2003 - 7 NIH: ad hoc member, ZRG1 IDM-G [illegible] (2003-5), ZRG1 IRA [illegible]
2004 - Editorial Board, [illegible]
2005 - NIAID: Steering Com[illegible]
2010 - Editor-in-Chief, [illegible] Member of IOM Forum on [illegible]
DHS and Kansas State Univ. Ctr. of Excellence for Emerging & Zoonotic Animal Diseases (CEEZAD)
2011 - Steering Committee, NIAID Workshop on Arboviruses
2014 - Member NRC [illegible] Committee to advise the US Global Change Research Program (USGCRP)
2015 - Member of Supervisory Board, One Health Platform; Editorial Board *One Health*
2016 - Member, WHO Expert group on Public Health Emergency Disease Prioritization
2016 - Member, Core Steering Committee & Co-Chair, Science & Technol WG, Global Virome Project
2017 External Review Committee, CSIRO Health & Biosecurity Business Unit
2017 - Chair, Forum on Mic[illegible]

Honors

1999 Meritorious service award, CDC
2000 CSIRO silver medal for collaborative research
2002 Honored by the naming of a new species of centipede, *Cryptops daszaki* (J Nat Hist 36: 76[illegible]
2003 6th Annual Lecturer, Medicine & Humanities, Texas A&M
2007 Finalist, [illegible] Director's Pioneer Award
2008 President's Lecturer, University of Montana
2012 Elected member of the Cosmos Club, Washington DC
2013 Honored by the naming of a new parasite species, [illegible]
2013 Hsu-Li Distinguished Lectureship in International Epidemiology, Univ. Iowa
2015 Robert Leader Endowed Lecture in Food Safety, Michigan State Univ.
2018 - Member, National Academy of Medicine (NAM), USA

C. Contribution to Science

1. Research on the bat origins of emerging viruses. Numerous high impact emerging viruses appear to have bat reservoirs (e.g. SARS-CoV, EBOV, NiV, HeV, MERS-CoV, SADS-CoV). As PI [illegible] on bat-origin viruses, my work has helped demonstrate the bat origin of SARS [illegible] SADS-CoV, analyze the drivers of bat vir[illegible]gence and risk factors fo[illegible]er. Collaborating with virologists in China, we have isola[illegible] and characterized SARS[illegible]-CoVs from bats that use the sam[illegible] host cell receptor (ACE-2) as SARS-CoV. This [illegible] provid[illegible] [illegible]tical reagents and resources that have helped advance und[illegible] virus-host binding and may contribute to vaccine development. My other work identified factors leading [illegible] the emergence of NiV from *Pteropus* bats in Malaysia and Bangladesh; a likely bat origin for MERS-CoV, and proof that bats harbor a significantly higher proportion of zoonoses than all other mammalian groups.

a. Ge X-Y, Li J-L, Yang X-L, Chmura AA, Zhu G, Epstein JH, [illegible] Y-J, Luo C-M, Tan B, Wang N, Zhu Y, Crameri G, Zhang S-Y, Wang L-F, **Daszak P***, Shi Z-L (20[illegible]) Isolation and characterization of a bat SARS-like Coronavirus that [illegible] ACE2 receptor. **Nature** 503: 535-538.

b. Memish ZA, Mishra N, Olival KJ, Fagbo SF, Kapoor V, Epstein JH, Al Hakeem R, Durosinl[illegible] Al Asmari M, Islam A, Kapoor A, Briese T, **Daszak P**, Al Rabeeah A, Lipkin WI. (2013). Middle East respiratory syndrome coronavirus in bats, Saudi Arabia. **EID** 19(11) [illegible]

c. Zhou P, Fan H, Lan T, Yang X-L, Shi W-F, Zha[illegible] Li B, Li J-M, Guo H, Pei G-Q, [illegible]ang L-B, Li S-Y, Mi Z-Q, He T-T, [illegible] Zhang X-L-L, Wang Y-Y[illegible]

Ma J-Y* (2018). Fatal Swine Acute [illegible] Syndrome caused by an HKU2-related Coronavirus of Ba[illegible] O[illegible]

d. Nikolay B, Salje H, Ho[illegible] Khan AKMD, Sazzad HMS, Rahman M[illegible] JRC, Kilpatrick AM, Nichol ST, Klena JD, Sultana S[illegible] Luby SP, Cauchemez S & Gurley ES (2019). Transmission of Nipah Virus 14 Years of Investigations in Bangladesh. **New England Journal of Medicine** 380:1804-1814

2. **Analyzing the process of disease [illegible]** global health. However, their emergence is sporadic, and involves a complex process that is hard to predict. In the early 2000s I started to use analytical approaches to identify predictable patterns in the process of disease [illegible] EID events, identifying their point origins, and correcting for reporting biases, I published the first ever predictive 'hotspots' maps of where future disease emergence is most likely. I have continued this line of research, publishing spatial analyses of the drivers of disease spread, and outlining strategies to predict pandemic emergence.

   a. Kilpatrick AM, Chmura AA, Gibbons DW, Fleischer RC, Marra PP & [illegible] (2006). Predicting the global spread of H5N1 avian influenza. **PNAS** 103: 19368-19373.

