Ruian Ke (Curriculum Vitae)

T-6 Theoretical Biology and Biophysics,
Los Alamos National Laboratory
Los Alamos, NM87545, U.S.A.

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Research Interests

Multiscale modeling of viral and immune interactions; HIV, SARS-CoV-2, influenza and HCV;
Data science; Machine learning; Systems biology

Appointments

2018 - present **Staff Scientist**, T-6: Theoretical Biology and Biophysics, **Los Alamos National Laboratory,** U.S.A.
2015 - 2018 **Assistant Professor** (tenure track), Precision Medicine Faculty cluster and Department of Mathematics, **North Carolina State University**, U.S.A.

Education

2013 – 2015 **Post-doc**, T-6: Theoretical Biology and Biophysics, **Los Alamos National Laboratory**, U.S.A.
2010 - 2013 **Post-doc**, Ecology and Evolutionary Biology, **University of California, Los Angeles,** U.S.A.
2006 - 2010 **Ph.D.** in Mathematics/Systems Biology, **Imperial College London,** London, U.K.
2003 - 2006 **B.Sc.** (1st Class Honors) in Mathematics**, Heriot-Watt University,** Edinburgh, U.K.
- ✧ Watt-Club Medal - the greatest academic distinction

Grants **(Total amount of the grants where my role is P.I.: $ 9.6 millions)**

External

2021 - 2022	NIH, 'Mechanistic Modeling for the UIUC SHIELD SARS-CoV-2 longitudinal study' **(role: P.I.)**	Total: **$223,164**
2021 - 2026	NIAID, 'RID HIV - Reversing Immune Dysfunction for HIV-1 eradication' (role: key personnel; P.I.: Chanda; LANL P.I.: Ribeiro)	Direct to LANL: **$737,350**
2020 - 2025	NIAID, 'Modeling the HIV Latent Reservoir, Latency Reversal and Immunotherapeutics for HIV' (**role: P.I.**)	Total: **$2,961,350**
2020 - 2025	NIAID, 'Reconstructing HIV Epidemics from HIV Phylogenetics' (role: key personnel; P.I.: Leitner)	Total: **$4,676,504**
2020 - 2021	NSF, 'RAPID: Mathematical Models for Understanding Key Epidemiological Parameters and Transmission of SARS-CoV-2' (role: co-P.I.; P.I.: Perelson)	Total: **$200,000**
2020 - 2021	DARPA, BTO, Rapid Response to COVID-19 (**role: P.I.**)	Total: **$265,000**
2018 - 2024	NIH/OD, 'Modeling Viral and T Lymphocyte Dynamics' (role: key personnel; P.I.: Perelson)	Direct: **$1,250,000**
2018 - 2022	DARPA, BTO, 'Multiscale modeling of influenza defective/therapeutic interfering particles' (**role: P.I.**)	Total: **$838,066**
2017 - 2021	DARPA INTERCEPT program, 'VIPER: Viral Interdiction through Population Engineering and Restructuring' (**role: P.I.**)	Total: **$5,172,020**
2016 - 2017	UNC-CH CFAR Developmental Award – NIH (**role: P.I.**)	Total: **$30,000**
2016 - 2017	Simons Collaboration Grant (**role: P.I.**)	Total: **$5,000**

Internal

2020 - 2021	LANL LDRD Reserve (role: co-P.I.; P.I.: Cuellar)	Total: **$150,000**
2020	LANL LDRD Special R&D Call COVID-19 (role: co-P.I.; P.I.: Ribeiro)	Total: **$125,000**
2020	LANL LDRD-CNLS Rapid Response to COVID-19 (**role: P.I.**)	Total: **$125,000**
2016 - 2017	NCSU Summer Interdisciplinary Research Internship (**role: P.I.**)	Total: **$10,000**
2016 - 2017	NCSU Faculty Research & Professional Development (**role: P.I.**)	Total: **$4,000**

AWARDS

2022	Lewis Wolpert prize (best paper award) from Journal of Theoretical Biology.
2015	Young Investigator Travel Award from the 7th HIV Persistence Workshop.
2015	Landahl Travel Award from Society of Mathematical Biology.
2006	Dorothy-Hodgkin Postgraduate Award at Imperial College London, U.K.
2006	Watt-Club Medal for achieving the greatest academic distinction in the Department of Mathematics, Heriot-Watt University, U.K.

