computed tomography liver radiomic features in a nonhuman primate model of diet-induced steatosis. ***J Med Imaging (Bellingham)***. 2023. 10(6):066004. PMCID: PMC10711681

6. **Jaeger AS**, Marano J, **Riemersma KK**, Castaneda D, Pritchard EM, Pritchard JC, Bohm EK, Baczenas JJ, O'Connor SL, Weger-Lucarelli J, **Friedrich TC**, Aliota MT. Gain without pain: adaptation and increased virulence of Zika virus in vertebrate host without fitness cost in mosquito vector. ***J Virol.*** 2023. 97(10):e0116223. PMCID: PMC10653995

7. Boehm EC, **Jaeger AS**, **Ries H**J, Castañeda D, **Weiler AM**, Valencia CC, Weger-Lucarelli J, Ebel GD, O'Connor SL, **Friedrich TC**, Zamanian M, Aliota MT. Wolbachia-mediated resistance to Zika virus infection in Aedes aegypti is dominated by diverse transcriptional regulation and weak evolutionary pressures. ***PLoS Negl Trop Dis.*** 2023. 17(10):e0011674. PMCID: PMC10569609

8. Krabbe NP, Razo E, Abraham HJ, Spanton RV, Shi Y, Bhattacharya S, Bohm EK, Pritchard JC, **Weiler AM**, Mitzey AM, Eickhoff JC, Sullivan E, Tan JC, Aliota MT, **Friedrich TC**, O'Connor DH, Golos TG, Mohr EL. Control of maternal Zika virus infection during pregnancy is associated with lower antibody titers in a macaque model. ***Front Immunol.*** 2023. 14:1267638. PMCID: PMC10556460

9. Harwood OE, Matschke LM, Moriarty RV, Balgeman AJ, Weaver AJ, Ellis-Connell AL, **Weiler AM**, Winchester LC, Fletcher CV, **Friedrich TC**, Keele BF, O'Connor DH, Lang JD, Reynolds MR, O'Connor SL. CD8+ cells and small viral reservoirs facilitate post-ART control of SIV replication in M3+

Mauritian cynomolgus macaques initiated on ART two weeks post-infection. ***PLoS Pathog.*** 2023. 19(9):e1011676. PMCID: PMC10553806

10. Koenig MR, Mitzey AM, Zeng X, Reyes L, Simmons HA, Morgan TK, Bohm EK, Pritchard JC, Schmidt JA, Ren E, Leyva Jaimes FB, Winston E, Basu P, **Weiler AM**, **Friedrich TC**, Aliota MT, Mohr EL, Golos TG. Vertical transmission of African-lineage Zika virus through the fetal membranes in a rhesus macaque (Macaca mulatta) model. ***PLoS Pathog.*** 2023. 19(8):e1011274. PMCID: PMC10434957

11. **Jaeger AS**, **Crooks CM**, **Weiler AM**, **Bliss M**I, **Rybarczyk S**, Richardson A, Einwalter M, Peterson E, Capuano S 3rd, Barkhymer A, Becker JT, Greene JT, Freedman TS, Langlois RA, **Friedrich TC**, Aliota MT. Primary infection with Zika virus provides one-way heterologous protection against Spondweni virus infection in rhesus macaques. ***Sci Adv.*** 2023 eadg3444. PMCID: PMC10313173

12. Koenig MR, Mitzey AM, Morgan TK, Zeng X, Simmons HA, Mejia A, Leyva Jaimes F, Keding LT, **Crooks CM**, **Weiler AM**, Bohm EK, Aliota MT, **Friedrich TC**, Mohr EL, Golos TG. Infection of the maternal-fetal interface and vertical transmission following low-dose inoculation of pregnant rhesus macaques (Macaca mulatta) with an African-lineage Zika virus. ***PLoS One.*** journals.plos.org; 2023 May 4;18(5):e0284964. PMCID: PMC10159132

13. **Braun KM***, **Haddock LA** III*, **Crooks CM**, **Barry GL**, **Lalli J**, Neumann G, Watanabe T, Imai M, Yamayoshi S, Ito M, **Moncla LH**, Koelle K, Kawaoka Y, **Friedrich TC**. Avian H7N9 influenza viruses are evolutionarily constrained by stochastic processes during replication and transmission in mammals. 2023. ***Virus Evol.*** 2023. 9:vead004. PMC9939568

14. Sakai-Tagawa Y, Yamayoshi S, Halfmann PJ, Wilson N, Bobholz M, Vuyk WC, **Wei W**, **Ries H**, O'Connor DH, **Friedrich TC**, Sordillo EM, van Bakel H, Simon V, Kawaoka Y. Sensitivity of rapid antigen tests for Omicron subvariants of SARS-CoV-2. 2023. ***J Med Virol.*** 95:e28788.

15. Rosinski JR, Raasch LE, Barros Tiburcio P, Breitbach ME, Shepherd PM, Yamamoto K, Razo E, Krabbe NP, **Bliss M**I, Richardson AD, **Einwalter MA**, **Weiler AM**, Sneed EL, Fuchs KB, Zeng X, Noguchi KK, Morgan TK, Alberts AJ, Antony KM, Kabakov S, Ausderau KK, Bohm EK, Pritchard JC, Spanton RV, Ver Hoove JN, Kim CBY, Nork TM, Katz AW, Rasmussen CA, Hartman A, Mejia A, Basu P, Simmons HA, Eickhoff JC, **Friedrich TC**, Aliota MT, Mohr EL, Dudley DM, O'Connor DH, Newman CM. Frequent first-trimester pregnancy loss in rhesus macaques infected with African-lineage Zika virus. 2023. ***PLoS Pathog.*** 19:e1011282. PMC10081769

16. Harwood OE, Balgeman AJ, Weaver AJ, Ellis-Connell AL, **Weiler AM**, Erickson KN, Matschke LM, Golfinos AE, Vezys V, Skinner PJ, Safrit JT, Edlefsen PT, Reynolds MR, **Friedrich TC**, O'Connor SL. Transient T Cell Expansion, Activation, and Proliferation in Therapeutically Vaccinated Simian Immunodeficiency Virus-Positive Macaques Treated with N-803. 2022. ***J Virol.*** 96:e0142422. PMC9749465

17. Ellis-Connell AL, Balgeman AJ, Harwood OE, Moriarty RV, Safrit JT, **Weiler AM**, **Friedrich TC**, O'Connor SL. Control of Simian Immunodeficiency Virus Infection in Prophylactically Vaccinated, Antiretroviral Treatment-Naive Macaques Is Required for the Most Efficacious CD8 T Cell Response during Treatment with the Interleukin-15 Superagonist N-803. ***J Virol.*** Am Soc Microbiol; 2022. 96:e0118522. Available from: http://dx.doi.org/10.1128/jvi.01185-22 PMCID: PMC9599604

18. Rosinski JR, Raasch LE, Barros Tiburcio P, Breitbach ME, Shepherd PM, Yamamoto K, Razo E, Krabbe NP, **Bliss MI**, Richardson AD, **Einwalter MA**, **Weiler AM**, Sneed EL, Fuchs KB, Zeng X, Noguchi KK, Morgan TK, Alberts AJ, Antony KM, Kabakov S, Ausderau KK, Bohm EK, Pritchard JC, Spanton RV, Ver Hoove JN, Kim CBY, Nork TM, Katz AW, Rasmussen CA, Hartman A, Mejia A, Basu P, Simmons HA, Eickhoff JC, **Friedrich TC**, Aliota MT, Mohr EL, Dudley DM, O'Connor DH, Newman CM. Frequent first-trimester pregnancy loss in rhesus macaques infected with African-lineage Zika virus. 2023. ***PLoS Pathog.*** 19:e1011282. PMC10081769

19. **Riemersma KK**, **Haddock LA** 3rd, Wilson NA, Minor N, Eickhoff J, Grogan BE, Kita-Yarbro A,

Halfmann PJ, Segaloff HE, Kocharian A, **Florek KR**, Westergaard R, Bateman A, Jeppson GE, Kawaoka Y, O'Connor DH, **Friedrich TC**, Grande KM. Shedding of infectious SARS-CoV-2 despite vaccination. 2022. ***PLoS Pathog.*** 18:e1010876. PMC9555632

20. Takashita E, Yamayoshi S, Halfmann P, Wilson N, **Ries H**, Richardson A, Bobholz M, Vuyk W, Maddox R, Baker DA, **Friedrich TC**, O'Connor DH, Uraki R, Ito M, Sakai-Tagawa Y, Adachi E, Saito M, Koga M, Tsutsumi T, Iwatsuki-Horimoto K, Kiso M, Yotsuyanagi H, Watanabe S, Hasegawa H, Imai M, Kawaoka Y. In Vitro Efficacy of Antiviral Agents against Omicron Subvariant BA.4.6. 2022. ***N Engl J Med*** 387:2094–2097. PMC9730936

21. Halfmann PJ, Minor NR, **Haddock LA** III, Maddox R, Moreno GK, **Braun KM**, Baker DA, Riemersa KK, Prasad A, Alman KJ, Lambert MC, **Florek K**, Bateman A, Westergaard R, Safdar N, Andes DR, Kawaoka Y, Fida M, Yao J, **Friedrich TC**, O'Connor DH. Evolution of a globally unique SARS-CoV-2 Spike E484T monoclonal antibody escape mutation in a persistently infected, immunocompromised individual. 2022. ***Virus Evol.*** 2022.

22. Ellis-Connell AL, Balgeman AJ, Harwood OE, Moriarty RV, Safrit JT, **Weiler AM**, **Friedrich TC**, O'Connor SL. Control of Simian Immunodeficiency Virus Infection in Prophylactically Vaccinated, Antiretroviral Treatment-Naive Macaques Is Required for the Most Efficacious CD8 T Cell Response during Treatment with the Interleukin-15 Superagonist N-803. 2022. ***J Virol.*** 96:e0118522. PMC9599604

23. Raasch LE, Yamamoto K, Newman CM, Rosinski JR, Shepherd PM, Razo E, **Crooks CM**, **Bliss MI**, Breitbach ME, Sneed EL, **Weiler AM**, Zeng X, Noguchi KK, Morgan TK, Fuhler NA, Bohm EK, Alberts AJ, Havlicek SJ, Kabakov S, Mitzey AM, Antony KM, Ausderau KK, Mejia A, Basu P, Simmons HA, Eickhoff JC, Aliota MT, Mohr EL, **Friedrich TC**, Golos TG, O'Connor DH, Dudley DM. Fetal loss in pregnant rhesus macaques infected with high-dose African-lineage Zika virus. 2022. ***PLoS Negl Trop Dis.*** 16:e0010623. PMC9380952

24. Amato KA*, **Haddock LA** 3rd*, **Braun KM**, Meliopoulos V, Livingston B, Honce R, Schaack GA, Boehm E, Higgins CA, **Barry GL**, Koelle K, Schultz-Cherry S, **Friedrich TC**, Mehle A. 2022. Influenza A virus undergoes compartmentalized replication in vivo dominated by stochastic bottlenecks. ***Nat Commun*** 13:3416. PMC9197827.

25. Dudley DM, Koenig MR, Stewart LM, Semler MR, Newman CM, Shepherd PM, Yamamoto K, Breitbach ME, Schotzko M, Kohn S, Antony KM, Qiu H, Tunga P, Anderson DM, Guo W, Dennis M, Singh T, **Rybarczyk S**, **Weiler AM**, Razo E, Mitzey A, Zeng X, Eickhoff JC, Mohr EL, Simmons HA, Fritsch MK, Mejia A, Aliota MT, **Friedrich TC**, Golos TG, Kodihalli S, Permar SR, O'Connor DH. 2022. Human immune globulin treatment controls Zika viremia in pregnant rhesus macaques. ***PLoS One*** 17:e0266664. PMC9282477.

26. Halfmann PJ, Kuroda M, Armbrust T, Theiler J, Balaram A, Moreno GK, Accola MA, Iwatsuki-Horimoto K, Valdez R, Stoneman E, Braun K, Yamayoshi S, Somsen E, Baczenas JJ, Mitamura K, Hagihara M, Adachi E, Koga M, McLaughlin M, Rehrauer W, Imai M, Yamamoto S, Tsutsumi T, Saito M, **Friedrich TC**, O'Connor SL, O'Connor DH, Gordon A, Korber B, Kawaoka Y. 2022. Characterization of the SARS-CoV-2 B.1.621 (Mu) variant. ***Sci Transl Med*** 14:eabm4908. PMC9392899.

27. Amjadi MF, Adyniec RR, Gupta S, Bashar SJ, Mergaert AM, **Braun KM**, Moreno GK, O'Connor DH, **Friedrich TC**, Safdar N, McCoy SS, Shelef MA. 2022. Anti-membrane Antibodies Persist at Least One Year and Discriminate Between Past Coronavirus Disease 2019 Infection and Vaccination. ***J Infect Dis*** jiac263. PMC9278254.

28. **Braun KM***, Moreno GK*, Wagner C, Accola MA, Rehrauer WM, Baker DA, Koelle K, O'Connor DH, Bedford T, **Friedrich TC***, **Moncla LH***. 2021. Acute SARS-CoV-2 infections harbor limited within-host diversity and transmit via tight transmission bottlenecks. ***PLoS Pathog.*** 17:e1009849. PMC8412271.