   b. Morse SS, Mazet JAK, Woolhouse M, Parrish CR, Carr[illegible] Karesh WB, [illegible] Lipkin WI, **Daszak P*** (201[illegible]) Prediction and prevention of the next pandemic zoonosis. **Lancet** 380:1956-1965.

   c. **Daszak P***, Zambrana-Torrelio C, Bogich T[illegible] Epstein JH, Murray KA, Hamilton H (2013). Interdisciplinary approaches to understanding disease [illegible] of [illegible] **PNAS** 110: 3681-3688

   d. Allen T, Murray KA, Zambrana-Torrelio C, Morse SS, Rondinini C, Di Marco M, Breit N, Olival KJ, **Da[illegible]** (2017). Glob[illegible] and correlates of emergin[illegible] **Nature Comm** 8: 1124

3. **Studies of wildlife [illegible] ecology to unde[illegible] emerge[illegible]** zoonotic, w[illegible] 2000 and in a more recent paper in *Nature* on the links among biodiversity and health. During the last tw[illegible] decades, I have led collaborative research programs on how the ecology of specific wildlife-origin zoonoses can help explain patterns of risk to people. Thi[illegible] my role as PI on 4 R01s, as [illegible] lead for USAID-EPT-PREDICT, and Chief of Party for USAID-IDEEAL. This work includes estimations of the diversity of yet-to-be discovered viruses which forms the rationale for the Global Virome Projec[illegible]

   a. **Daszak P***, Cunningham AA, Hyatt [illegible] (2000). Emerging infectious diseases of wildlife - threats to biodiversity and hu[illegible]ealth. **Science** 287: 44[illegible]

   b. Keesing F, Belden LK, **Daszak P**, Dobson A, Harvell CD, Holt RD, Hudson P, Jolles A, Jones KE, Mitchell CE, Myers SS, Bogich T & Ostfeld RS. (2010). Impacts of biodiversity on the emergence and transmission of infectious diseases. **Nature** 468:6[illegible]652.

   c. Anthony SJ, Epstein JH, Murray KA, Navarrete-Macias I, Zambrana-Torrelio CM, Solovyov A, Ojeda-Flores R, Arrig[illegible]NC, Islam A, Ali Khan S, Hosseini P, Bogich TL, Olival KJ, Sanche[illegible]D, Karesh W, Goldstein T, Luby SP, [illegible] u[illegible]own viral diversity in mammals [illegible]

   d. Mandl JN, Ahmed R, Barreiro LB, **Daszak P**, Epstein JH, Virgin HW, Feinberg MB. (2015). Reservoir host immune responses to emerging zoonotic viruses. **Cell** 160: 20-35

4. **Na[illegible]se research.** I have tr[illegible] to use my [illegible] pro[illegible] multidisciplinary collaborat[illegible]on an[illegible]

to primary data and [illegible] linkages, including 5 Policy Forums and editorials in Sc[illegible]. I have served as a member of the NAS[illegible] Forum on Microbial Thre[illegible] over 10 years, and no[illegible] Chair, where I help set the [illegible] am a new and active memb[illegible] the NRC Committee to Advise the US Global Change Re[illegible] Program. I have served on advisory and review boards at CSIRO, Australia and on the Australian Biosecurity CRC, and on all annual meetings of the WHO R[illegible] Blueprint Pathogen Prioritization Committee. I have managed meetings among senior leadership of the US NSF and NSFC China to promote US-China collaboration, and am an active member of a series of One Health editorial boards and international organization boards, as well as a Commissioner of *The Lan[illegible]*

a. [illegible] DR, Shadduck JA, Shaw DH, Swayne DE, Tolwani RJ (2005). Critical needs for research in veterinary science. ***National Aca[illegible]mies P[illegible]*** [illegible]22 pp.

b. Rodriguez JP, Taber AB, **Daszak P**, Sukumar R, Valladares-Padua C, Padua S, Aguirre LF, Medellin R, Acosta M, Aguirre AA, Bon[illegible], Bordino P, B[illegible], Buchori [illegible] Mendez M, Mugica L, Pacheco LF, D[illegible], Pea[illegible] [illegible] Policy Forum: The globalization of conservatio[illegible] [illegible]5-756.

c. Smith KF*, Behrens M, [illegible]hloegel LM, [illegible] P* (2009). Reducing the risks of the wildlife trade. **Science** [illegible]595.

d. **Daszak P** (20[illegible]). Anatomy of a pandemic. **Lancet** 380: 1883-18[illegible]. Lead article as Guest Editor for a ***Lancet Series*** on Zoonoses.