INVITED TALKS/WORKSHOPS

2021	Colloquium, Department of Mathematics, Arizona State University, AZ
2021	(Virtual) PRedicting Emergence of Virulent Entities By Novel Technologies (NSF-PREVENT) Symposium
2021	(Virtual) Emory Theory and Modeling of Living Systems Symposium
2021	(Virtual) Indiana CTSI Modelling and Simulation Virtual Symposium
2020	(Virtual) Seminar, University of New Mexico
2020	(Virtual) The CDC modeling group on COVID-19 epidemiological characteristics
2020	(Virtual) the Pandemic Prediction and Forecasting S&T Working Group (commissioned by the White House) seminar.
2020	(Virtual) BEES Webinar, Georgia Southern University, GA
2019	UCLA Biophysics seminar, Los Angeles, CA
2018	SFI Working Group - Integrating Critical Phenomena and Multi-scale Selection in Virus Evolution, Santa Fe Institute, Santa Fe, NM
2018	SAMSI opening workshop - Statistical, Mathematical, and Computational Methods for Precision Medicine (PMED), Raleigh, NC
2018	SFI workshop - Aging and Adaptation in Infectious Diseases, Santa Fe Institute, Santa Fe, NM
2018	NCI Workshop - Linking Computational and Experimental Biology in HIV Research, National Cancer Institute, Fredrick, MD
2018	MBI Workshop – Host-Pathogen Dynamics, Mathematical Biology Institute, Columbus, OH
2017	SIAM Dynamical Systems Meeting 2017, Snowbird, UT
2017	2017 SIAM SEAS meeting, Tallahassee, FL
2016	AMS regional meeting, Raleigh, NC
2016	Seminar, School of Veterinary Medicine, NCSU, Raleigh, NC
2016	The 11th AIMS Conference on Dynamical Systems, Differential Equations and Applications, Orlando, FL
2016	SIAM Life Science Meeting 2016, Boston, MA
2016	ENAR meeting at Austin, TX

2015 Triangle Center for Evolutionary Medicine Symposium, Raleigh, U.S.

2015 Mathematical Biology Seminar, Pennsylvania State University, State College, U.S.

2015 Society of Mathematical Biology Annual Meeting, Atlanta, U.S.

2015 Colloquium, Department of Applied Mathematics and Statistics, University of California, Santa Cruz, U.S.

2015 Colloquium, Department of Mathematics, North Carolina State University, Raleigh, U.S.

2014 q-bio hour, CNLS, Los Alamos National Laboratory, Los Alamos, U.S.

CONTRIBUTED ORAL PRESENTATIONS

2022 The 29th International Dynamics & Evolution of Human Viruses conference, San Diego, CA

2022 CROI 2022 - Conference on Retroviruses and Opportunistic Infections

2021 (Virtual) 28th International Dynamics & Evolution of Human Viruses

2021 (Virtual) CROI 2021 - Conferences on Retroviruses and Opportunistic Infections

2020 (Virtual) COVID-19 Dynamics & Evolution - Part 2

2020 (Virtual) eSMB2020 (Annual Meeting of the Society of Mathematical biology)

2020 (Virtual) CAIMS –PIMS Coronavirus Modelling Conference, Pacific Institute for the Mathematical Sciences

2020 (Virtual) 27th International Dynamics & Evolution - Part 1

2019 4th Workshop on Viral Dynamics, Paris, France

2019 SIAM Dynamical Systems Meeting 2019, Snowbird, UT

2017 Viral Dynamics, the past, the present, the future, Santa Fe, NM

2017 Keystone Symposia on Modeling Viral Infections and Immunity, Estate Park, CO

2016 2nd Annual Conference of the International Society for Evolution Medicine & Public Health, Durham, NC