29. **Braun KM***, Moreno GK*, Buys A, Somsen ED, Bobholz M, Accola MA, Anderson L, Rehrauer WM,

Baker DA, Safdar N, Lepak AJ, O'Connor DH, **Friedrich TC**. 2021. Viral Sequencing to Investigate Sources of SARS-CoV-2 Infection in US Healthcare Personnel. ***Clin Infect Dis.*** 73:e1329-e1336. PMC8083259.

30. Moriarty RV, Golfinos AE, Gellerup DD, Schweigert H, Mathiaparanam J, Balgeman AJ, **Weiler AM**, **Friedrich TC**, Keele BF, Davenport MP, Venturi V, O'Connor SL. 2021. The mucosal barrier and anti-viral immune responses can eliminate portions of the viral population during transmission and early viral growth. ***PLoS One.*** 16:e0260010. PMC8639003.

31. Moreno GK, **Braun KM**, Pray IW, Segaloff HE, Lim A, Poulsen K, Meiman J, Borcher J, Westergaard RP, Moll MK, **Friedrich TC**, O'Connor DH. 2021. Severe Acute Respiratory Syndrome Coronavirus 2 Transmission in Intercollegiate Athletics Not Fully Mitigated With Daily Antigen Testing. ***Clin Infect Dis.*** 73:S45-S53. PMC8136076.

32. Valesano AL, Fitzsimmons WJ, Blair CN, Woods RJ, Gilbert J, Rudnik D, Mortenson L, **Friedrich TC**, O'Connor DH, MacCannell DR, Petrie JG, Martin ET, Lauring AS. 2021. SARS-CoV-2 Genomic Surveillance Reveals Little Spread From a Large University Campus to the Surrounding Community. ***Open Forum Infect Dis.*** 8:ofab518. PMC8600169.

33. **Crooks CM**, **Weiler AM**, **Rybarczyk SL**, **Bliss M**I, **Jaeger AS**, Murphy ME, Simmons HA, Mejia A, Fritsch MK, Hayes JM, Eickhoff JC, Mitzey AM, Razo E, **Braun KM**, Brown EA, Yamamoto K, Shepherd PM, Possell A, Weaver K, Antony KM, Morgan TK, Newman CM, Dudley DM, Schultz-Darken N, Peterson E, Katzelnick LC, Balmaseda A, Harris E, O'Connor DH, Mohr EL, Golos TG, **Friedrich TC**, Aliota MT. 2021. Previous exposure to dengue virus is associated with increased Zika virus burden at the maternal-fetal interface in rhesus macaques. ***PLoS Negl Trop Dis.*** 15:e0009641. PMC8357128.

34. Ausderau K, Kabakov S, Razo E, Mitzey AM, Bach KM, **Crooks CM**, Dulaney N, Keding L, Salas-Quinchucua C, Medina-Magües LG, **Weiler AM**, **Bliss M**, Eickhoff J, Simmons HA, Mejia A, Antony KM, Morgan T, Capuano S, Schneider ML, Aliota MT, **Friedrich TC**, O'Connor DH, Golos TG, Mohr EL. 2021. Neonatal Development in Prenatally Zika Virus-Exposed Infant Macaques with Dengue Immunity. ***Viruses***. 13:1878. PMC8473338.

35. Currie DW, Moreno GK, Delahoy MJ, Pray IW, Jovaag A, **Braun KM**, Cole D, Shechter T, Fajardo GC, Griggs C, Yandell BS, Goldstein S, Bushman D, Segaloff HE, Kelly GP, Pitts C, Lee C, Grande KM, Kita-Yarbro A, Grogan B, Mader S, Baggott J, Bateman AC, Westergaard RP, Tate JE, **Friedrich TC**, Kirking HL, O'Connor DH, Killerby ME. 2021. Interventions to Disrupt Coronavirus Disease Transmission at a University, Wisconsin, USA, August-October 2020. ***Emerg Infect Dis.*** 27:2776-2785. PMC8544969.

36. Newman CM, Ramuta MD, McLaughlin MT, Wiseman RW, Karl JA, Dudley DM, Stauss MR, Maddox RJ, **Weiler AM**, **Bliss MI**, Fauser KN, **Haddock LA**, Shortreed CG, Haj AK, Accola MA, Heffron AS, Bussan HE, Reynolds MR, Harwood OE, Moriarty RV, Stewart LM, **Crooks CM**, Prall TM, Neumann EK, Somsen ED, Burmeister CB, Hall KL, Rehrauer WM, **Friedrich TC**, O'Connor SL, O'Connor DH. 2021. Initial Evaluation of a Mobile SARS-CoV-2 RT-LAMP Testing Strategy. ***J Biomol Tech.*** 32:137-147. PMC8730517.

37. Temte JL, Barlow S, Temte E, Goss M, **Florek K**, **Braun KM**, **Friedrich TC**, Reisdorf E, Bateman AC, Uzicanin A. 2021. Evidence of Early Household Transmission of SARS-CoV-2 Involving a School-aged Child. ***WMJ.*** 120:233-236. PMC8721881.

38. **Crooks CM**, **Weiler AM**, **Rybarczyk SL**, **Bliss M**, **Jaeger AS**, Murphy ME, Simmons HA, Mejia A, Fritsch MK, Hayes JM, Eickhoff JC, Mitzey AM, Razo E, **Braun KM**, Brown EA, Yamamoto K, Shepherd PM, Possell A, Weaver K, Antony KM, Morgan TK, Zeng X, Dudley DM, Peterson E, Schultz-Darken N, O'Connor DH, Mohr EL, Golos TG, Aliota MT, **Friedrich TC**. 2021. African-Lineage Zika Virus Replication Dynamics and Maternal-Fetal Interface Infection in Pregnant Rhesus Macaques. ***J Virol.*** 95:e0222020. PMC8312872.

39. **Braun KM***, Moreno GK*, Halfmann PJ, Hodcroft EB, Baker DA, Boehm EC, **Weiler AM**, Haj AK, Hatta M, Chiba S, Maemura T, Kawaoka Y, Koelle K, O'Connor DH, **Friedrich TC**. 2021. Transmission of SARS-CoV-2 in domestic cats imposes a narrow bottleneck. ***PLoS Pathog.*** 17:e1009373. doi:10.1371/journal.ppat.1009373.

40. **Riemersma KK***, **Jaeger AS***, **Crooks CM**, **Braun KM**, Weger-Lucarelli J, Ebel GD, **Friedrich TC***, Aliota MT*. 2021. Rapid evolution of enhanced Zika virus virulence during direct vertebrate transmission chains. ***J Virol.*** 10.1128/JVI.02218-20.

41. Juang DS, Juang TD, Dudley DM, Newman CM, Accola MA, Rehrauer WM, **Friedrich TC**, O'Connor DH, Beebe DJ. 2021. Oil immersed lossless total analysis system for integrated RNA extraction and detection of SARS-CoV-2. ***Nat Commun*** 12:1–9. 10.1038/s41467-021-24463-4.

42. Newman CM, Tarantal AF, Martinez ML, Simmons HA, Morgan TK, Zeng X, Rosinski JR, **Bliss MI**, Bohm EK, Dudley DM, Aliota MT, **Friedrich TC**, Miller CJ, O'Connor DH. 2021. Early Embryonic Loss Following Intravaginal Zika Virus Challenge in Rhesus Macaques. ***Front Immunol*** 12:686437. 10.3389/fimmu.2021.686437.

43. Cai Y, Yu S, Fang Y, Bollinger L, Li Y, Lauck M, Postnikova EN, Mazur S, Johnson RF, Finch CL, Radoshitzky SR, Palacios G, **Friedrich TC**, Goldberg TL, O'Connor DH, Jahrling PB, Kuhn JH. 2021. Development and Characterization of a cDNA-Launch Recombinant Simian Hemorrhagic Fever Virus Expressing Enhanced Green Fluorescent Protein: ORF 2b' Is Not Required for In Vitro Virus Replication. ***Viruses*** 13.

44. Hangartner L, Beauparlant D, Rakasz E, Nedellec R, Hozé N, McKenney K, Martins MA, Seabright GE, Allen JD, **Weiler AM**, **Friedrich TC**, Regoes RR, Crispin M, Burton DR. 2021. Effector function does not contribute to protection from virus challenge by a highly potent HIV broadly neutralizing antibody in nonhuman primates. ***Sci Transl Med.*** 1310.1126/scitranslmed.abe3349.

45. Dudley DM*, Newman CM*, **Weiler AM**, Ramuta MD, Shortreed CG, Heffron AS, Accola MA, Rehrauer WM, **Friedrich TC**, O'Connor DH. 2020. Optimizing direct RT-LAMP to detect transmissible SARS-CoV-2 from primary nasopharyngeal swab samples. ***PLoS One.*** 15:e0244882. doi:10.1371/journal.pone.0244882.

46. Moreno GK*, **Braun KM***, **Riemersma KK***, Martin MA, Halfmann PJ, **Crooks CM**, Prall T, Baker D, Baczenas JJ, Heffron AS, Ramuta M, Khubbar M, **Weiler AM**, Accola MA, Rehrauer WM, O'Connor SL, Safdar N, Pepperell CS, Dasu T, Bhattacharyya S, Kawaoka Y, Koelle K, O'Connor DH*, **Friedrich TC***. 2020. Revealing fine-scale spatiotemporal differences in SARS-CoV-2 introduction and spread. ***Nat Commun.*** 11:5558. doi:10.1038/s41467-020-19346-z.

47. Kropp Schmidt JA, Mean KD, Puntney RC, Alexander ES, Sullivan R, Simmons HA, Zeng X, **Weiler AM**, **Friedrich TC**, Golos TG. 2020. Zika virus in rhesus macaque semen and reproductive tract tissues: a pilot study of acute infection†. ***Biol Reprod***. 10.1093/biolre/ioaa137.

48. Safdar N, Moreno GK, **Braun KM**, **Friedrich TC**, O'Connor DH. 2020. Using Virus Sequencing to Determine Source of SARS-CoV-2 Transmission for Healthcare Worker. ***Emerg Infect Dis.*** 2610.3201/eid2610.202322.

49. Koenig MR, Razo E, Mitzey A, Newman CM, Dudley DM, Breitbach ME, **Semler MR**, Stewart LM, **Weiler AM**, **Rybarczyk S**, Bach KM, Mohns MS, Simmons HA, Mejia A, Fritsch M, Dennis M, Teixeira LBC, Schotzko ML, Nork TM, Rasmussen CA, Katz A, Nair V, Hou J, Hartman A, Ver Hoeve J, Kim C, Schneider ML, Ausderau K, Kohn S, **Jaeger AS**, Aliota MT, Hayes JM, Schultz-Darken N, Eickhoff J, Antony KM, Noguchi K, Zeng X, Permar S, Prabhakaran V, Capuano S, **Friedrich TC**, Golos TG, O'Connor DH, Mohr EL. 2020. Quantitative definition of neurobehavior, vision, hearing and brain volumes in macaques congenitally exposed to Zika virus. ***PLoS One.*** 15:e0235877. doi:10.1371/journal.pone.0235877.

50. **Jaeger AS**, **Weiler AM**, Moriarty RV, **Rybarczyk S**, O'Connor SL, O'Connor DH, Seelig DM, Fritsch

MK, **Friedrich TC**, Aliota MT. 2020. Spondweni virus causes fetal harm in Ifnar1^-/-^ mice and is transmitted by Aedes aegypti mosquitoes. Virology. 547:35-46. doi:10.1016/j.virol.2020.05.005.

51. Pomplun NL, Vosler L, Weisgrau KL, Furlott J, **Weiler AM**, Abdelaal HM, Evans DT, Watkins DI, Matano T, Skinner PJ, **Friedrich TC**, Rakasz EG. 2020. Immunophenotyping of Rhesus CMV-Specific CD8 T-Cell Populations. ***Cytometry A.*** 10.1002/cyto.a.24197.

52. **Moncla LH***, Bedford T, Dussart P, Horm SV, Rith S, Buchy P, Karlsson EA, Li L, Liu Y, Zhu H, Guan Y, **Friedrich TC**, Horwood PF*. 2020. Quantifying within-host diversity of H5N1 influenza viruses in humans and poultry in Cambodia. ***PLoS Pathog.*** 16:e1008191. doi:10.1371/journal.ppat.1008191.

53. **Florek K**, **Mutschler JP**, McLean HQ, King JP, Flannery B, Belongia EA, **Friedrich TC**. 2020. Antibody-dependent cell-mediated cytotoxicity antibody responses to inactivated and live-attenuated influenza vaccination in children during 2014-15. Vaccine. 38:2088-2094. doi:10.1016/j.vaccine.2019.10.060.