D. Additional Information: R[illegible]

Ongoing Research Support

USAID Emerging Pandemic Threats Mazet (PI) 10/01/14 – 09[illegible]
PREDICT-2
The goal is to co[illegible] in wildlife [illegible] risk behavior, analyze EID risk, and design interventions in >20 countri[illegible]
Role: PI on Subcontract

2R01 AI110964 D[illegible]zak (PI) 0[illegible]
Understanding the Risk of Bat Coronavirus Emergence
The goal of this work is to c[illegible]ize the virolo[illegible]ical, behavioral and demographic factors that presen[illegible] risk of future emerge[illegible] of SARSr-CoVs in pe[illegible]nd iden[illegible]al outcome[illegible]
Role: PI

Completed Research Support [illegible]

1R01 AI110964 Daszak (PI) 06/01/14 – 0[illegible]/19
Understanding the Risk of Bat Coronavirus Emergence
The goal [illegible] ecological and virolo[illegible] on bat-origin SARSr-CoVs in China [illegible] surve[illegible]s and testing in people, to id[illegible]
Role: PI

USAID 141437 [illegible]MA, Thailand) Daszak (CoP) 10/01/13 - 03/30/19
Infectious Dis[illegible] Emergence and Economics of Al[illegible]
Cooperative agreement to analyze how land u[illegible]hange affects eco[illegible]
Role: Chief of Party

NSF DE[illegible]1437[illegible]
US-UK Collab: Risks of Animal and Plant Infectious Diseases th[illegible]
The goal is to a[illegible] [illegible]ging disease risk globally.
Role: Co-I[illegible]

HD[illegible] [illegible] Allen (PI) 0[illegible]/15/15 - 04/14/17
Global Rapid Identification [illegible] of undiagnosed EID Events
The goal was to design software for the DoD biosurveillance ecosystem to diagnose novel EID events.
Role: Co-Investigator

1R01GM100471 (NIGMS) P[illegible] (PI) 0[illegible]
MASpread: Modeling Anthropogenic Effects in [illegible]
The goal was to analyze the social decisions involved in disease spread through [illegible]
Role: Co-Investigator

NSF Daszak (PI) 07/01/10-06/30/15
EcoHealthNet - a Research Coordination Network
F[illegible]nding for st[illegible]
Role: PI

3. Memish ZA, Mishra N, Olival KJ, Fa[illegible] [illegible]m A, Kapoor A, B[illegible] [illegible]zak P, Al Rabeeah AA, Lipkin WI (2013). Mi[illegible] [illegible]espiratory Syndr[illegible] Coronavirus in Bats, Saudi Arabia. EID 19(1[illegible]
4. **Ol[illegible]** [illegible]J*, Hosseini P, Zambrana-Torrelio C, Ross N, Bogich T, Daszak P* (2017). Host and viral traits predict zoonotic spillover from mammals. **Nature** 546(7660): 646-650.

*corresponding author

B. Positions and Honors

Positions and Employment

1999 -02	Research Associate, Kewalo Marine Laboratory, University of Hawaii
2003 -07	US Environmental Protection Agency STAR Fellow
2006 -13	Instructor, Columbia University Secondary School Summer Program
2010 -12	NIH Fogarty US Global Health Post-Doc Fellow
2012 -15	Senior Research Scientist, EcoHealth Alliance
2015 -17	Associate Vice President for Research, EcoHealth Alliance
[illegible]	Visiting Scientist, American Museum of Natural History
2009 -	Adjunct Faculty, Earth Institute Center for Environmental Sustainability, Columbia University
2017 -	Vice President f[illegible], EcoHealth Alliance

Other Experience and Professional Memberships

199[illegible]	[illegible]merican Association for the Adva[illegible] [illegible]ence
2000 -02	Mentor, NSF Undergraduate Mentoring in Environmental Biology (UM[illegible]) [illegible] University
2003 -05	Member, American Society of Mammalogists
2005 -06	Member, New York Academy of Sciences
2011 -	Scientific Steering Committee Member, Southeast Asian Bat Conservation Research Unit
20[illegible]	Scientific Advisory Board Member, Lubee Bat Conservancy, FL
2011 -	Scientific Advisor, Bat Conservation International
2011 -	Review Editor, EcoHealth
2015 -	US White-Nose Syndrome Stakeholder Committee and Communications Committee Member
2017 -	DoD D[illegible]RA: Stee[illegible] [illegible]mittee Member, Bat One Health Research Network
2017 -	Founder, Western Asia Bat Research Network

Honors

[illegible]	Colorado State University Distinguished Scholar Award
[illegible]	NSF Graduate Student Fellowship, Honorable Mention
2005 -07	Bat Conservation International Student Award and Scholarship
2[illegible]	[illegible]PA STAR Fellowship Award
2008	PhD D[illegible]rtation with Distinction [illegible]
2013	Plena[illegible] [illegible]
2013 -14	Institute of Medicine, Forum on Microbial Threats: invited speaker, briefings on MERS-CoV and Emerging Viral Diseases
2016	Plenary Speaker, NYC Medtech conference – Global Virome Project
2017 -18	Three papers awarded the InCites Highly Cited Paper™ designation (top 1% in field) for Immunology and Microbiology
2019	Keynote Speaker, World-Wide Human Geography Data Working Group, Harvard University, MA
2019	Keynote Speaker, 18[illegible] International Bat Research Conference, Phuket, Thailand