2016 Biology and Medicine Through Mathematics (BAMM!) Conference, Richmond, VA

2016 The 23rd HIV Dynamics & Evolution meeting held at Woods Hole, MA

2015 Phylogenetics and Evolutionary Biology seminar, North Carolina State University, Raleigh, U.S.

2015 Ecology and Evolution of Infectious Diseases (EEID) conference, Atlanta, U.S.

2014 Post-doc Research Day, Los Alamos National Laboratory, Los Alamos, U.S.

2014 The 21st International HIV Dynamics and Evolution conference, Tucson, U.S.

2014 Theoretical Biology and Biophysics Group Talk, Los Alamos National Laboratory, Los Alamos, U.S.

2013 Annual Meeting of the Society for the Study of Evolution (Evolution2013), Snowbird, U.S.

2012 The 11th International Conference on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases, New Orleans, U.S.

2012 MBI Young Researchers in Mathematical Biology, Ohio, U.S.

STUDENT/POSTDOC MENTORING

2018 - **Los Alamos National Laboratory, U.S.A.**

- Tin Phan (2021 -), Postdoc, PhD in Mathematics, Arizona State University.
- Steven Sanche (2019 - 2021), CNLS Postdoc, PhD in Mathematics, Montreal University.
- Garrett Nieddu (2018 - 2020), Postdoc, PhD in Mathematics, Montclair State University.
  Current position: R&D scientist at Merck, Co.

- Michael Kupperman (2019 -), Graduate research assistant, graduate student from University of Washington.
- Sarah Pungitore (2020), Summer intern, graduate student from University of Arizona.
- Celine Snedden (2019), Summer intern, graduate student from University of California, Los Angeles.

2015 – 2018 **North Carolina State University, U.S.A.**

Long-term lab members

- Alex Farrell (2017-2018), Postdoc researcher, PhD in Mathematics, Arizona State University, *Current position:* Post-doc at University of Arizona.
- Yufan Huang (2017-2019), (thesis co-chair with Huaiyu Dai) Electrical and Computer Engineering graduate student.
  Current position: Google Inc.
- G. Michael Lavigne (2016-2020), Applied Mathematics graduate student, Provost Fellow, NSF-RTG fellow.
  Current position: Teaching assistant professor, Georgia Institute of Technology
- Marco Hamins-Puertolas (2016-2020), Biomathematics graduate student, NSF-RTG fellow, 2-year research assistant.
  Current position: Post-doc at UC Berkeley
- Savannah Bates (2017-2018), Biomathematics graduate student, NSF fellowship, Year-long research assistant.
- Ryan Brandt (2016-2017), Undergraduate student in Physics, year-long research assistant.
  Current position: Graduate Student at Stanford University
- Hayley Russell (2016-2018), Undergraduate student in Mathematics, 2-year research assistant.
  Current position: Facebook.

Short-term rotation students

- Ethan King (2016), Applied Mathematics graduate student, rotation.
- Jiabin Yu (2016), Applied Mathematics graduate student, rotation.
- Ricardo Wehrhahn (2016), Applied Mathematics graduate student, rotation.

2013 – 2015 **Los Alamos National Laboratory, U.S.A.**

- David E. Li (2014), postbachelor student from Rice University (currently a PhD student at UT Austin)

2010 – 2013 **University of California, Los Angeles, U.S.A.**

- Aurélien Puiseux (2011), visiting student from École Normale Supérieure, Paris.
- Prianna Ahsan (2013), undergraduate student at UCLA.

TEACHING

2015 - 2018 **North Carolina State University, U.S.A.**

- MA341H – Applied Differential Equations (Spring 2016; Fall 2016)
- BMA772 – Stochastic Processes in Biology (Spring 2017, Spring 2018)
- MA591 – Parameter Estimation and Quantitative Immunology (Spring 2017)

2016 **q-bio summer school (UNM campus)**

2010 – 2013 **University of California, Los Angeles, U.S.A.**

- Mathematical and computational modeling in ecology (EEB119/219, leading a series of lectures)
- Quantitative bootcamp for EEB graduate students (Teaching assistant)
- Molecular mechanisms of human diseases (M252A/B, leading discussion classes)

2006 – 2009 **Imperial College London, U.K.**

Teaching assistant for Calculus for Engineers; Complex analysis; Dynamical systems; Matlab and

Maple; Multivariable calculus; Numerical analysis; Real analysis.