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162. Vogel TU*, **Friedrich TC***, O'Connor DH, Rehrauer W, Dodds EJ, Hickman H, Hildebrand W, Sidney J, Sette A, Hughes A, Horton H, Vielhuber K, Rudersdorf R, De Souza IP, Reynolds MR, Allen TM, Wilson N, Watkins DI. 2002. Escape in one of two cytotoxic T-lymphocyte epitopes bound by a high-frequency major histocompatibility complex class I molecule, Mamu-A*02: a paradigm for virus evolution and persistence. ***J Virol.*** 76:11623-11636

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I.A.2. Invited publications

1. Dudley DM, Aliota MT, Mohr EL, Newman CM, Golos TG, **Friedrich TC**, O'Connor DH. 2019. Using macaques to address critical questions in Zika virus research. ***Annu Rev Virol.*** 10.1146/annurev-virology-092818-015732.

2. **Braun KM**, **Friedrich TC**. 2019. Influenza evolution with little host selection. ***Nat Ecol Evol.*** 10.1038/s41559-018-0782-1.

3. Aliota MT, Bassit L, Bradrick SS, Cox B, Garcia-Blanco MA, Gavegnano C, **Friedrich TC**, Golos TG, Griffin DE, Haddow AD, Kallas EG, Kitron U, Lecuit M, Magnani DM, Marrs C, Mercer N, McSweegan E, Ng LFP, O'Connor DH, Osorio JE, Ribeiro GS, Ricciardi M, Rossi SL, Saade G, Schinazi RF, Schott-Lerner GO, Shan C, Shi PY, Watkins DI, Vasilakis N, Weaver SC. 2017. Zika in the Americas, year 2: What have we learned? What gaps remain? A report from the Global Virus Network. ***Antiviral Res.*** 144:223-246. doi:10.1016/j.antiviral.2017.06.001.

4. Newman C, **Friedrich TC**, O'Connor DH. 2017. Macaque monkeys in Zika virus research: 1947-present. ***Curr Opin Virol.*** 25:34-40. doi:10.1016/j.coviro.2017.06.011.

5. **Moncla LH**, **Florek NW**, **Friedrich TC**. 2017. Influenza Evolution: New Insights into an Old Foe. ***Trends Microbiol.*** 25:432-434. doi:10.1016/j.tim.2017.04.003.

6. Johnson R, Yingyun C, Wahl-Johnson V, Fang Y, **Friedrich TC**, Radoshitzky SR, Kota K, O'Connor D, Bavari S, Jahrling PB, Goldberg TL, Kuhn JH. 2011. Simian hemorrhagic fever virus as a model for risk group 4 pathogens. In: Proceedings of the 2nd International Conference on Fundamental and Applied Aspects of Medical Primatology, vol. 1. August 8-10, Sochi-Adler, Krasnodar Krai, Russia.

7. **Friedrich TC**, Watkins DI. 2008. Wanted: correlates of vaccine-induced protection against simian immunodeficiency virus. ***Curr Opin HIV AIDS.*** 3:393-398. doi:10.1097/COH.0b013e3282faa461.

8. **Friedrich TC**, Watkins DI. 2005. The role of the SIV model in AIDS vaccine research. ***IAVI Rep.*** 9:1, 6-8

9. **Friedrich TC** and Watkins DI. Truth or consequences: understanding the functional significance of AIDS virus escape from immune responses. In: Proceedings of the Cent Gardes meeting organized by the Fondation Mérieux in partnership with Aventis Pasteur and with the participation of IAVI, Annecy (France), 27-29 October 2002 Marc Girard, Marissa Vicari, Betty Dodet (Eds.) Amsterdam: Elsevier, 2003.

10. **Friedrich TC** and Watkins DI. Influence of MHC gene products on immune control of AIDS virus infection: consideration for use in nonhuman-primate resources. In: International Perspectives: The future of nonhuman primate resources, proceedings of the workshop held April 17-19, 2002 John L. VandeBerg et al. (Eds.) Washington, DC: National Academies Press, 2002.

11. O'Connor D, **Friedrich T**, Hughes A, Allen TM, Watkins DI. 2001. Understanding cytotoxic T-lymphocyte escape during simian immunodeficiency virus infection. ***Immunol Rev*** 183:115-26.

I.A.3. Manuscripts submitted or in preparation

1. Finch CL, Crozier I, Lee JH, Byrum R, Cooper TK, Liang J, Sharer K, Solomon J, Sayre PJ, Kocher G, Bartos C, Aiosa NM, Castro M, Larson PA, Adams R, Beitzel B, Di Paola N, Kugelman JR, Kurtz JR, Burdette T, Nason MC, Feuerstein IM, Palacios G, St Claire MC, Lackemeyer MG, Johnson RF, **Braun KM**, Ramuta MD, Wada J, Schmaljohn CS, **Friedrich TC**, O'Connor DH, Kuhn JH. 2020. Characteristic and quantifiable COVID-19-like abnormalities in CT- and PET/CT-imaged lungs of SARS-CoV-2-infected crab-eating macaques (Macaca fascicularis). bioRxiv. 10.1101/2020.05.14.096727.

I.B. Research support

I.B.1. Active research support

CDC 75D30122C15355 (O'Connor/Friedrich) 09/30/22-09/29/25 1.8 calendar
CDC $6,349,744 total award
Impact of local differences in vaccine uptake on SARS-CoV-2 evolution and spread across three Upper Midwestern states
The goal of this project is to understand how regional differences in COVID vaccine uptake, access to medical care, and other sociodemographic factors affect the evolution and transmission of SARS-CoV-2.
Role: co-PI

R01 AI 132563 (Aliota/Friedrich) 01/01/18-12/31/24 NCE no effort in NCE
NIAID $492,174
Previous exposure to dengue as a risk factor for Zika virus during pregnancy
The mechanism by which Zika virus infection can cause birth defects is unknown. Zika virus is closely related to dengue viruses, which also circulate in areas of the Americas where Zika-induced birth defects have occurred. This project will test the hypothesis that pre-existing immunity to dengue virus can affect the outcome of Zika virus infection during pregnancy.
Role: co-PI

R01 AI AI170737 (O'Connor/O'Connor) 01/01/23-12/31/28 0.6 calendar
NIAID $3,887,920 total award
Anticipating and rapidly responding to respiratory virus outbreaks with continuous air sampling in K-12 schools
This project will deploy air samplers to 16 K-12 schools to explore whether air sampling accurately assesses SARS-CoV-2 and influenza virus risk in schools and forecasts transmission of these viruses in the communities where the schools are located. Viral sequencing of air samples will also be performed to ascertain which viral variants are circulating and spreading within and between schools and the broader community.
Role: Contact PI

P01 AI 132132 (O'Connor) 08/01/18-07/31/23 1.2 calendar
NIH $1,967,057 (Total DCs in year 1)
Zika virus pathophysiology during pregnancy
In this Program Project we will test the hypothesis that prolonged detection of Zika virus in maternal blood during pregnancy predicts neonatal injury and birth defects, both of which we predict are more common than currently thought. We will also evaluate how pre-existing immunity to related dengue viruses and passive immunity to Zika virus modulate the duration of sustained Zika virus detection and/or risk of congenital Zika syndrome in fetuses; completion of this project could provide pregnant women with a better way of assessing the risk of congenital Zika virus infection and offer new therapeutic options to reduce this risk during the later stages of pregnancy.
Role: co-I of Project 2; Virology Core PI

P51 OD 011106 (Ackerman) 05/01/23-04/30/27 1.2 calendar
NIH-ORIP $50,665,021 total support; $208,184 to my lab
WNPRC base grant
These funds support the Virology Services Unit, which provides research support to WNPRC and extra-mural investigators performing virology research in nonhuman primates.
Role: PI of Virology Services core

435100-A22-ELCProjE-01 (O'Connor, D) 8/1/2021-7/31/2024 0.12 calendar
Wisconsin Dept of Health Services $600,000
ELC Project: Enhancing Detection Expansion
This contract is for sequencing of SARS-CoV-2 genomes over the next two years to the Wisconsin DHS/DPH. These sequences will be placed into public repositories (GISAID and/or NCBI Genbank) ensuring these sequences are available to DHS/DPH.
Role: co-PI

Pending research support

Title: Evolutionary pathways to antiviral resistance for influenza virus

Major Goals: A major question in influenza virus evolution is how evolutionary processes that appear to be dominated by random effects on small scales are connected to the global scale, where viral evolution seems to be shaped by natural selection for immune escape. We hypothesize that a temporal disconnect between virus replication and selective pressures weakens the activity of natural selection on the scale of individual hosts. We will test this hypothesis using a novel barcoded influenza virus that allows for unprecedented resolution of the fate of individual viruses within and between hosts.

Status of Support: Pending
Project Number: R01
Name of PD/PI: Friedrich and Mehle
Source of Support: National Institutes of Health
Primary Place of Performance: University of Wisconsin - Madison
Project/Proposal Start and End Date: 07/2024-06/2026
Total Proposal Subaward amount: $ 415,367
Year Person Months
1. 2024 1.2 calendar
2. 2025 1.2 calendar

Title: Vertical transmission, pregnancy outcomes and treatment of MPXV infection in a translational pregnant macaque model
Major Goals: We will develop a preclinical rhesus macaque model of mpox disease in pregnancy. We hypothesize that MPXV will be vertically transmitted with inoculation in early gestation, that there will be an increase in adverse pregnancy outcomes with maternal infection, and that the antiviral drug tecovirimat will decrease maternal disease and improve pregnancy outcomes. My role on this project is to provide expertise in virology and nonhuman primate models of viral infection.
Status of Support: Pending
Project Number: 1R01AI182082-01
Name of PD/PI: Emma Mohr (Contact) and Thaddeus Golos
Source of Support: National Institutes of Health
Primary Place of Performance: University of Wisconsin - Madison
Project/Proposal Start and End Date: 04/2024-03/2029
Total Proposal Subaward amount: $ 3,814,057
Year Person Months
1. 2025 0.3 calendar
2. 2026 0.3 calendar
3. 2027 0.3 calendar

4. 2028 0.3 calendar
2. 2029 0.3 calendar

Title: The paradox of flavivirus antigenic non-reciprocity

Major Goals: Pre-existing immunity to one flavivirus can affect the outcome of subsequent exposures to different flaviviruses. Mounting evidence shows that the outcome of these subsequent exposures differs depending on the order in which the host has been exposed to other viruses previously. This multi-PI project seeks to integrate novel nonhuman primate models of flavivirus immune cross-reactivity with well-defined human cohorts to understand antibody determinants of these non-reciprocal immune interactions.

Status of Support: Pending
Project Number: 1R01AI183302-01
Name of PD/PI: Thomas Friedrich (contact), Matthew Aliota, Eva Harris
Source of Support: National Institutes of Health
Primary Place of Performance: University of Wisconsin - Madison
Project/Proposal Start and End Date: 04/2024-03/2029
Total Proposal Subaward amount: $ 3,814,057
Year Person Months
1. 2025 0.3 calendar
2. 2026 0.3 calendar
3. 2027 0.3 calendar
4. 2028 0.3 calendar
2. 2029 0.3 calendar

Title: Covert COVID: Role of tissue reservoirs in persistent SARS-CoV-2 evolution and pathogenesis

Major Goals: SARS-CoV-2 can cause unusually prolonged infections in some individuals. These prolonged infections typically occur in immunocompromised persons who are at risk for severe disease or death. They are significant because they pose unique challenges to treatment and because such prolonged infections are likely to be a major source of highly evolved variant viruses like Alpha and Omicron. We hypothesize that tissue reservoirs outside the upper respiratory tract are important in maintaining SARS-CoV-2 persistence and in promoting extensive within-host viral evolution. This program project assembles a unique multidisciplinary team to investigate this hypothesis in distinct but interconnected projects focusing on human patients, environmental sampling, and novel animal models.
Status of Support: Pending
Project Number: 1P01AI186769-01
Name of PD/PI: David O’Connor (contact), Thomas Friedrich
Source of Support: National Institutes of Health
Primary Place of Performance: University of Wisconsin - Madison
Project/Proposal Start and End Date: 2/1/2025-1/31/2030
Total Proposal amount: $ 22,926,145
Year Person Months
1. 2025 2.4 calendar
2. 2026 2.4 calendar
3. 2027 2.4 calendar
4. 2028 2.4 calendar
2. 2029 2.4 calendar

I.B.2. Completed research support

R01 AI 125392 (Friedrich/Mehle) 01/01/17-12/31/23 NCE 2.4 calendar
NIAID $240,715 (UW-Madison share of total year 1 DCs)
Mechanisms of influenza transmission bottlenecks: impact on viral evolution
My group recently showed that airborne transmission of influenza viruses can impose genetic bottlenecks that dramatically impact viral evolution. If funded, this project will determine the host and viral determinants of these bottlenecks in a ferret model. The findings of these experiments will elucidate how influenza viruses evolve during airborne transmission and help determine whether transmission bottlenecks might favor or hinder the emergence of novel viruses in humans.
Role: Contact PI

(Friedrich and Mehle) 08/01/18-07/31/23 NCE 0.6 calendar
NIH NIAID 5R01AI125392 Supplement in response to NOT-AI-18-030 $235,692 (total DCs)
Mechanisms of influenza transmission bottlenecks: impact on viral evolution
For the parent award we have developed a unique set of influenza viruses bearing "molecular barcodes" that allow us to track viral evolution with high precision. The goal of this proposed supplement will be to adapt these barcoded viruses to understand how influenza virus antigenic variants can escape the forces of genetic drift and come to dominate a population.
Role: PI