3. **Mode[illegible] [illegible]obal disease emerg[illegible]** [illegible] develop new models that he[illegible] the environmental drivers of bat virus spillover to h[illegible]s, cross-species transmission am[illegible] spatial analysis of emer[illegible] zoon[illegible] dis[illegible] estimating viral host range. These models explicit[illegible] data from PCR [illegible] serology-ba[illegible] field studies, combined with an understanding of wildlife [illegible]gy, ecology, and host phylogenetics and evolution, to assess the environmental and dem[illegible]phic drivers of disease transmission -- brid[illegible] the gap betw[illegible] field investigations and transmission risk.

   a. [illegible] [illegible]otic [illegible] vir[illegible]

   b. Willoughby AR, Phelps K, PREDICT Consortium, **Olival KJ*** (2017). A Comparative Analysis of Viral Richness and Viral Sharing in Cave-Roosting [illegible]ts. Diversity 9(3): 35.

   c. Al[illegible]n T, Murray KA, Zambrana-Torr[illegible], Morse SS, Rondinini C, Di Marco M, Breit N, **Olival KJ**, Daszak P ([illegible]17). Global hotspots and correlates of emerging [illegible]onotic diseases. Nature Comm 8(1124): 1-10.

   d. Wa[illegible] A, Crowley DE, [illegible] KJ, Taylor M, Munster VJ, Plowright RK (2018). Taxonomic patterns in the zoonotic potential of mammalian v[illegible]

4. **Elucida[illegible]g host-vector-pathogen interacti[illegible] [illegible]nary biology**. I started using evolutionary and phylog[illegible]etic tools to improve the understanding of host and vector disease biology during my PhD dissertation. I continued this through my NIH post-doctoral fellowship research on Nipah virus [illegible]ics using [illegible] host phylogeographic analyses of *Pt[illegible]* spp. fruit bats and [illegible]tors. O[illegible] examples include DNA barcoding analysis of mosquito bloodmeals to understand bunyavirus vertebrate host range; co-phylog[illegible] [illegible]ents; and analyzing patterns of [illegible]

   a. Murdock C, **Olival KJ**, and Perkins SL (2010). Feeding prefe[illegible]ces of snow[illegible] mosquitoes (Culicidae: *Culiseta* and *Oche[illegible]* [illegible] (Bunya]viridae: Orthobunyavirus) and humans. **Journal of Medical Entomology**. 47(2): 226-229.

   b. **Olival KJ***, Dick CW, Simmons NB, Mora[illegible] JC, Melnick DJ, Dittmar K, Perkins SL, Das[illegible] R (20[illegible]). Lack of population genetic structure [illegible] across species of Pteropus bats in Southeast Asia. **Parasites & Vectors**. 8(6): e231.

   c. Lei BR, **Olival KJ*** (2014). Contrasting Patterns in Mammal-Bacte[illegible] *Bartonella* and *Leptospira* in Bats and Rodents. **PLOS NTD**. 8(3): e2738.

   d. Wacharapluesade[illegible] Duengkae P, Rodpan A, Kae[illegible]om T, Maneeorn P, Kanchanasaka B, Yins[illegible] C, Sittidetboripat N, Charees[illegible]n C, Khlangsap N, Pidthong A, Leadp[illegible]om K, Ghai S, Epstein JH, Daszak P, **Ol[illegible]** [illegible] (2015). Diversit[illegible] Coronavirus in Bats from Eastern Thailand. **Virology J**[illegible]

D. Additional Information: Research [illegible]

Ongoing Research Support

HDTRA11710064 Olival (PI) 10/02/17-10/01/22

Understanding the Risk of Bat Born[illegible] Asia

The goal of this project is to characterize pathogen diversity, strength[illegible] zoo[illegible] diseas[illegible] capacity, and test key hypotheses about the risk of bat bo[illegible]

Role: PI

USAID Emerging Pandemic Threats [illegible] Mazet (PI) [illegible]/14-09/30/19
PREDICT 2
The goal of this project is to create and implement a global virus surveillance [illegible] systems in animals and humans [illegible]
and analyze spillover risk.
Role: Modeling and Analytics Coordinator; Country lead for Indonesia [illegible] Thailand

Completed Research Support

R01 AI110964 Daszak (PI) 06/01/14-05/31/19
Understanding Risk [illegible]
The goal of this study is to analyze the risk of coronavirus spillover from bats to humans in South[illegible]
Role: co[illegible]

platform identifies threat posed by a SARS-like [illegible] of circulating bat coronavirus. **Nature Med** 21(12):1508-13.

4. Cockrell AS, Yount BL, Scobey T, Jensen K, Douglas M, Beall A, Tang XC, Marasco WA, [illegible] **Baric RS** (2016). A mouse model for MERS coronavirus-induced acute respira[illegible] **Nat Microbiol** 28;2:16226.