SERVICES

Editorial board member:

- Frontiers in Immunology
- Mathematical Biosciences and Engineering
- Viruses

Editor of special issues:

- *Multiscale dynamics of infectious diseases, immune responses and therapeutics* at Mathematical Biosciences and Engineering
- *Mathematical Modeling of Viral Infection* at Viruses

Grant proposal review panel:

- NSF - Math Biology
- NIAID – HIV (ad-hoc)

Guest editor for:

- PLoS Pathogens

Mini-symposium organizer

- 2019 SIAM Dynamical Systems Meeting, Snowbird, UT
- 2017 SIAM Dynamical Systems Meeting, Snowbird, UT
- 2016 SIAM Life Science Meeting, Boston, MA
- 2015 Society of Mathematical Biology Annual Meeting, Atlanta, U.S.

Workshop/Program co-organizer

- SAMSI Program on Statistical, Mathematical, and Computational Methods for Precision Medicine (PMED)

Manuscript reviewer (selected)

- American Journal of Epidemiology; Antimicrobial Agents and Chemotherapy; BMC Biology; Cell Host & Microbe; Cell Reports Medicine; Communications Medicine; EBioMedicine; Emerging Infectious Diseases; Epidemics; Frontiers in Immunology; Frontiers in Pharmacology; Frontiers in Public Health; International Journal of Infectious Diseases; Journal of Biological Engineering; Journal of Infectious Diseases; Journal of Mathematical Biology; Journal of the Royal Society Interface; Nature Communications; PLoS Computational Biology; PLoS Neglected Tropical Diseases; PLoS Pathogens; PNAS; Proceedings of the Royal Society of London, B; Retrovirology; Science Advances; Science Translational Medicine; The Lancet Regional Health – Americas

Committee member at LANL

- Physics/Theory Colloquium

External PhD thesis examiner

- David Dick (advisor, Lindi Wahl), Western University, ON, CAN
- Tanja Laske (advisor, Udo Reichl), University of Magdeburg, Germany

SOCIETY MEMBERSHIP

Society of Mathematical Biology

PUBLICATIONS

(Google Scholar: https://scholar.google.com/citations?user=38sWL14AAAAJ&hl=en)

Preprints

Kupperman, M.D., Leitner, T., **Ke, R.,** A deep learning approach to real-time HIV outbreak detection using genetic data. [Link]

Choudhary, M. C., Chew, K. W., Deo, R., Flynn, J. P., Regan, J., Crain, C. R., ... **Ke, R.,** … Li, J., & ACTIV-2/A5401 Study Team. ACTIV-2/A5401 Study Team. Emergence of SARS-CoV-2 Resistance with Monoclonal Antibody Therapy. [Link]

Ke, R., Sanche, R., Romero-Severson, E., Hengartner, N. Fast spread of COVID-19 in Europe and the US suggests the necessity of early, strong and comprehensive interventions. [Link]

Ke, R., Zitzmann, C., Ribeiro, R.M., Perelson, A.S. Kinetics of SARS-CoV-2 infection in the human upper and lower respiratory tracts and their relationship with infectiousness. [Link]

Sanche, S., Lin, Y.T., Xu, C., Romero-Severson, E., Hengartner, N.W., **Ke, R.** The novel coronavirus, 2019-nCoV, is highly contagious and more infectious than initially estimated. [Link]

Ke, R., Deng, K., The dynamics of the HIV-1 latent reservoir – considering the heterogeneous subpopulations. [Link]

Farrell, A., Brooke, C.B., Koelle, K., **Ke, R.** Coinfection of semi-infectious particles can contribute substantially to influenza infection dynamics. [Link]

Articles

2022

Chaturvedi, S., Pablo, M., Wolf, M., Rosas-Rivera, D., Calia, G., Kumar, A. J., Vardi, N., Du, K., Glazier, J., **Ke, R.**, Chan, M.F., Perelson, A.S., Weinberger, L.S. Disrupting autorepression circuitry generates "open-loop lethality" to yield escape-resistant antiviral agents. **Cell** 185(12), 2086-2102