R01 AI 127565 (Legge/Narasimhan/Waldschmidt/Friedrich) 07/01/17-06/30/23 NCE 0.6 calendar as of 7/1/20
NIAID $113,031 (Share of total year 4 DCs to my lab)
Nanovaccine-mediated immune protection against influenza virus
This multi-PI proposal seeks to evaluate a novel method for generating broadly protective immunity against influenza. In years 1-3, Dr. Legge and other investigators will define a "lead candidate" vaccine formulation in mice and define cellular and humoral correlates of protection. In years 4-5, my group will lead a preclinical evaluation of this lead vaccine candidate's protective efficacy against influenza challenge in our translational nonhuman primate model of influenza. Thus I will not have committed effort on this award until 2020.
Role: co-PI

75D30120C09870 (O'Connor/Friedrich) 05/17/21-05/16/23 0.6 calendar
CDC $1,913,800 total costs
Impact of immune failure on SARS-CoV-2 evolutionary potential
In this project we will rapidly sequence SARS-CoV-2 genomes from potential cases of immune failure, including vaccine breakthrough, reinfection, or persistent infection, to characterize patterns of viral evolution and detect potential variants of concern.
Role: MPI

R01 AI 132519 (Golos) 04/25/18-03/31/23 0.9 calendar
NIH $512,115 (Total year 1 DCs to UW)
Pathways of vertical Zika virus transmission in nonhuman primate pregnancy
The goal of this project is to determine whether prolonged viremia in ZIKV-infected pregnant macaques is associated with adverse fetal outcomes. I provide virology expertise to this project.
Role: co-I

Marshfield Clinic Research Institute (McLean, H) 4/1/2021-03/31/23 0.36 calendar
Seqirus, Inc. $126,436 total subaward costs
Genotyping and within-host evolutionary analysis of human influenza viruses
For this project we will use deep sequencing to confirm influenza subtyping analyses and characterize within-host diversity of influenza viruses infecting volunteers in a vaccine study.
Role: PI-subaward

2U01AI102456-06 (Kaufman) 3/1/20-7/31/22 0.6 calendar

NIAID $76,282 total award to Friedrich lab
Tomotherapy and Hematopoietic Stem Cells for Tolerance to Kidney Transplants
The goal of this pilot project is to develop standardized molecular diagnostic assays for opportunistic viral pathogens of nonhuman primates, principally cytomegalovirus (CMV), which cause morbidity after allogeneic solid organ transplants. CMV and other viral pathogens are common opportunistic agents in human transplant recipients also, and currently no standardized assays exist to detect macaque CMV.
Role: PI of pilot project

75D30120C09870 (O'Connor/Friedrich) 09/15/20-09/14/22 0.6 calendar
CDC $1,028,200 total direct costs
Defining the role of college students in SARS-CoV-2 spread in the Upper Midwest
The goal of this project is to use rapid genome sequencing of SARS-CoV-2 viruses from college students in Wisconsin and Michigan together with epidemiological data to understand the role college students play in spreading the virus in the communities in which they live.
Role: MPI

MSN253819/2021 HTH 011 (O'Connor/O'Connor/Friedrich) 06/01/21-05/31/22 0.12 calendar
Rockefeller Foundation $339,999 direct costs
Upper Midwest Regional Accelerators for Genomic Surveillance
The major goal of this project is to enhance interactions among clinical and public health professionals and researchers to apply innovative methods in pathogen genomic sequencing for public health benefit.
Role: MPI

MSN248683/2240 (O'Connor/Friedrich) 01/01/21-12/31/21 0.24 calendar
Emergent Ventures/Mercatus Center $120,000 total costs
Urgent sequencing of travel-associated SARS-CoV-2 viruses in Wisconsin
We will rapidly sequence SARS-CoV-2 viruses from PCR+ individuals in Wisconsin who have traveled internationally in the past 14 days or have had close contact with someone who traveled internationally in the last 14 days.
Role: MPI

(no award number) 05/01/20-06/30/21 0.6 calendar
Wisconsin Partnership Program $184,464 total costs
Genetic surveillance of SARS-CoV-2 spread in Wisconsin to inform outbreak control
The goal of this project is to use rapid genome sequencing of SARS-CoV-2 viruses together with real-time data sharing to inform our understanding of the temporal and geographic dynamics of the pandemic in Wisconsin.
Role: PI

(O'Connor) 11/01/20-12/31/20 0.12 calendar
Wisconsin Partnership Program
Genetic epidemiology of SARS-CoV-2 in hospitals and care facilities
The goal of this project is to use viral genomics to determine sources of SARS-CoV-2 infections among health care workers in UW Hospital and Clinics.
Role: co-I

NIH Rapid Acceleration of Diagnostics for COVID-19 (RADx)
07/08/20-09/07/20 0.1 calendar
Flambeau Diagnostics (Beebe)
Massively parallel centralized and decentralized ultrafast COVID-19 infectiousness testing
This project was funded as part of an NIH/FDA effort to accelerate the devleopment of diganostic testing for SARS-CoV-2 infection. My laboratory contributed to the development and validation of a rapid nucleic acid-based test for SARS-CoV-2 that could be used in a mobile laboratory. Flambeau Diagnostics, led by David Beebe, was our commercial partner. In October 2020, Flambeau was chosen as one of 6 recipients of Phase 2 RADx-Tech awards, which will provide $12 million in funding to scale up development of

an automated mobile testing lab run from a minivan.
Role: Co-I

R21 AI 128400 (Aliota) 04/01/17-03/31/19 0.24 calendar
NIAID
Zika virus evolutionary dynamics in host adaptation
The goal of this project was to determine whether Wolbachia infection inhibits mosquitoes' susceptibility to Zika virus and their potential to transmit it to mammalian hosts. My role was to assess the potential for Zika virus to evolve under selection pressure from Wolbachia in infected hosts.
Role: co-I

R24 OD 017850 (O'Connor) 09/01/14-05/31/19 1.2 calendar (reduced due to reduced role in final year of project)
NIH-ORIP
Identifying common CD8+ T cell responses to major pathogens in rhesus macaques
The goal of this project is to identify CD8+ T cell epitopes derived from multiple clinically important pathogens presented by common MHC class I molecules in the rhesus macaque. Identifying these epitopes will provide "benchmarks" by which to compare T cell responses across studies and will therefore enhance macaque models of infectious disease. My role is to collaborate with the PI on design, execution, and interpretation of experiments to identify epitopes derived from influenza viruses.
Role: co-Investigator

WNPRC pilot award (Suresh/Friedrich) 12/01/14-11/30/18
WNPRC/NIH-ORIP
Priming protective mucosal CD8 T cell immunity
This project was supported by pilot funding from the Wisconsin National Primate Research Center. The aims were to test the ability of a novel adjuvant to induce potent cellular immunity to influenza in the respiratory mucosae of rhesus macaques, and determine whether adjuvanted vaccines provide protection against influenza challenge. This project did not provide salary support.
Role: co-PI

UW2020 Initiative (Mehle) 04/01/16-07/31/17
Wisconsin Alumni Research Foundation
Genomic approaches to identify host factors and mechanisms that modulate pathogen infections
This project developed new genetic approaches to identify critical host factors exploited by pathogens during infection. My role was to generate and analyze deep sequence data for viruses and vRNA.
Role: co-Investigator

R01 AI 069274 (Kawaoka) 09/01/14-08/31/16
NIH-NIAID
NIH diversity supplement to support graduate training
This supplement to Dr. Kawaoka's R01 on the transmissibility of H5N1 influenza viruses in mammals supported training of my PhD student Jorge Dinis, who worked on collaborative projects with Dr. Kawaoka.
Role: co-PI of supplement

R13 OD024607 (O'Connor/Friedrich) 04/04/17/03/31/18
NIH/ORIP
NHP Symposium on AIDS - Madison WI
This award supported the 35th Annual Suymposium on Nonhuman Primate Models for AIDS. "NHP AIDS" is the major conference focused on nonhuman primate AIDS research and brings together >250 delegates annually. I co-organized this meeting in Madison, WI with Shelby O'Connor.
Role: co-PI

U01 IP000471 (Belongia) 09/01/11-06/30/16
NIH/CDC
Influenza Vaccine Effectiveness in a Wisconsin Population
This award supported a longitudinal, multicenter study of influenza vaccine effectiveness. My laboratory's role in this project was to evaluate human immune responses to influenza vaccination and infection and to sequence viruses infecting study participants.
Role: PI of subaward

R01 AI084787 (Friedrich/O'Connor) 09/01/09-08/31/15
NIH/NIAID
Defining the importance of CD8+ T cell breadth in SIV/HIV protective immunity
This project sought to understand whether a broadly directed CD8+ T cell response is necessary for control of AIDS virus replication.
Role: co-PI

no award ID (Friedrich) 09/01/14-05/31/15
UW Graduate School
Correlates of broadly cross-protective immunity against influenza
This project, supported in part by bridge funding from the Graduate School, used a novel "mosaic" immunogen to identify immune responses that confer "cross-protection" against influenza in a translational macaque model.
Role: PI

P51 RR000167 (Cadwallader/Friedrich) 09/28/09-04/30/12
NCRR
WNPRC base grant
This administrative supplement funded the development of nonhuman primate models for influenza vaccine and pathogenesis research.
Role: PI of subaward

MSN136980 07/01/10-06/30/12
(Friedrich) UW-Madison Vilas Associates
Human T cell immunity and susceptibility to severe influenza H1N1 disease
The goal of this project was to identify cellular immune correlates of susceptibility to severe influenza disease in patients admitted to UW Hospital and Clinics.
Role: PI

(no ID) (Goldberg) 07/01/10-06/30/12
UW-Madison Wisconsin Center of Infectious Diseases
Novel tools for viral discovery and pandemic prevention
My laboratory provided virology expertise to this multidisciplinary project aimed at discovering novel viruses infecting nonhuman primates.
Role: co-I

ICTR 07012011 (Coleman) 07/01/11-06/30/13
UW Institute for Clinical and Translational Research (UW–Madison CTSA)
Epidemiologic and viral predictors of 2009 H1N1 influenza
In collaboration with investigators at the Marshfield Clinic in northern Wisconsin, my group is testing the hypothesis that viral escape from CD8+ T cell responses contributed to human cases of recurrent influenza infection during the 2009 pandemic.
Role: PI of subaward

ICTR 09032008 (Friedrich) 08/01/08-02/28/2010
UW Institute for Clinical and Translational Research (UW–Madison CTSA)
Nonhuman primate models for pandemic influenza
This project aimed to indentify CTL epitopes in influenza virus utilizing the unique cohort of MHC-defined rhesus macaques available at WNPRC.
Role: PI

R21 AI068586 (Friedrich) 08/15/2006-07/31/2009
NIH/NIAID
Correlates of elite control of SIV
The goal of this project was to dissect the contribution of Mamu-B*17-restricted CD8 T-cell responses to immune control of pathogenic SIV.
Role: PI

I.C. Invited research presentations

1. [Multiple SARS-CoV-2 research presentations in 2020-23]
2. Evolutionary dynamics of avian influenza virus host switching: implications for the next pandemic? Invited research seminar, Peter Doherty Institute of the University of Melbourne, Australia 2019
3. Evolution and transmission of H7N9 avian influenza viruses in ferrets. Respiratory Virology Interest Group seminar, Peter Doherty Institute of the University of Melbourne, Australia 2019
4. Infection via mosquito bite alters Zika virus populations and replication kinetics in rhesus macaques. Flash talk and poster. 2nd Conference on Viral Genomics and Evolution, Wellcome Genome Campus, Hinxton, England 2018
5. Making sense of Zika: building new rapid-response animal models to understand emerging viruses. Iowa Nanovaccines Institute, Iowa City, IA 2018
6. From zero to Zika: building new NHP models to understand emerging viruses. Dept. of Microbiology, Immunology, and Pathology/Arthropod-borne and Infectious Diseases Laboratory, Colorado State University, Fort Collins, CO 2018
7. Oropharyngeal mucosal transmission of ZIKV in rhesus macaques. Second International Meeting on Arboviruses and Their Vectors (IMAV), University of Glasgow, Scotland 2017
8. Team ZEST: Adventures in understanding Zika. Pathology Department Grand Rounds, University of Iowa Medical School, Iowa City, IA 2017
9. Passing through: the role of transmission bottlenecks in influenza virus host adaptation. Invited seminar, Fred Hutchinson Cancer Research Center, Seattle, WA 2016
10. Deep sequencing reveals potential antigenic drift variants at low frequency in influenza-A-infected humans. Influenza Vaccines for the World, Albufeira, Portugal 2015
11. ADCC antibodies in heterosubtypic immunity to influenza. 4th GTC Conference on Influenza Vaccines, Boston, MA 2015
12. Transmission bottlenecks: Effects on influenza virus evolution. Dept. of Homeland Security/Fogarty International Center Research and Policy for Infectious Disease Dynamics (RAPIDD): Modeling and Predicting Influenza Phenotypes, University of Cambridge, England 2015
13. MVA encoding hemagglutinin induces heterosubtypic immunity in macaques. Fifth European Scientific Working Group for Influenza (ESWI) Conference, Riga, Latvia 2014
14. Blurred Lines: HIV DNA, RNA, and detection limits. Clinton Health Access Initiative/CDC task force on Alternative Technologies for Viral Load Testing in African Treatment Programs, Centers for Disease Control and Prevention, Atlanta, GA 2014