B. Position and Honors

Positions and Employment

1986 -1992	Assistant Professor, Department of [illegible] Epidemiology, University of North Carolina (UNC) [illegible] Hill, NC
1992 -2001	Associate Professor, Departments of Epidemiology and Microbiology & Immunology, UNC Chapel Hill
2001 -	Professor, Departments of Epidemiology and Microbiology [illegible]

Other Experience and Professional Membership

2005 -[illegible]	Permanent Member, NIH VirB Study Section
2005 -[illegible]	[illegible] Review Board, J. Virology
2006 -07	Acting Chair and [illegible] Division T RNA Viruses, American [illegible] Microbiology
2007 -08	Associate Editor, Plos Pathogens
2008	Nat'l Acad Sci: Working Group: Gene Sequence Methods for Classification of [illegible]
20[illegible] -17	Senior Editor, Plos Pathogens
2014	National Academy of Sciences Working Group on Risks and Benefits of Gain of Function Research
2015	MERS-CoV Stakeholders Workshop, Organizer and invited panelist, NIH
2015	Natl. Acad. Of Sciences “China-U.S. Workshop on the Challenges of Emerging Infections, Laboratory Safety, and Global Health [illegible]
2017	Natl. Acad. Of Sciences “China-U.S. Workshop on the Challenges of Emerging Infections, Laboratory Safety, and Global Health Security” Jan 16-18th in Galveston-Texas.
2018	Natl. Acad. Of Sciences “[illegible] Workshop on the Challenges of Emerging Infections, Laboratory Safety, [illegible]

Honors

1984 -86	Harvey Weaver Scholar, National Multiple Sclerosis Society
1984 -87	Established Investigator, American Heart Association
2005	Finalist/Runner-up, World Technology Award
2011	Innovation/Inspiration Award [illegible] Research, UNC Gillins School of Public Health
2019	Kenan Distinguished Professor

C. Contributions to Science

1. **Contributi**[illegible] coronavirus, norovir[illegible] biology, virus-host interactions, [illegible] and new technologies like struc[illegible] synthetic genome design, and systems genetics. We developed new approaches to identify and [illegible]
   a. Yount B, Curtis K, Fritz L, Hensley L, Jahrling P, Prentice L, Denison M, Geisbert T, **Baric RS** (2005). Reverse Genetics with a full-length infectious cDNA for the [illegible] **Proc Natl Acad Sci USA** [illegible]
   b. Lindesmith LC, Donaldson EF, Lobue AD, Cannon JL, Zheng DP, Vinje J, **Baric RS** (2008). Mechanisms of GII.4 NoV persistence in humans. **PLoS Med** 5(2):e31.
   c. Sheahan TP, Sims AC, Graham RL, Menachery VD, Gralinski [illegible] st SR, Pyrc K, Fe[illegible] Trantcheva I, Bannister R, Park Y, Babusis D, Clarke MO, Mackman RL, Spahn JE, Palmiotti CA, Siegel D, Ray AS, Cihlar T, Jordan R, Denison MR, **Baric RS** (2017). [illegible] 5734 inhibits both epidemic and zoonotic CoV. **Sci Transl Med** 28:9(396).

   d. Menachery VD, [illegible]ount BL, Jr. (+15 other authors) and Baric RS (2016). SARS-like WIV1-CoV poised for human emergence. **Proc Natl Acad Sci USA** 113:3048-3053.

2. **Viral Immunity**. New diagnostic m[illegible]cs [illegible] needed to identify precis[illegible] the molecular level. Our group has pioneered [illegible] structure-guided immunogen design, coupled with reverse genetic strategies, to tra[illegible] viral proteins), using noroviruses and dengue/zikv virus as model platforms.
   a. Lindesmith LC, Ferris MT, Mullan CW, Ferreira J, Debbink K, Swanstrom J, Richardson C Goodwin RR, Baehner F, Mendelman PM, Bargatze RF, **Bari**[illegible] Broad blockade antibody responses in human volunteers after immunization with a multivalent norovirus VLP candidate vaccine: immunological analyses [illegible]
   b. Gallichotte EN, Baric TJ, Yount BL Jr. Widman DG. Durbin A [illegible]ead S. **Baric RS**, de Silva AM (2018). Human dengue virus serotype 2 neutralizing antibodies target two distinct quaternary epitopes. **PLoS Pathog** [illegible]14(2):e1006934.
   c. Gallichotte EN, Baric TJ, Nivarthi U, Delac[illegible] Whitehead SS, de Silva AM, **Baric RS** (2018). Genetic Variation between Dengue Virus Type 4 Strains Impacts Human Antibody Binding and Neutralization. **Cell Rep** 30;25(5):1214-1224.
   d. Lindesmith LC, McDaniel JR, Changela A, Verardi R, Kerr SA, Costantini V, Brewer-Jensen PD, Mallory ML, Voss WN, Boutz DR, Blazeck JJ, Ippolito GC, Vinje J, Kwong PD, Georgiou G, **Baric RS**. Sera Antibody Repertoire Analyses Reveal Mechanisms of Broad and Pandemic Strain Neutralizing Responses after Human Norovirus Vaccination. **Immunity** [illegible] 1541.e8.