Ke, R., Martinez, P. P., Smith, R. L., Gibson, L. L., Mirza, A., Conte, M., ... & Brooke, C. B. Daily sampling of early SARS-CoV-2 infection reveals substantial heterogeneity in infectiousness. **Nature Microbiology** 7 (5), 640-652

Sanche, S., Cassidy, T., Chu, P., Perelson, A.S., Ribeiro, R., **Ke, R.,** A simple model of COVID-19 explains disease severity and the effect of treatments. **Scientific Reports.** (accepted) [Link]

Ke, R., Martinez, P., Smith, R. L., Gibson, L., Achenbach, C., McFall, S., ... & Brooke, C. B. Longitudinal analysis of SARS-CoV-2 vaccine breakthrough infections reveal limited infectious virus shedding and restricted tissue distribution. **Open Forum Infectious Diseases**, 9(7), ofac192

Allender, M. C., Adkesson, M. J., Langan, J. N., Delk, K. W., Meehan, T., Aitken-Palmer, C., ... & **Ke, R.,** … & Wang, L. (2022). Multi-species outbreak of SARS-CoV-2 Delta variant in a zoological institution, with the detection in two new families of carnivores. **Transboundary and Emerging Diseases.** doi: 10.1111/tbed.14662

Cuéllar, L., Torres, I., Romero-Severson, E., Mahesh, R., Ortega, N., Pungitore, S., Hengartner, N.W., **Ke, R.** Excess deaths reveal the true spatial, temporal, and demographic impact of COVID-19 on mortality in Ecuador. **International Journal of Epidemiology** 51(1), 54-62

Cuéllar, L., Torres, I., Romero-Severson, E., Mahesh, R., Ortega, N., Pungitore, S., **Ke, R.,** Hengartner,

N.W. Assessing the Impact of Human Mobility to Predict Regional Excess Death in Ecuador. **Scientific Reports** 12(1), 1-12

2021 van Dorp, C.H., Goldberg, E.E., Hengartner, N., **Ke, R.,** Romero-Severson, E.O. Estimating the strength of selection for new SARS-CoV-2 variants. **Nature Communications** 12(1), 1-13

Ke, R., Zitzmann, C., Ribeiro, R.M., Perelson, A.S. In vivo kinetics of SARS-CoV-2 infection and its relationship with a person's infectiousness. **Proceedings of the National Academy of Sciences** 118(49)

Cuéllar, L., Torres, I., Romero-Severson, E., Mahesh, R., Ortega, N., Pungitore, S., **Ke, R.,** Hengartner, N.W. Excess deaths reveal unequal impact of COVID-19 in Ecuador. **BMJ global health** 6 (9), e006446

Perelson, A.S., **Ke, R.** Mechanistic modeling of SARS-CoV-2 and ther infectious diseases and the effects of therapeutics. **Clinical Pharmacology & Therapeutics** 109 (4), 829-840

Kim, K.S., Ejima, K., Iwanami, S., Fujita, Y., Ohashi, H., Koizumi, Y., … **Ke, R.**, … & Iwami, S.A quantitative model used to compare within-host SARS-CoV-2, MERS-CoV, and SARS-CoV dynamics provides insights into the pathogenesis and treatment of SARS-CoV-2. **PLoS Biology** 19 (3), e3001128.

Smith, R.L., Gibson, L.L., Martinez, P.P., **Ke, R.**, Mirza, A., … & Brooke, C.B, Longitudinal assessment of diagnostic test performance over the course of acute SARS-CoV-2 infection. **Journal of Infectious Diseases** 224(6), 976-982.