15. Selection on hemagglutinin imposes a genetic bottleneck during mammalian transmission of H5N1 influenza viruses. Options for the Control of Influenza VIII, Cape Town, South Africa 2013
16. Reinventing vaccines. University of Wisconsin Festival of Ideas (organized by Wisconsin Union Directorate's Distinguished Lecture Series), Madison, WI 2013
17. Harnessing immunity to stop HIV. University of Wisconsin School of Veterinary Medicine Board of Visitors meeting, Madison, WI 2013
18. The next pandemic? Hunting for RNA viruses in African primates. University of Wisconsin-La Crosse, La Crosse, WI 2013
19. Characterizing antigenic variation in circulating influenza viruses using rapid, massively parallel deep sequencing. Marshfield Clinic Research Foundation, Marshfield, WI 2013
20. Understanding the impact of viral variation on influenza vaccine effectiveness. Marshfield Clinic Research Foundation, Marshfield, WI 2013
21. When (neutralizing) antibodies fail: Modeling cross-protective immunity to emerging influenza viruses. Marshfield Clinic Research Foundation, Marshfield, WI 2012
22. Cross-reactive T cells are involved in rapid clearance of 2009 pandemic H1N1 influenza virus infection by nonhuman primates. Keystone Symposium: Pathogenesis of Influenza: Virus-Host Interactions, Hong Kong SAR, China 2011
23. Cross-reactive CD8 T cells enable early clearance of 2009 pandemic influenza virus from the lower respiratory tract in nonhuman primates. Options for the Control of Influenza VII, Hong Kong SAR, China 2010
24. Can memory CD8+ T cells protect macaques against 2009 H1N1 influenza viruses? Johns Hopkins University School of Medicine, Baltimore, MD 2010
25. Can memory T cell responses protect against pandemic influenza? Rakai Health Sciences Project, Kalisizo, Uganda
26. SIV elite controllers resist superinfection with multiple CD8+ T cell escape mutant viruses. 27th Annual Symposium on Nonhuman Primate Models for AIDS, Boston, MA 2009
27. Targeting an AIDS vaccine: macaque models for human "elite control" and identifying correlates of protection. Animal Biotechnology and its Application to Animal and Human Health, Cambridge Genome Campus, Hinxton, England 2007
28. Domination or Cooperation? A role for subdominant CD8+ T cell responses in control of AIDS virus infection. Laboratory of Molecular Microbiology, National Institutes of Health, Bethesda, MD 2007
29. Reversion of CTL escape mutant simian immunodeficiency virus in vivo: implications for HIV vaccine development. XV International AIDS Conference, Bangkok, Thailand *Young Investigator award
30. Understanding rhesus macaque MHC diversity. NCRR Nonhuman Primate Genomics Working Group, Southwest Primate Research Center, San Antonio, TX 2003
31. Understanding the functional significance of AIDS virus escape from CTL responses. Deutsches Primatenzentrum (German Primate Center), Göttingen, Germany 2002
32. Association of particular MHC class I alleles with control of AIDS virus infection. International Perspectives: The Future of Nonhuman Primate Resources, National Academy of Sciences, Washington, DC 2002

I.D. Contributed abstracts

*** presenting author**

1. **CM Crooks**, AS Jaeger, **AM Weiler**, **SL Rybarczyk**, **M Bliss**, **EA Brown**, HA Simmons, JM Hayes, A Mejia, K Yamamoto, PM Shepherd, ME Murphy, TG Golos, A Possell, K Weaver, TK Morgan, DM Dudley, N Schultz-Darken, E Peterson, DH O'Connor, MT Aliota, and **TC Friedrich**. African-lineage Zika virus causes placental pathology in pregnant rhesus macaques. American Society for Tropical Medicine and Hygiene 2019 meeting, National Harbor, MD.
2. **K Braun***, **G Barry**, G Neumann, T Watanabe, Y Kawaoka, and **TC Friedrich**. Stochastic transmission bottlenecks constrain adaptation of H7N9 influenza viruses to mammalian hosts. Options X for the Control of Influenza, Singapore, 2019.
3. DM Dudley*, P Shepherd, K Yamamoto, M Breitbach, **M Bliss**, **SL Rybarczyk**, **AM Weiler**, M Schotzko, E Sneed, **C Crooks**, N Schultz-Darken, **TC Friedrich**, SR Permar, and DH O'Connor.
4. **LH Moncla***, P Dussart, P Buchy, H Zhu, T Bedford, **TC Friedrich**, and PF Horwood. Characterization of H5N1 spillover infection in humans and poultry in Cambodia. Young Flu 2018, Hanoi, Vietnam.
5. **T Friedrich***, D Dudley, C Newman, **J Lalli**, L Stewart, M Koenig, **A Weiler**, M Semler, **G Barry**, K Zarbock, M Mohns, M Breitbach, N Schultz-Darken, E Peterson, W Newton, E Mohr, S Capuano III, J Osorio, S O'Connor, D O'Connor, and M Aliota. Infection via mosquito bite alters Zika virus populations and replication kinetics in rhesus macaques. 2nd Conference on Viral Genomics and Evolution, Wellcome Genome Campus, Hinxton, England 2018.
6. CM Newman, DM Dudley, MT Aliota, **AM Weiler**, **GL Barry**, MS Mohns, ME Breitbach, LM Stewart, CR Buechler, ME Graham, J Post, N Schultz-Darken, E Peterson, W Newton, EL Mohr, S Capuano III, DH O'Connor, and **TC Friedrich***. Oropharyngeal mucosal transmission of ZIKV in rhesus macaques. Second International Meeting on Arboviruses and Their Vectors (IMAV), University of Glasgow, Scotland 2017.
7. **AM Weiler***, MT Aliota, J Weger, **G Barry**, DM Dudley, C Newman, SL O'Connor, DH O'Connor, G Ebel, and **TC Friedrich**. Resources for nohuman primate models of Zika virus. 35th Annual Symposium on Nonhuman Primate Models for AIDS, Madison, WI 2017.
8. **LH Moncla***, G Zhong, CW Nelson, **JM Dinis**, J Mutschler, AL Hughes, T Watanabe, Y Kawaoka, and **TC Friedrich**. Selective bottlenecks shape evolutionary pathways taken during mammalian adaptation of a 1918-like avian influenza virus. Macrae Foundation XVIII International Symposium on Respiratory Viral Infections, Lisbon, Portugal 2016. My student Louise Moncla won a Young Investigator Award for this abstract.
9. **LH Moncla***, G Zhong, CW Nelson, **JM Dinis**, AL Hughes, T Watanabe, Y Kawaoka, and **TC Friedrich**. Selective bottlenecks shape evolutionary pathways taken during mammalian adaptation of a 1918-like avian influenza virus. First International Meeting on Respiratory Pathogens, Singapore 2015. My student Louise Moncla won a Pasteur Institute Young Investigator Award for this abstract.
10. **TC Friedrich***. ADCC antibodies in heterosubtypic immunity to influenza. 4th GTC Conference on Influenza Vaccines, Boston, MA 2015.
11. **LH Moncla***, G Zhong, CW Nelson, AL Hughes, T Watanabe, **TC Friedrich**, and Y Kawaoka. Selective bottlenecks shape evolutionary pathways taken during mammalian adaptation of a 1918-like avian influenza virus. International Society for Influenza and other Respiratory Viruses (ISIRV) Workshop on Next-Generation Viral Sequencing, Pasteur Institute, Paris, France 2015.
12. **N Florek**, **JT Weinfurter**, ML Budde, JM Greene, BT Cain, NH Pham, SL O'Connor, E Gostick, DA Price, M Piatak Jr, JD Lifson, DH O'Connor, and **TC Friedrich***. Acute-phase T cell activation does not predict control of SIVmac239 in MHC-defined Mauritian cynomolgus macaques. 32nd Annual Symposium on Nonhuman Primate Models for AIDS, Portland, OR 2014.
13. A Das, **AM Weiler**, **TC Friedrich**, and NJ Maness*. Maintenance of multiple Nef functions limits and dictates pathways of immune escape. 32nd Annual Symposium on Nonhuman Primate Models for

AIDS, Portland, OR 2014.

14. **NW Florek**, **JT Weinfurter**, **S Jegaskanda**, JN Brewoo, TD Powell, GR Young, SC Das, M Hatta, KW Broman, O Hungnes, SG Dudman, Y Kawaoka, SJ Kent, DT Stinchcomb, JE Osorio, and **TC Friedrich***. Modified vaccinia Ankara encoding influenza hemagglutinin induces heterosubtypic immunity in macaques. Fifth Conference of the European Scientific Working Group on Influenza (ESWI), Rīga, Latvia 2014.
15. P Wilker, **J Dinis***, G Starrett, M Imai, M Hatta, C Nelson, D O'Connor A Hughes, G Neumann, Y Kawaoka, and **TC Friedrich**. Selection on hemagglutinin imposes a genetic bottleneck during mammalian transmission of H5N1 influenza viruses. Conference of Ford Foundation Fellows, Washington, DC 2014.
16. ME Sundaram*, HQ McLean, JK Meece, RK Zimmerman, MP Nowalk, CJ Lin, **TC Friedrich**, S Spencer, and EA Belongia. Antibody Response to Intradermal and High Dose Influenza Vaccine in 2012-13 Among Adults Who Did and Did Not Respond to Standard Dose Vaccine in 2011-12. IDWeek: Advancing Science, Improving Care, a joint meeting of the Infectious Disease Society of America and other groups. Philadelphia, PA 2014.
17. Y Cai, EN Postnikova, S Yú, S Mazur, NM Deiuliis, SR Radoshitzky, JG Bernbaum, MG Lackemeyer, V Haucke, V Wahl-Jensen, **TC Friedrich**, DH O'Connor, TL Goldberg, LE Hensley, PB Jahrling, and JH Kuhn*. CD163-dependent clathrin-mediated endocytosis is the preferred cell–entry pathway of simian hemorrhagic fever virus. XIIIth International Nidovirus Symposium, Salamanca, Spain, 2014.
18. P Wilker, **J Dinis**, G Starrett, M Imai, M Hatta, C Nelson, D O'Connor A Hughes, G Neumann, Y Kawaoka, and **TC Friedrich***. Selection on hemagglutinin imposes a genetic bottleneck during mammalian transmission of H5N1 influenza viruses. Options for the Control of Influenza VIII, Cape Town, South Africa 2013.
19. Y Hatta, S Seymour, T Ross, C Crevar, A Kelvin, D Kelvin, D Banner, **T Friedrich**, S Watanabe, G Neumann, Y Kawaoka, and P Bilsel*. Single replication flu vaccine M2SR elicits long-lasting, cross-protective immunity. Options for the Control of Influenza VIII, Cape Town, South Africa 2013.
20. TL Goldberg*, M Lauck, WM Switzer, D Hyeroba, A Tumukunde, J Kuhn, CA Chapman, N Ting, **TC Friedrich**, and DH O'Connor. Co-infection of wild African primates with SIV and simian hemorrhagic fever viruses. 20th Conference on Retroviruses and Opportunistic Infections, Atlanta, GA 2013.
21. WM Switzer*, M Lauck, **JT Weinfurter**, A Shankar, D Hyeroba, A Tumukunde, G Weny, CA Chapman, N Ting, **TC Friedrich**, DH O'Connor, TL Goldberg. Discovery of novel and highly divergent SIVs in three wild monkey species in Kibale National Park, Uganda. 20th Conference on Retroviruses and Opportunistic Infections, Atlanta, GA 2013.
22. M Lauck*, SD Sibley, **TC Friedrich**, TL Goldberg, DH O'Connor. Discovery of novel RNA viruses in non-human primates from Kibale National Park, Uganda. Great Plains Emerging Infectious Diseases Conference, Iowa City, IA 2012.
23. M Harris, CM Burns, EA Becker, AT Braasch, E Gostick, DA Price, **TC Friedrich**, SL O'Connor*. Subdominant T cell responses elicited by a pre-stabilized SIV select for sequence variants during acute infection. Keystone Symposium on HIV Vaccines, Keystone, CO 2012.
24. M Budde, J Weinfurter, A Ericsen, J Greene, E Becker, D Price, S O'Connor, **T Friedrich**, D O'Connor*. CD8+ T cell responses in macaques with restricted genetic diversity. Keystone Symposium on HIV Vaccines, Keystone, CO 2012.
25. SL O'Connor*, A Braasch, CM Burns, MD Alpert, DT Evans, **TC Friedrich**, EG Kallas and DH O'Connor. Defining the need for immunodominant CD8+ T cell responses in an HIV/SIV vaccine. 29th Annual Symposium on Nonhuman Primate Models for AIDS, Seattle, WA 2011.
26. **JT Weinfurter**, K Brunner, SV Capuano III, C Li, K Broman, Y Kawaoka and **TC Friedrich***. Cross-reactive T cells are involved in rapid clearance of 2009 pandemic H1N1 influenza virus infec-

tion by nonhuman primates. Keystone Symposium: Pathogenesis of Influenza: Virus-Host Interactions, Hong Kong SAR, China 2011.