3. **Vi**[illegible] **Molecu**[illegible] **Genetics/Im**[illegible] analyse[illegible] flaviviruses, including recently emerg[illegible] CoV, PEDV, conventional human and [illegible]onaviruses like MHV and HCoV NL63 [illegible] coronaviruses. We have also built full length infectious cDNA clones for DENV1-4 serotypes, several Zikv strains, as well as panels of isogenic DENV serotypes encoding genotype distinct E glycoproteins. We demonstrated that coronaviruses and influenza viruses regulate host expression, by epigenetics.
   a. Douglas G, Widman DG, Ellen Y[illegible] Gallichotte EN, [illegible] Plante [illegible] Swanstrom J [illegible] the Zika virus family tree. **MBio** 7:8(2). pii: e[illegible]614-16.
   b. Swanstrom JA, Plante JA, Plante KS, Young EF, McGowan E, Gallichotte EN, Widman DG, Heise MT, [illegible] Isolated from Dengue Patients Are Protective against Zik[illegible]
   c. Lindesmith LC, Beltramello M, Donaldson EF, Corti D, Swanstrom J, Debbink K, Lanzavecchia A, **Baric RS** (2012). Immunogenetic [illegible] **Pathog** 8(5):e1002705.
   d. Menachery VD, Eisfeld AJ, (+23 other authors) and Baric RS. Pathogenic influenza viruses and coronaviruses utilize similar and contrasting approaches to control interferon stimulated gene responses. **Mbio** 5[illegible]174-14. 2[illegible]

4. **Host Suscepti**[illegible] causes of human morbidity and mortality worldwide. [illegible] ho[illegible] alleles that regulate SARS-CoV [illegible] epigeneti[illegible]
   a. Gralinski LE, Fer[illegible] SARS-CoV Susceptibility Loci Using the Collaborative Cross. **PLoS Genet** 11:e1005504,
   b. Gralinski L, Menachery V, (+9 other authors) and **Baric RS** (2017). *Ticam2* contributes to SARS-CoV pathogenesis. **G3** 7:7(6):1653-1663.
   c. Rasmussen AL, Okumura A, (**Baric RS** + 18 others) a[illegible] MG (2014). Host genetic diversity enables Ebola hemorrhagic fever pathogenesis and resistance. **Science** 346:987-991. PMC4241145.

[illegible] Y, Xing SZ, Chen YS, Sun Y, Li J, Daszak P, Wang L-F, Shi ZL, Tong YG, Ma JY (2018). Fatal swine acute diarrhoea syndrome caused by an HKU2-related coronavirus of bat origin. **Nature** 556: 255-258.

B. Positions and Honors

Positions and Employment

1982 -86	Doctoral Candidate, Department of Biochemistry, University of California, Davis, [illegible]
1986 -89	Post-doctoral Fellow, Department of Biochemistry, University of California, Davis, USA
1990	Senior Research Officer, Ctr for Molecular Bio. and Med., Monash University, Clayton, Australia
1990 -92	Research Scientist, CSIRO Australian Animal Health Laboratory (AAHL), Geelong, Australia
1992 -96	Senior Research Scientist, CSIRO AAHL, Geelong, Australia
1996 -04	Principal Research Scientist, CSIRO AAHL, Geelong, Australia
2004 -08	[illegible]
2008 -	OCE Science Leader, CSIRO AAHL, Geelong, Australia
2012 -	Professor and Director, Program in [illegible] Singapore

Other Experience and Professional Membership

1996 -	Editorial Board, Asia-Pacific Journal of Molecular Biology and Biotechnology
2003	WHO SARS Scientific Research Advisory Committee
[illegible] -	Honorary Professor, Wuhan Institute of Virology, Chinese Academy of Sciences
2006 -	Editorial Board, Chinese Journal of Virology
2006 -	Editorial Board, Zoonoses and [illegible]
2006 -07	NH[illegible]
2008 -15	Chair ,ICTV Study Group, Paramyxoviridae
2009 -	Honorary Professor, The University of Melbourne, Australia
2010 -	Editorial Board, Frontiers in Virology
2012 -	Editor-in-Chief, Virology Journal
2012 -	Board of Directors, Singapore Eye Research Institute
2012 -	Executive Committee, Australasian Society of Virology
2013 -	WHO International Health Regulations Roster of Experts
2015 -	Editorial Board, Scien[illegible]

Honors

20[illegible]6	CSIRO Award for Excellence in Partnership
2007	Finalist, Eureka Prize for Scientific Research
2008	CSIRO CEO Science Leader Award
2010	Elected fellow of the Australian Academy of Technological Sciences and Engineering
2011	Gardner Lecture Award, European Society of Clinical Virologist
2013	CSIRO Chairman's Medal for Research
20[illegible]4	Winner, Eureka Prize for Infectious Disease Research

C. Contributions to Science

1. **Identification** [illegible] wildlife, livestock and humans, coupled with [illegible] experimental infections under BSL-2, -3, and -4, and laboratory assays to identify evidence that bats are the reservoir for a series of emerging viruses in people, including [illegible] current interest in bats in EID research globally.

a. Chua KB, Crameri C, Hyatt A, Yu M, T[illegible]pang MR, Rosli J, McEachern J, Crameri S, Kur[illegible]asamy V, Eaton BT, **Wang L-F** (2007). A previously unknown reovirus of bat origin is [illegible]ted with an acute respiratory disease in humans. **Proc. Natl. Acad. Sci. USA** 27: 11424-11429.