Lavigne, G.M., Russell, H., Sherry, B., **Ke, R.** Autocrine and paracrine interferon signaling as 'ring vaccination' and 'contact tracing' strategies to suppress virus infection in a host. **Proceedings of the Royal Society B.** 288 (1945), 20203002

Schreiber, S., **Ke, R.**, Loverdo, C., Park, M., Ahsan P., Lloyd-Smith, J. O., Cross scale dynamics and disease emergence. **Virus Evolution** 7 (1), veaa105

Ke, R., Romero-Severson, E., Sanche, S., Hengartner, N. Estimating the reproductive number R0 of SARS-CoV-2 in the United States and eight European countries and implications for vaccination. **Journal of Theoretical Biology** 517, 110621

Mavigner, M., Liao, L.E., Brooks, A.D., **Ke, R.**, Mattingly, C., Schoof, N., McBrien, J., Carnathan, D., Liang, S., Vanderford, T.H., Paiardini, M. et al. CD8 lymphocyte depletion enhances the latency reversal activity of the SMAC mimetic AZD5582 in ART-suppressed SIV-infected rhesus macaques. **Journal of Virology.** 95 (8), e01429-20.

2020 Sun, J., Vera, J.C., Drnevich, J., Lin, YT, **Ke, R.**, Brooke, C.B. Single cell heterogeneity in influenza A virus gene expression shapes the innate antiviral response to infection. **PLoS Pathogens.** 16(7):e1008671.

Romero-Severson, E.O., Hengartner, N., Meadors, G., **Ke, R**. Change in global transmission rates of COVID-19 through May 6 2020. **PLoS One** 15 (8), e0236776.

Gonçalves, A., Bertrand, J., **Ke, R.**, Comets, E., de Lamballerie, X., Malvy, D., Pizzorno, A., Terrier, O., Calatrava, M.R., Mentré, F., Smith, P., Perelson, A.S., and Guedj, J. Timing of antiviral treatment initiation is critical to reduce SARS‐CoV‐2 viral load. **CPT: pharmacometrics & systems pharmacology** 9(9), 509-514.

Sanche, S., Lin, Y. T., Xu, C., Romero-Severson, E., Hengartner, N., **Ke, R.** High Contagiousness and Rapid Spread of Severe Acute Respiratory Syndrome Coronavirus 2. **Emerging Infectious Diseases** 26(7), 1470-1477.

2019 Huang, Y., Dai, H., **Ke, R.** Principles of effective and robust innate immune response to viral infections: a multiplex network analysis. **Frontiers in Immunology** 10, 1736.

Koelle, K., Farrell, A., Brooke, C.B., **Ke, R.** Within-host infectious disease models accommodating cellular coinfection, with an application to influenza. **Virus Evolution** 5 (2), vez018.

2018 Gallagher, M.E., Brooke, C.B., **Ke, R.**, Koelle, K. Causes and consequences of spatial within-host viral spread. **Viruses** 10(11),627.

Ke, R., Conway, J.M., Margolis, D.M., Perelson, A.S. Determinants of the efficacy of HIV latency reversing agents and implications for drug and treatment design. **JCI Insight** 3(20):e123052.

Ke, R., Li, H., Wang, S., Ding, W., Ribeiro, R.M., Giorgi, E.E., Bhattacharya, T., Barnard, R.J.O, Shaw, G.M., Perelson, A.S. Superinfection and cure of infected cells as mechanisms for hepatitis C virus expansion and persistence. **Proceedings of the National Academy of Sciences** 115(30):E7139-E7148.

Chang, C.C., Naranbhai, V., Perelson, A.S., Hengartner, N., Dantanarayana1, A., **Ke, R.**, Tennakoon, S., Solomon, A., Roche, M., Hoh, R., Hartogensis, W., Bacchetti, P., Hecht, F., Sikaris, K., Elliott, J.H., Deeks, S.G., Cameron, P., Lewin, S.R., Variation in cell associated unspliced HIV RNA on antiretroviral therapy is associated with the circadian regulator BMAL-1. **AIDS** 32(15):2119.

2017 Shan, L.*, Deng, K.*, Xing, S, Rabi, S.A., Kim, M., Hosmane, M.N., Durand, C.M., Yang, H.C., **Ke, R.**, Siliciano, J.D. and Siliciano, R.F. Unique features of effector to memory transition render CD4+ T cells permissive for latent HIV infection. **Immunity** 47(4), 766-775.