27. EN Chin*, **JT Weinfurter**, EA Becker, **TC Friedrich** and DH O'Connor. Ultradeep pyrosequencing reveals that the extent of acute phase viral diversification is variable in MHC-identical macaques infected with clonal SIVmac239. 18th Conference on Retroviruses and Opportunisitic Infections, Boston, MA 2011

28. **BF Wolter**, **JT Weinfurter**, K Brunner, SV Capuano III, C Li, Y Kawaoka and **TC Friedrich***. Cross-reactive CD8 T cells enable early clearance of 2009 pandemic influenza virus from the lower respiratory tract in nonhuman primates. Options for the Control of Influenza VII, Hong Kong SAR, China 2010

29. **BF Wolter**, **JT Weinfurter**, K Brunner, SV Capuano III, C Li, Y Kawaoka and **TC Friedrich***. Can recent infection with H1 or H3 seasonal influenza viruses protect macaques against 2009 H1N1 challenge? Keystone Symposium on Viral Immunity and HIV Vaccines, Banff, AB, Canada 2010

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32. N Wilson, B Keele, J Reed, S Piaskowski, **C Mac Nair**, A Bett, X Liang, F Wang, E Thoryk, G Heidecker, M Citron, L Huang, J Lin, S Vitelli, CD Ahn, M Kaizu, N Maness, MR Reynolds, **T Friedrich**, J Loffredo, E Rakasz, S Erickson, DB Allison, M Piatak Jr, J Lifson, J Shiver, D Casimiro, G Shaw, B Hahn and D Watkins*. Vaccine-induced cellular responses control acute SIV replication after heterologous challenge. 26th Annual Symposium on Nonhuman Primate Models for AIDS. San Juan, PR 2008

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36. **TC Friedrich***, EG Rakasz, **GE May**, **EJ León**, SM Piaskowski, K Weisgrau, J Furlott, **T Soma**, **CE Mac Nair**, NJ Maness, J Reed, NA Wilson and DI Watkins. SIV elite controllers resist challenge with multiple escape mutant viruses. HIV Vaccines: Progress and Prospects. Banff, Alberta, Canada 2008

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40. **TC Friedrich***, AB McDermott, MR Reynolds, S Piaskowski, S Fuenger, IP de Souza, R Rudersdorf, C Cullen, LJ Yant, L Vojnov, J Stephany, S Martin, DH O'Connor, N Wilson and DI Watkins. Consequences of CTL escape: common escape mutations in SIV are not recognized in naïve hosts. HIV Vaccine Development: Progress and Prospects. Whistler, BC, Canada 2004 (Young Investigator Scholarship)

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I.E. Patents

1. Watkins DI, **Friedrich TC**, Sacha JB, Yant LJ and O'Connor DH. 2006. Novel Approach to Broaden and Strengthen Cellular Immune Responses For a Global AIDS Vaccine. Provisional US 60/898,644.

2. Friedrich T, O'Connor DH and Watkins, DI. 2002. A Multivalent, "Pre-Escaped" Epitope Vaccine for AIDS. In Process.

I.F. Grant review service

agency	review group	role	grant type(s)	year(s)
NIH	Special Emphasis panel: Virology member conflicts	member	R01, R21, R33	2017, 2018, 2019, 2020
NIH	Vaccines Against Microbial Diseases (VMD); became Vaccines Against Infectious Diseases (VID) in 2023	ad hoc member 2019, permanent member 2020	R01, R15, R21, R03	2019-24
NIH	Special Emphasis Panel: Explorations of Antimicrobial Resistances and Therapeutics	member	R21, R03	2018
Dept. of Defense	Congressionally Directed Medical Research Program (CDMRP) research programs (similar to NIH P01)	member	program	2018
NIH	Special Emphasis Panel: Immunity in Aging	member	R01	2018
NIH	Special Emphasis Panel: Complications in Zika	member	R21	2017
NIH	Special Emphasis Panel: NHP Core Virology Lab	member	contract	2017
NIH	Special Emphasis Panel: Centers for AIDS Research	member	P30	2016
NIH	Special Emphasis Panel: Investigator-Intitated proposals on influenza/antiviral immunity	member	P01	2016
UK Medical Research Council	Infections and Immunity	ad hoc member	Research Grant	2016

agency	review group	role	grant type(s)	year(s)
NIH	Special Emphasis Panel: Integrated Clincal/Preclinical Program for HIV Topical Microbicides and Biomedical Prevention	member	U19	2015
NIH	Special Emphasis Panel: Innovation in HIV Vaccine Discovery	member	R01	2014
NIH	HIV Vaccines (VACC)	ad hoc member	R01	2014
NIH	Special Emphasis Panel: Innovation in HIV Vaccine Discovery	member	R01	2012, 2013
NIH	Special Emphasis Panel: AIDS Immunity and Pathogenesis (AIP) member conflicts	member	R01, R21	2012
NIH	Special Emphasis Panel: Centers for AIDS Research	member	P30	2009, 2010, 2011, 2012
NIH	Special Emphasis Panel: Nonhuman Primate Reagent Resource	member	contract	2009
UK Wellcome Trust	Research Training Fellowships	ad hoc member	training fellowships	2006

I.G. Academic journal peer review

I have not served on editorial boards. I have performed ad hoc peer review for the following journals:

BMC Genomics (2014)

Clinical and Experimental Immunology (2014–15)

Clinical Infectious Diseases (2016)

Comparative Medicine (2012)

EcoHealth (2011)

Ecology and Evolution (2017)

Emerging Microbes & Infections (2018–23)

Evolution, Medicine, and Public Health (2018)

Immunity (2018)

iScience (2020)

Journal of AIDS (2016)

Journal of the American Association of Aging (AGE) (2011)

Journal of Clinical Immunology (2019)

Journal of Infectious Diseases (2018)

Journal of Virology (2011, 2013–)

Nature (2021–)

Nature Communications (2015–)

Nature Ecology and Evolution (2017–2019)

Pathogens and Immunity (2017)

PLoS Biology (2014–15)

PLoS Genetics (2018)

PLoS Medicine (2014–15)

PLoS ONE (2011–2013, 2015, 2017, 2019)

PLoS Pathogens (2010, 2017, 2020–)

PNAS (2009, 2020–)

Retrovirology (2007)

Science (2016)

Science Translational Medicine (2020–)

Scientific Reports (2016–2019)

Tissue Antigens (2007, 2008)

Tohoku Journal of Experimental Medicine (2012)

Vaccine (2010, 2011, 2014, 2017–)

Viral Immunology (2011)

Virulence (2016)

Viruses (2016)

Virus Evolution (2021–)

II. Teaching accomplishments

II.A. Didactic teaching

Faculty course director, Pathology/PBS 210: HIV: Sex, Science and Society (2008-)

This is my primary teaching responsibility. I direct this survey course on the biological, sociological and economic aspects of HIV/AIDS together with my colleague Dr. David O'Connor. From 2008–2022, the course enrolled ~100 undergraduate students each fall semester. In addition to directing the course, I also taught 5-7 lectures per year and led one of four small discussion groups (15 meetings per semester). This course consistently received high approval ratings from students, including a high proportion of students who do not plan to major in biological sciences. However, after the end of the 2022 fall semester, after 3 years of teaching the course online or as an online/in-person hybrid, Dave and I felt that students were becoming less engaged by the large lecture format. In consultation with Dr. Jenny Safran, the director of the undergraduate Honors Program, we decided to completely revise our course and offer it as a 30-person freshman seminar for Honors students. We decided to design the course "like it was 1992" (the year I entered college), which is to say that we made it completely analogue, with no PowerPoint slides and no online assessments. (Reading materials, syllabi, etc were still distributed online.) In true seminar fashion, the course has become more interactive. We are now able to take detours into topics that arise from student questions or interests, which keeps us and the students more engaged than before.

Faculty course director, PBS 528: Immunology (2014-17)

Core instructor, PBS 528: Immunology (2018-20)

This is my second major teaching responsibility. This course enrolls ~100 students per year, mostly upper-level undergraduates, but also some graduate students. This is a survey course intended to provide students with a thorough background in all aspects of immunology. I took over as instructor of record in

2014 after the retirement of the previous course director, who had run the course for over 25 years. Matt Reynolds took over as course director in fall 2018. I continued to give lectures in the course through the fall of 2020. Throughout my involvement with the course, it received consistently high evaluations from students, despite its academic rigor. Matt is a superb director who has only improved the content and organization of the course.

PBS 930: Graduate Student Seminar (2013–2020; co-director 2016–2020)

PBS 930 is a seminar course for MS and PhD students in the Comparative Biomedical Sciences (CBMS) program. This one-credit course is designed to provide students with a comfortable and yet structured environment in which to learn to give effective research presentations. Students prepare and give a research seminar (one student per week) and then receive structured feedback from faculty and their peers; this feedback is used to assign a letter grade for the presentation. I participated in this course as a faculty mentor beginning in fall of 2013, and in 2016 I became co-director along with my departmental colleague Lyric Bartholomay. In 2018-19 we extensively restructured the course to include low-stakes homework assignments designed to help students develop verbal and graphic design skills necessary to make effective presentations. After co-directing the course for 5 years, in 2021 Lyric and I stepped aside and course directorship was taken over by Leandro Teixeira and Wilmara Salgado Pabon.

Lecturer, PBS 513: Veterinary Virology (2008-)

Each year I give lectures on retroviruses to second-year veterinary students.

Lecturer, Medical Microbiology and Immunology (MMI) 555: Vaccines (2018-19)

This is a team-taught course for senior undergraduates and MS students on applying immunology and microbiology concepts to vaccine design. In 2018 I was invited by course coordinator Peter Schult to give a lecture on Zika vaccines; I returned in 2019 to give an updated talk on the same topic.

Lecturer, Pathology 803: Pathogenesis of Major Human Diseases (2008-10, 2012-14, 2020)

Through 2014 I taught a unit on influenza immunity and pathogenesis to Ph.D. students in this course each year except for 2011, when the course was not offered. I gave 2 didactic lectures to provide students with the background necessary to discuss an issue in contemporary influenza research. They were then asked to read, evaluate and discuss a research paper I selected. I taught a section in this course again in 2020.

Lecturer, Pathology 807: The Immune System in Health and Disease (2015, 18, 20, 22, 24)

Pathology 807 is a team-taught course for graduate students on current topics in immunology. Each lecturer presents a focused lecture on a current topic and then assigns students a research paper from the field to evaluate. The faculty member then leads a discussion of the assigned paper. Each student is expected to turn in a written critique of the paper, which the faculty member provides comments on and assigns a numerical grade. In 2015 and 2018 I led sessions on influenza immunity and pathogenesis. In 2020, 2022, and 2024 I led a session on COVID-19 immunity and pathogenesis.

Lecturer, Pathology 709: Special Topics in Immunopathology (2009-10, 2012)

In this course for Ph.D. students I taught a unit on the role of the host immune response in influenza pathogenesis. Here I provided a single, focused lecture giving background necessary to understand a research paper in the field, which I choose for them. In the next class period, a team of students was asked to lead a journal-club-style seminar describing the paper, its strengths, weaknesses and "take-home messages" to the class.

Lecturer, Pathology 809: Professional Development: Grantsmanship in Pathogene-

sis of Human Diseases (2012)

In 2012 I participated in this semester-long professional development course for Ph.D. students. The overall goal of the course is to help students learn to generate testable hypotheses, write effective proposals and present their results. I led interactive seminars on how to generate (and write) specific aims based on an incisive hypothesis, and how to give effective research presentations.

Lecturer/discussion leader, MMI 810: Current Issues in Microbiology (2011)

This was a seminar course designed to expose new Ph.D. students to important emerging topics in biological research. I presented a seminar about using "unbiased" deep sequencing to discover novel viruses, which I used to stimulate discussion about "omics" research and the role of hypotheses in systems biology. In the next class period, I led the students in discussion of a research paper illustrating these topics. According to the course organizer, I was the highest-rated instructor in this year-long course.

Instructor, PBS 518: Recitation in Infectious Disease Pathobiology (2009)

In this epidemiology course for veterinary students, I led a team of instructors to design an "outbreak scenario" to test students' ability to diagnose and control an infectious disease. My partners were veterinarians from the Wisconsin National Primate Research Center; we presented an outbreak of respiratory disease in a captive rhesus macaque colony. Our role was to guide a team of students in thinking through diagnostic and control procedures, a process of a few weeks. The students then presented their solutions to the class in a "morbidity and mortality rounds" style talk.