b. Mahalingam S, [illegible]ero LJ, Playford G, Spann K, Herring B, Rolph R, Middleton D, Mc[illegible] **Wang L-F** (2012). Hendra virus: an emerging paramyxovirus in Australia. **Lancet Infectious Diseases** 12: 799-807.

c. Zhou P, Fan H, Lan T, Yang X[illegible] W-F, Zhang W, Zhu Y, Zhang Y-W, [illegible] Xie Q-M, Mani S, Zheng X[illegible] Li [illegible], Pei G-Q, An X-P, Ch[illegible]ein J-W, Zhou L, Mai K-J, Wu Z-X, Li D, Anderson DE, [illegible] L-B, Li [illegible]Y, Mi Z-Q, He T-T, Cong F, Guo P-J, Hu[illegible] R, Luo Y, Liu X-L, Chen J, Huang Y, [illegible] Zhang H-L, Wang Y-Y, Xing S-Z, Chen Y-S, Sun Y, Li J, Daszak P, **Wang L-F**, Shi ZL, Tong YG, Ma JY (2018). Fatal swine acute diarrhoea syndrome caused by an HKU2-related coronavirus of bat origin. **Nature** 556:255-258.

d. Yang XL, Tan CW, [illegible] DE, Jiang RD, Li B, Zhang W, Zhu Y, Lim XF, Zhou P, Liu X[illegible] [illegible] (2019). Characterization of a filovirus [illegible] Rousettus bats in China. **Nat Microbiol.** 4:390-395.

2. **Establishment of bat [illegible] host interaction and evolutionary biology.** Working with collaborators around the world, my lab has amassed an unprecedented collection of serological, tissue and other samples from bat surveillance programs. I have used these to develop and disseminate primary and immortalized bat cell lines, and a host of reagents which my team and collaborators are using to test hypotheses about why bats are able to host so many distinct viruses. Current projects include bat genomics and proteomics; examining the bat MHC, using gene knockout technology to identify links between flight, viral resistance, and [illegible].

a. Wynne JW, Shiell BJ, Marsh G-A, Boyd V, Monaghan P, Zhou P, Klein R, Todd S, Mok L, Green D, Tachedjian M, Baker M, Matthews D, **Wang L-F** (2014). Proteomics informed by transcriptomics reveals Hendra virus sensitizes bat cells to TRAIL mediated apoptosis. **Genome Biology** [illegible]

b. Xie J, Li Y, Shen X, Goh G, Zhu Y, Cui J, **Wang L-F**, Shi ZL, Zhou P (2018). Dampened STING-Dependent Interferon Activation in Bats. **Cell Host Microbe** 23(3):297-301.e4.

c. Ahn M, Anderson DE, Zhang Q, Tan CW, Lim BL, Luko K, [illegible] JHJ, Sobota [illegible] Dutertre C-A, [illegible] F, Shi Z[illegible] mediated inflammation in bats and [illegible] 799.

3. **Application of both molecular and serological platforms to pathogen discovery.** My work at CSIRO AAHL, and now at Duke-NUS has focused on the development and use of PCR and serological assays to identify novel pathogens in wildlife, livestock and [illegible] outbreak conditions. This includes the discovery of bats as [illegible]servoir for [illegible] developed.

a. Bossart KN, McEachern JA, Hickey AC, Choudhry V, [illegible] Neutralization assays for differential henipavirus serology using Bio-Plex Protein Array Systems. **J. Viol. Meth.** 142: 29-40.

b. Kaku Y, Nog[illegible] K, Baza[illegible] Yamada A, Inoue [illegible], **Wang L-F** (2012). Second generation of pseudotype-based serum neutralization assay for Nipah virus antibodies: sensitive and high-throughput analysis utilizing secreted alkaline phosphatise. **J. Virol. M**[illegible]

c. Mani S, Tan CW, **Wang L-F**, Anderson DE (2018). Serological [illegible] Dengue Viruses in Experim[illegible]

BIOGRAPHICAL SKETCH

NAME: Anderson, Danielle Elizabeth

eRA COMMONS U[illegible] (credential, e.g., agency login):

[illegible]TION TITLE: Research Assistant Professor

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date	FIELD OF STUDY
Deakin Uni[illegible] Australia	BSc (Hons)	12/2000	Biology
Curtain University of Technology, Australia	PhD	02/2007	Virology

A. Personal Statement

As a Research Ass[illegible] School, my research aims to identify [illegible] serve as Scientific Director of the Duke[illegible] ABSL3 laboratory, [illegible]h provides infra[illegible]ructure, expertise [illegible] support for research with pathogens requiring high co[illegible]ainment. I have a backgroun[illegible] specific training and expertise in hi[illegible]ghput screening. In my current role, my visio[illegible] to create a world[illegible] lab with an [illegible] safety record. A facility that not only Duke-NUS, but Singapore can be pro[illegible]ud of, and that enhances the biomedical research activi[illegible]ngapore by providing the opportunity for *in vitro* and *in vivo* experimentation with BSL3 patho[illegible] I was involved in the design and accreditation process of commissioning the Duke-NUS A[illegible]SL3, so I am intimately familiar with capacities of the facility and the regulatory framework it is embedded in. In addition to my laboratory expertise, I have extensi[illegible] in designing animal experiments with ferrets, non-human primates and bats. As I have trained and wo[illegible] (Duke-NUS Medical School) and the [illegible] University), and the BSL4 facility in China (Wuhan Institute of Virology). I [illegible]elieve that I have the necessary broad expertise and the international network to co[illegible]ntinue m[illegible] research. The current a[illegible]plication not only builds logically on my prior work and expertise in this field but is aligned with my future res[illegible]