Ke, R., Cong, M., Li, D., Garcia-Lerma, G., Perelson, A. S., On the death rate of abortively infected cells: estimation from simian/human immunodeficiency virus infection. **Journal of Virology** 91(18).

2016 Benzine, T., Brandt, R., Lovell, W. C., Yamane, D., Neddermann, P., de Francesco, R., Lemon, S. M., Perelson, A. S.; **Ke, R.**, McGivern, D. R., NS5A inhibitors unmask differences in functional replicase complex half-life between different hepatitis C virus strains. **PLoS Pathogens** 13(6): e1006343.

Lau, G.K., Benhamou, Y., Chen, G., Li, J., Shao, Q., Ji, D., Li, F., Li, B., Liu, J., Hou, J., Sun, J., Wang, C., Chen, J., Wu, V., Wong, A., Wong, C.L.P., Tsang, S.T.Y., Wang, Y., Bassit, L., Tao, S., Jiang, Y., Hsiao, H-M., **Ke, R.**, Perelson, A.S., Schinazi, R.F., Efficacy and safety of 3-week response-guided triple direct-acting antiviral therapy for chronic hepatitis C infection: a phase 2, open-label, proof-of-concept study. **The Lancet Gastroenterology & Hepatology** 1.2: 97-104.

Sherman, K.E., **Ke, R.**, Rouster, S.D., Abdel-Hameed, E.A., Park, C., Palascak, J., Perelson, A.S., Viral dynamic modeling of hepatitis C response to telaprevir-based regimen in hemophiliacs. **Haemophilia** 22.4: 543-548.

2015 **Ke, R.**, Elliott, J., Lewin, S. R., Perelson, A.S., Modeling the effects of vorinostat in vivo reveals both transient and delayed HIV transcriptional activation and minimal killing of latently infected cells. **PLoS Pathogens.** 11(10): e1005237.

Ke, R., Loverdo, C., Qi, H., Sun, R., Lloyd-Smith, J. O., Rational design and adaptive management of HCV antiviral treatment. **PLoS Computational Biology**. 11(6): e1004040.

2014 **Ke, R.**, Loverdo, C., Qi, H., Olson, A., Wu, N., Sun, R., Lloyd-Smith, J. O., Modelling clinical data shows active tissue concentration of daclatasvir is ten-fold lower than its plasma concentration. **Journal of Antimicrobial Chemotherapy.** 69 (3): 724-727.

Qi, H., Olson, A., Wu, N., **Ke, R.**, et al. A quantitative high-resolution genetic profile rapidly identifies sequence determinants of hepatitis C viral fitness and drug sensitivity. **PLoS Pathogens.** 10 (4),

e1004064.

2013 **Ke, R.**, Aaskov, J., Holmes, E.C., Lloyd-Smith, J.O. Phylodynamic analysis of the emergence and epidemiological impact of transmissible defective dengue viruses. **PLoS Pathogens.** 9(2): e1003193.

Ke, R., Lloyd-Smith J.O. Coadaptive stability of interfering particles with HIV-1 when there is an evolutionary conflict. [Letter] **Journal of Virology.** 2013; 87 (17), 9959-9959.

Ke, R., Ingram, P., Haynes, K. An integrative model of ion regulation in yeast. **PLoS Computational Biology**. 9(1): e1002879.

Ke, R., Haynes, K., Stark, J. Modelling the activation of the alkaline pH response transcription factor PacC in *Aspergillus nidulans* reveals the involvement of a negative feedback loop. **Journal of Theoretical Biology.** 326:11-20.

2012 **Ke, R.**, Lloyd-Smith J.O. Evolutionary analysis of human immunodeficiency virus type 1 therapies based on conditionally replicating vectors. **PLoS Computational Biology.** 8(10): e1002744.

Conference proceedings

1. Yu, Y., **Ke, R.,** Tran, H. (2021) Ensemble UNet++ for Locating the Exponential Growth Virus Samples **Proceedings of SAI Intelligent Systems Conference**, 465-480

2. Huang, Y., Dai, M., Zhang, Z., **Ke, R.** (2018) Network analysis of virus-innate immune interaction within a host. **Information Sciences and Systems (CISS), 52nd Annual Conference on,** 1-6.