Instructor, Pathology 210: HIV: Sex, Science and Society (2007)

I gave multiple lectures in the first semester in which Pathology 210 was offered. At that time, the course director was Dr. David Watkins, though I played a role in designing and organizing the course under his direction. This included designing curriculum and assessments, as well as grading and advising students. One year later, Dr. Watkins stepped down as course director, and I assumed the role, together with Dr. O'Connor. We dramatically changed the course organization and syllabus.

Guest lecturer, Med Micro 677: HIV: Sex, Science and Society (2005, 2006)

I gave multiple lectures in the original version of the "Sex, Science and Society," which was conceived as a 1-credit seminar course for upper-level undergraduates majoring in microbiology or related fields.

Guest lecturer, Biochem 875: Special Topics of Interest to Graduate Students (2004)

I presented a talk on immunodeficiency virus escape from immune detection to this Ph.D. student class.

Guest lecturer, Biochem 550: Topics in Medical Biochemistry (2002)

I presented a lecture on MHC-associated control of immunodeficiency viruses to this class for graduate and upper-level undergraduate students.

Teaching assistant, Biocore 304: Honors Biology Laboratory (2000)

I led a discussion section for this rigorous, writing-intensive laboratory course. The Biology Core Curriculum (Biocore) is an intensive, interdisciplinary 2-year course in biology for outstanding undergraduate students at UW-Madison. Biocore 304 is a 2-credit laboratory course in cellular and molecular biology designed to complement a 3-credit lecture course. Students are expected to learn to formulate hypotheses, design and conduct appropriate experiments, and communicate their results in the style of peer-reviewed scientific papers. Since learning all these things at once is very challenging, even for honors students, I designed a new curriculum module aimed at helping students learn to write in the precise and concise style demanded in the sciences. This "burgerology" assignment required students to design and test a hypothesis about hamburgers (or veggie burgers), and to write a brief scientific paper on their study. Students reported that they enjoyed the assignment, since it allowed them to focus on writing effectively in an unfamiliar style without having to grapple with difficult scientific content. Most students felt this assignment helped prepare them to write their "real" research papers later in the semester.

Undergraduate teaching assistant, Biocore 304: Honors Biology Laboratory (1996)

As an undergraduate alumnus of the Biocore program, I took the opportunity to be an "undergrad TA" for the same Biocore 304 course described above. I assisted a Ph.D. student with all aspects of the course—leading discussions, answering student questions, and grading assignments.

II.B. Mentoring

II.B.1. Postdoctoral mentees

Heather Machkovech, MD, PhD. 2023–. Heather joined the lab in fall 2023 as a fellow supported by UW's Physician Scientist Training Program (PSTP), which supports MD-PhDs in both their clinical residency and in a research laboratory. Heather completed her PhD at the University of Washington in the lab of Jesse Bloom, studying within-host evoultion of influenza viruses. Her UW residency is in infectious disease, so her interests, skills, and background are well-suited to my lab's work. Heather's research in my lab focuses on respiratory virus evolution within and between hosts. She has taken over the lead on our collaborative studies using barcoded influenza viruses to investigate mechanisms of transmission bottlenecks in animal models. Given her interests and expertise, she is also working on studies of SARS-CoV-2 evolution in persistently infected humans. In her first months in lab, Heather led a critical review and editorial on the importance of studying these persistent infections, which appeared in ***Lancet Infectious Disease***.
Research topic: Within- and between-host evolution of respiratory RNA viruses.

Kasen Riemersma, DVM, PhD. 2019–21. Kasen joined my lab in August 2019, having completed his PhD studying arbovirus evolution and pathogenesis with Lark Coffey at UC-Davis. Kasen's main research contribution in the lab was to lead multiple studies of within- and between-host evolution of flaviviruses. He also coordinated our group's SARS-CoV-2 genomic epidemiology studies beginning in summer 2021, after the departure of the senior PhD students who established that program. Kasen was instrumental in our group's early observation that fully vaccinated individuals who became infected with the SARS-CoV-2 Delta variant could still shed infectious virus at high levels, suggesting that people with breakthrouogh infections should take precautions to limit transmission to others. This work received wide attention as a preprint in summer 2021. Kasen decided to leave the academic track for an industry position in September 2021.
Research topic: Within- and between-host evolution and pathogenesis of Zika virus and related flaviviruses; SARS-CoV-2 molecular evolution and genomic epidemiology.

II.B.2. UW-Madison graduate program trainerships

Biophysics (2021–)

Cellular and Molecular Biology (2008–)

Cellular and Molecular Pathology (2008–)

Comparative Biomedical Sciences (2011–)

Genomic Sciences Training Grant (2020–)

Microbes in Health and Disease Training Grant (2016–)

Microbiology Doctoral Training Program (2010–)

Molecular Biosciences Training Grant (2008–19; training grant ended)

Medical Scientist Training Program (2011–)

Pathogen and Vector Biology Training Grant (2017–)

Virology Training Grant (2015–)

II.B.3. Current graduate students

Hunter Ries, CMP 2021- (pursuing PhD). Hunter joined my lab as a new PhD student in December 2021 and is developing his thesis work. His current project is aimed at understanding the mechanisms of natural selection acting on SARS-CoV-2 in immunocompromised individuals with prolonged infection.
Thesis topic: RNA virus evolution in immunocompromised hosts.

Wanting Wei, Biophsyics 2021- (pursuing PhD). Wanting joined my lab as a new PhD student in December 2021 and is developing her thesis project. Her current project is to use genomic epidemiology to trace the introduction and spread of the Omicron SARS-CoV-2 variant into Wisconsin.
Thesis topic: SARS-CoV-2 evolution and transmission.

II.B.4. Past graduate students

Luis Haddock Soto, PhD, CMB 2020-2023. Supported by fellowships from UW–Madison's **Science and Medicine Graduate Research Scholarships (GRS)** and the **Genomic Sciences Training Program T32**. Luis did a fourth rotation in my laboratory in February-March 2020 and joined as a PhD student in March 2020.
Thesis topic: Processes of RNA virus evolution within and between hosts.

Luis's research focused on respiratory RNA virus evolution. He had two main projects. First, he was a leader of my group's collaborative work on SARS-CoV-2 genomic surveillance and evolution, particularly after Dr. Kasen Riemersma left for a new position. Luis was central in analyzing data and overseeing the revision of our manuscript showing that people infected with SARS-CoV-2 despite vaccination could shed infectious virus. Luis's major contribution was in carrying forward our studies using the molecularly barcoded influenza virus to examine compartmentalization and viral evolutionary dynamics within and between hosts. He developed computational methods to reliably count "true" barcodes in Illumina sequence data and, working with Katie Amato in Andrew Mehle's lab, showed that influenza virus infections in directly inoculated ferrets show dramatic levels of anatomical compartmentalization, with different populations of viruses even within each lung lobe. These findings suggest that within-host compartmentalization serves as a barrier to the evolution and transmission of novel virus variants, by reducing local effective population sizes and limiting the ability of variants that arise in the lower respiratory tract from accessing the upper respiratory tract, from where they would be more efficiently transmitted. Luis also started crucial experiments using these barcoded viruses to examine transmission between hosts, which will be carried on by postdoc Dr. Heather Machkovech.

Chelsea Crooks, PhD, MDTP 2017-2022. Supported by **Pathogen and Vector Biology T32**, 2018–19.
Thesis topic: Mechanisms of Zika virus pathogenesis.

Chelsea's thesis research focused on the mechanisms of Zika virus (ZIKV) immunity and pathogenesis during pregnancy. She spearheaded the development of ZIKV research in my laboratory, becoming an expert in placental anatomy and vertical transmission of viruses. Chelsea's major contribution was to lead our multi-PI, multidisciplinary collaboratory in studies of ZIKV infection at the maternal-fetal interface. She found that pre-existing immunity to dengue virus (DENV) in pregnant macaques enhanced ZIKV infection of maternal-fetal interface tissues, although it was not associated with direct fetal harm. The 2015–16 outbreak in the Americas was caused by ZIKV of the Asian genetic lineage. Chelsea investigated the pathogenic potential of the distinct African-lineage ZIKV and found that it also caused placental damage in pregnant macaques. Follow-up studies showed that a higher dose of African-lineage ZIKV given slightly earlier in pregnancy dramatically increase the risk of fetal demise. Together these studies suggest that the understudied African lineage of ZIKV poses risks to fetal health. Chelsea's work opened up new areas of research for my lab, specifically focusing on the complex immune interactions among related flaviviruses. She is currently a postdoctoral fellow with Sallie Permar at Weill Cornell Medical School in New York City.

Katarina (Kat) Braun, MD, PhD, MSTP 2017–21. Supported by merit-based **UW–Madison Rath Fellowship,** then **NIH/NIAID F30**).
Thesis topic: Mechanisms of influenza and SARS-CoV-2 evolution within and between hosts.

Kat's thesis work used deep sequencing to understand how influenza and SARS-CoV-2 viruses evolve within and between hosts. Her initial work focused on using animal models to investigate the impact of transmission bottlenecks on influenza virus evolution. She established new laboatory and bioinformatic tools to enumerate influenza virus populations and to understand how natural selection operates on these populations during infection and transmission. When SARS-CoV-2 emerged, she worked closely with Gage Moreno, a PhD student in Dave O'Connor's laboratory, to establish methods for high-throughput sequencing and analysis of SARS-CoV-2 genomes. Kat and Gage almost single-handedly started SARS-CoV-2 genomic surveillance in Wisconsin, and their collaborative work led to many important insights. Kat's major contribution here was to be among the first in the world to show that SARS-CoV-2 evolution is constrained by frequent transmission bottlenecks during typical acute infections, which she showed in analysis of viral evolution in both humans and animal models. Kat and Gage's dedication and quick thinking established an extremely fruitful new research direction for the lab. Gage is now a postdoc with Pardis Sabeti at the Broad Institute, Harvard. Kat is working on a clinical fellowship in maternal-fetal medicine at Yale.

Joseph Lalli, MSTP 2019-21 (pursuing MD/PhD). Joe did an outstanding rotation in my laboratory in summer 2017 and began as a PhD student in April 2019.
Thesis topic: Mechanisms of protective immunity to influenza viruses in humans and animal models.

Joe began thesis work in my laboratory studying the evolution of influenza viruses during transmission in humans and the mechanisms of protective immunity against influenza in primate models. He left the lab in June 2021.

Kelsey Florek, MPH, PhD, MDTP 2013-17. Supported by fellowships from **SciMed-Graduate Research Scholars** (**GRS,** a fellowship for underrepresented minority students at UW–Madison) and the Molecular Biology Training Grant (**MBTG**) T32.
Thesis topic: Increasing the breadth of influenza immunity through informed vaccine design

Kelsey's thesis work bridged laboratory and clinical investigations of responses to influenza vaccination. She evaluated novel influenza vaccine platforms in our translational macaque model, showing that viral vector vaccines could elicit cross-protective antibodies against influenza that may work through antibody-dependent cellular cytotoxicity (ADCC). She also investigated responses to influenza vaccination in humans in collaboration with investigators at CDC and the Marshfield Clinic. She is currently a bioinformatics team lead at the Wisconsin State Laboratory of Hygiene using next-generation sequencing to characterize infectious disease outbreaks and antibiotic resistance.

Louise Moncla, PhD, MDTP 2012-17 (supported by **MBTG** fellowship and **UW–Madison Distinguished Graduate Fellowship**).
Thesis topic: The role of transmission bottlenecks in influenza host switching

Louise studied viral adaptation to new species. Her main contribution was showing how selective bottlenecks shape the pathways by which avian influenza viruses adapt to mammalian transmission. Her work showed that transmission bottlenecks were "loose" during the early adaptation process, and become tighter and more highly selective as avian viruses adapt to more efficient mammalian transmission. This work formed the basis for a successful R01 proposal to investigate the mechanisms of influenza transmission bottlenecks. Louise completed a postdoctoral fellowship with Trevor Bedford at the Fred Hutchinson Cancer Research Center and was recently appointed tenure-track assistant professor at the University of Pennsylvania in Philadelphia.

Jorge Dinis, PhD, MDTP 2011-15 (supported by **NSF** and **Ford Foundation fellowships**, and by an **NIH diversity supplement**).
Thesis topic: Within-host evolution of emerging and re-emerging influenza A viruses

Jorge's work showed that H5N1 avian influenza viruses undergo a selective bottleneck during airborne transmission in mammals, uncovering a previously unappreciated way in which natural selection might impact the emergence of new pandemic viruses. He is currently a research project manager at the University of California, Berkeley and a lecturer at San Jose State University.

Sinthujan Jegaskanda, PhD 2012. University of Melbourne, Australia.
Thesis topic: ADCC in influenza immunity.

Sinth was a PhD candidate in the laboratory of my colleague Stephen Kent. I hosted him in my group for 10 weeks in March-May 2012 as part of an informal scientific exchange. Working in my lab he found evidence that antibodies capable of mediating ADCC may play a role in broadly cross-reactive immunity to influenza. He did a postdoc with Dr. Kanta Subbarao at NIH from 2013-16 and is currently working in patent law in Australia.

Ben Wolter, MS 2010. (supported by **SciMed-GRS** and **MBTG fellowships**)
Thesis topic: Influenza A virus pathogenesis and immunity in nonhuman primates.

Ben came to my lab as a PhD student and helped establish my program in studying influenza pathogenesis and immunity in nonhuman primate models. He decided to leave science for personal reasons in his second year of graduate school.

II.B.5. Undergraduate researchers

Sarojshree Namasivayam Janaki, 2023–. Sarojshree joined the lab in fall 2023 as a sophomore interest in gaining research experience as an hourly before embarking on a Bio 152 independent project. She is currently working with Dr. Heather Machkovech on a project using barcoded influenza viruses to understand the mechanisms that constrain viral genetic diversity within and between hosts.

Aiden Cox, 2023–. Aiden joined the lab in spring 2023 as a freshman interested in gaining research experience. He has been working as a student hourly supporting various research projects.

Helena Gebremichael, 2022–23. Helena joined the lab in late 2022 as a senior population health sciences major interested in gaining some experience in a research lab. She graduated in 2023 and will soon start a position as a research technician in the lab of Matt Reynolds at UW–Madison. Helena is interested in applying for medical schools in the next 1-2 years.

Justina Tidaback, 2021–23. Justina joined the lab in 2021.She assisted Kasen Riemersma with projects on SARS-CoV-2 sequencing and worked as part of our large SARS-CoV-2 sequencing team. She is currently working as a laboratory technician at Northwestern University in Chicago.

Livia Romanov, 2021–. Livia joined the lab in 2021 as a sophomore interested in developing research experience. She is currently peforming a project on Zika virus evolution during prolonged infection of pregnant hosts, which started under the supervision of Chelsea Crooks and is continuing with Hunter Ries.

Siyang Peng, 2021–23. Siyang joined the lab in 2021 and worked with Luis Haddock to characterize influenza virus evolution within and between hosts. She will begin work on her PhD in fall 2023 at New York University.

Molly Monge, 2020. Molly, an undergraduate at Rensselaer Polytechnic Institute, joined my lab for a virtual fellowship during the pandemic summer of 2020. She was matched with us via a fellowship program for promising undergraduates from underrepresented groups organized by the American Physician Scientists Association. Molly was mentored by Kasen Riemersma and performed a project to evaluate methods to improve error correction for viral deep sequencing data. She presented this work at an ASPA South Regional Conference in 2020.

Hunter Ries, 2020-21. Hunter joined my lab as a senior in the summer of 2020. His project, almost entirely virtual due to the pandemic, used bioinformatic analysis of ZIKV genome sequences to understand patterns of viral adaptation to mammalian and mosquito hosts. He was mentored by Kasen Riemersma. He recently joined my lab as a new PhD student.

Emma Boehm, 2019-21. Emma joined the laboratory as a junior interested in gaining experience studying the biology of infectious diseases. Her project involved methods for improving the fidelity of deep sequencing approaches to define within-host population diversity of Zika and influenza viruses. She was mentored by Kat Braun. She is currently a laboratory technician at the University of Minnesota.

Nicole Minerva, 2019-21. Nicole joined the laboratory as a junior enrolled in the Entering Research course, which is designed to give motivated students a structured opportunity to learn how research is done in university labs. Her project was to develop techniques for high-fidelity sequencing of influenza viruses using Oxford Nanopore long-read technology. She was mentored by Joe Lalli. In fall 2021 she became a post-baccalaureate fellow in NIH's IRTA program.

Elizabeth Brown, 2018-21. Elizabeth was a member of the Biohouse Learning Community, a program sponsored by University Housing and several UW–Madison colleges that offers enhanced classes and training in biological sciences for motivated undergraduates. She earned a competitive research fellowship to join my lab in summer 2018. She was mentored by Chelsea Crooks oon a project to study Zika virus evolution within hosts with prolonged infections. She is currently applying to medical schools.

Macy Pell, 2015-18. Graduated 2018. Macy was mentored by Louise Moncla. She completed a senior honors thesis investigating influenza virus within-host population structure that will be part of a future manuscript submission from my laboratory. She is currently a PhD student at Michigan State University.

Luiza Campos, 2016. Performed an independent project for the Biology 152 course on optimizing a novel QRT-PCR assay for Zika virus. Luiza left the lab after completing her semester-long project. She was mentored by Andrea Weiler.

Mauricio Salvo, 2015. Graduated 2015. Completed a Master's degree with Dr. Jorge Osorio at UW–Madison in 2017 and subsequently worked in Dr. Osorio's laboratory. He is currently employed at Roche.

Omolayo Fatola, 2013. Omolayo, a sophomore at the University of Maryland–Baltimore County, was a research fellow in my laboratory during summer 2013, supported by a competitive scholarship from the University of Wisconsin Institute for Biology Education (the Integrated Biological Sciences Summer Research Program, or IBS-SRP). She was mentored by Jorge Dinis. She is currently in medical school.

Olivia Charlier, 2012-14. Graduated from UW–Madison in 2014. Attended UW–Madison medical school.

Pascale Stiles, 2012-13. Currently pursuing PhD at University of Glasgow.

Kristen Ross, 2011-12. Graduated from UW–Madison PharmD program.

Christopher Wier, 2010-12. Subsequently enrolled in PhD program at Ohio State University.

Ryan Zoellner, 2010-11. Graduated from UW–Madison in 2013.

Jasmyni Dias, 2008-2011. Subsequently enrolled in UW–Madison PharmD program.

Leif Evensen, 2009-2011. Graduated from UW–Madison in 2011.

Michael Romas, 2010-2011. Graduated from UW–Madison in 2012.

II.B.6. Supervised rotations for PhD students

Hunter Ries, CMP, 2021

Wanting Wei, Biophysics, 2021

Andrew Norton, Medical Scientist Training Program (MSTP), 2021

Dawid Maciorowski, MSTP, 2021. Dawid is planning to perform his PhD research at the University of Oxford, but sought out my lab to contribute to SARS-CoV-2 and other virology research until he departs.

Luis Haddock Soto, CMB, 2020

Mitchell Ramuta, CMB, 2019

Chelsea Crooks, MDTP, 2017

Joseph Lalli, MSTP, 2017

Katarina Braun, MSTP, 2015

Kelsey Florek, MDTP (GRS, MBTG), 2013

Louise Moncla, MDTP (MBTG), 2012

Tatum Mortimer, MDTP (MBTG), 2012.

Jorge Dinis, MDTP, 2011

Stephanie Lowry, CMP, 2010

Ben Wolter, CMB (GRS, MBTG), 2008

Christina Dang, CMB, 2008

II.B.7. PhD student thesis committee service

II.B.7.1. Current PhD student committee service

II.B.7.2. Completed PhD student committee service

1. Mitchell Ramuta (PI David O'Connor), CMB, 2020-23. PhD awarded 2023.
2. Sarmi Basnet (PI James Gern), MDTP, 2015-22. PhD awarded 2022.
3. Katie Amato (PI Andrew Mehle), MDTP, 2017-21. PhD awarded 2021.
4. Stephen Peinado (PI Lyric Bartholomay), Comparative Biomedical Sciences (CBMS), 2017-21. PhD awarded 2021.
5. Gage Moreno (PI David O'Connor), Cellular and Molecular Pathology (CMP), 2019-21. PhD awarded 2021.
6. Anna Heffron (PI David O'Connor), MSTP, 2017-21. PhD awarded 2021.
7. Andrew Bennett (PI Tony Goldberg), CBMS, 2014-20. PhD awarded 2020.
8. James Romero (PI David Evans), CMP, 2014-15. James left Dr. Evans's laboratory in 2015.
9. Adam Ericsen (PI David O'Connor), CBMS, 2013-2016. PhD awarded 2016.
10. Pedro Jiménez, DVM (PI Jorge Osorio), CBMS, 2013-2016. PhD awarded 2016.
11. Yat Yee Amos Wong (PI Lauren Trepanier), CBMS, 2012-2016. PhD awarded 2016.
12. Attapon Kamlangdee, DVM (PI Jorge Osorio), CBMS, 2012-2016. PhD awarded 2016.
13. Laura Felley (PI Jenny Gumperz), Medical Scientist Training Program (MSTP), 2012-15. I left Laura's committee when her research topic turned away from my expertise.
14. Brock Bakke, MS (PI Jorge Osorio), CBMS, 2012-2015. PhD awarded 2015.
15. David Gasper, DVM (PI M. Suresh), CBMS, 2012-2015. PhD awarded 2015.
16. Tony Hanson (PI Yoshihiro Kawaoka), CMB, 2010-16. PhD awarded 2016.
17. Eui Ho Kim (PI M. Suresh), CBMS, 2009-14. PhD awarded 2014.

18. Michael Lauck (PI David O'Connor), CMB, 2009-2013. PhD awarded 2013.
19. Emily Chin (PI David O'Connor), CMB, 2009-2011. Emily left the O'Connor lab in 2011 and received her PhD in 2015.
20. Melba Marie Tejera (PI M. Suresh), CMB, 2008-14. PhD awarded 2014.
21. Anna Jatzek (PI M. Suresh), CMB, 2008-12. PhD awarded 2012.
22. Melisa Budde (PI David O'Connor), CMB, 2008-10. PhD awarded 2010.

II.B.8. MS student thesis committee service

1. Mauricio Salvo, CBMS, 2015-17. MS awarded 2017.
2. Adam Ericsen, CBMS, 2012. MS awarded 2012.

III. Service and leadership

III.A. National and international service

III.A.1. National/international

Co-Organizer, **CoVen international collaborative on animal models for COVID-19**, Since January 2020. In January 2020, recognizing the threat to global health posed by what is now called COVID-19, my colleague David O'Connor and I organized a group of international investigators to openly share plans, protocols, and data relevant to developing and utilizing animal models. Our meetings contributed in particular to developing nonhuman primate models for SARS-CoV-2 infection. The group continues to meet biweekly as of December 2020 and has over 150 members in the USA, Brazil, UK, Europe, and Australia.

Member, **World Health Organization Working Group on Animal Models for COVID-19** Since February 2020. In February 2020, WHO began inviting investigators worldwide to share information and set research priorities for developing animal models for COVID-19. This group continues to meet frequently to discuss emerging data and coordinate the global research resposne to the pandemic.

Member, Scientific Committee, **38th Annual Symposium on Nonhuman Primate Models for AIDS**, Portland, OR, 2020. I am a member of the Scientific Committee for this NHP AIDS conference, which was to be hosted by the Oregon National Primate Research Center in 2020. The overall organizers are Afam Okoye, Jacob Estes, and Nancy Haigwood. This meeting has been postponed due to the COVID-19 pandemic.

Participant, **Global Health and Translational Sciences Summit: Translational immunology supporting countermeasure development for emerging vector-borne diseases**, Trudeau Institute, Saranac Lake, NY, 2018. This 2-day invitation-only summit sought to develop best practices for responding to outbreaks of novel potentially pandemic pathogens. Participants were drawn from industry, academia, foundations, and military research from multiple sites in the US and Europe. A condition for invitation was that participants must have had a demonstrated history of productive collaboration.

Co-Organizer, **35th Annual Symposium on Nonhuman Primate Models for AIDS**, Madison, WI, 2017. "NHP AIDS" is the premier scientific conference focusing on AIDS reserach in primate models. I served as overall co-organizer of this conference with my UW–Madison colleague Shelby O'Connor. We secured peer-reviewed funding from an NIH R13 grant to support this conference, which attracted over 250 delegates.

Participant, **Modeling and Predicting Influenza Phenotypes**, NIH Fogarty International Center/University of Cambridge, Cambridge, England, 2015. This 3-day invitation-only workshop was sponsored by the University of Cambridge and the Fogarty Center's Research and Policy for Infectious Disease Dynamics (RAPIDD) program. The goal of this workshop was to bring together investigators on the cutting edge of research into influenza host switching to summarize current understanding and identify key knowledge gaps to prioritize for future research on how new pandemic influenza viruses might emerge. I was invited to discuss influenza transmission bottlenecks, which my work had recently shown could play an important role in the evolution of host switching. I am co-author on a conference proceeding/concept paper in eLife, CV reference 79.

Member, Scientific and Organzing Committees, **26th Annual Symposium on Nonhuman Primate Models for AIDS**, San Juan, PR, 2008. I served as a member of the Organizing and Scientific Committees for this NHP AIDS conference, which was hosted by the Wisconsin National Primate Research Center, but took place in San Juan, PR. The overall organizer was David O'Connor.

Please note that service as a peer reviewer for grant applications and manuscripts is listed in the research section beginning in section **I.F**.

III.B. UW–Madison service

Pathobiological Sciences department bioinformatics faculty search committee (2019–20)

Pathobiological Sciences department immunology faculty search committee (2016–17)

Microbiology Doctoral Training Program Steering Committee (2015–18)

Wisconsin National Primate Research Center Executive Committee (2007–)

WNPRC Pathologist search committee (2010-11)

WNPRC Centralized Protocol Implementation Unit Head search committee Chair (2010)

Biological Safety Officer search committee (2008)

III.C. School of Veterinary Medicine service

Equity and Diversity Committee (2015–22; Chair 2017–21)

Undergraduate Curriculum Committee (2008–; Chair 2009–)