1. **DE Anderson***, K Pfeffermann*, [illegible] Saw[illegible], J Pearson, M Kovtun, DL Corcoran, Y Krebs, K Sigmundsson, SF Jamison, ZZJ Yeo, LJ Rennick, L-F Wang, PJ Talbot, WP Duprex, MA Garcia-Blanco and V von Messling (*Authors contribu[illegible]). Comparative Loss-of-[illegible] ABCE1 as an Essential Cellular Host Factor for E[illegible] Translation of *Pneumov*[illegible] 10.1128/mBio.00826[illegible] 2019
2. [illegible] T [illegible]an, **DE Anderson**, R-D Jiang, B Li, W[illegible] Guan, L Zhang, S-Y Li, Y-[illegible]Jiang, L-F W[illegible] from *Re*[illegible]
3. **DE Anderson***, A Islam*, G Crameri*, S [illegible] Mendenhall, SP Luby, ES Gurley, P Daszak, JH Epstein and L-F Wang (*Authors contributed equally). Isolation and full-genome characterization of multiple Nipah viruses from bats, Bangladesh. **Emerging infectious Diseases**. 25(1): [illegible]-170, **2019**.
4. P Zhou, H Fan, T Lan, X-L Yang, W-F Shi, W Zhang, Y Zhu, Y-W Zhang, Q[illegible] Xie, S Mani, X-S Zheng, B Li, J-M Li, H Guo, G-Q Pei, X-P An, J-W Chen, L Zhou, K-J Mai, Z-X Wu, D Li, **DE Anderson**, L-B Zhang, S-Y Li, Z-Q Mi, T-T He, F Cong, P-J Guo, R Huang, [illegible] X-L Liu, J Chen, Y Huang, [illegible] X-L-L[illegible]

3. **Wacharapluesadee S**, Duengkae P, Chaiyes A, Kaewpom T, Rodpan A, Yingsakmongkon S, Petcharat S, Phengsakul P, Maneeorn P, Hema[illegible] [illegible]9). Longitudinal study [illegible] coronavirus infection in Lyle's flying fox (Pteropus lylei) in Thailand. [illegible] 2020;15(1):38.
4. **Wacharapluesadee S**, Sintunawa C, Kaewpom T, [illegible] [illegible]rinan K, [illegible] [illegible]al KJ, Epstein JH, Rodpan A, Sangsri P, Intarut N, Chindamporn A, Suksawa K, Hemachudha T (2013). Group C betacoronavirus in bat guano fertilizer, Thailand. [illegible]

B. Positions and Honors

Positions and Employment

1994 -97	Biochemical Technician, Department of Entomology, A[illegible]RIMS, Thailand
1997	Researcher, Department of Immunology, Chulabhorn Research Institute, Thailand
[illegible]	[illegible]
2000 -16	Laboratory Chief, Neuroscience Centre for Research and Development & WHO Collaborating Centre for Research and Training on Viral Zoonoses, Faculty of Medicine, Chulalongkorn University Hospital, Thai Red Cross Society, Thailand
2016 -	Deputy Chief of Thai Red Cross Emerging Infectious Diseases Health Science Centre, Faculty of Medicine, Chulalongkorn University Hospital

Other Exper[illegible]

2010 -	PREDICT Thailand Country Coordinator
2014 -	Thai Ministry of Public Health (M[illegible]) [illegible] Diagnostic Committee
2015 -	PREDICT 2 Thailand Country [illegible]
2016 -	Steering committee, Bat One Health Research Network, BTRP-DTRA

C. Contribution to Science

1. **Research on [illegible] coronavirus prevalence** [illegible] have bat reservoirs. Our surveillance projects study the diversity of coronavirus (CoV) in bats in Thailand. We have isolated and characterized CoVs from many bat species, and detected and sequenced CoV in bat guano miner. Our surveillance studies continue to analyze the drivers of their emergence, and risk factors for spillover.

   a. Joyjinda Y, Rodpan A, Chart[illegible], Suthum K, Y[illegible] [illegible]aemsakul S, Cheun-Arom T, Bunp[illegible] S, Olival KJ, Stokes MM, Hemachudha T, **Wacharapluesadee S** (2019). [illegible] Complete Genome [illegible] Coronavirus HKU1 from a Nonill Bat Guano Miner in Thailand. **Microbiol Resour Announc** 8(6).pii:e01457-18.

   b. **Wacharapluesadee S**, Duengkae P, Chaiyes A, Kaewpom T, Rodpan A, Yingsakm[illegible] S, Phengsakul P, Maneeorn P, Hema[illegible] [illegible]9). Longitudinal study [illegible] coronavirus infection in Lyle's flying fox (Pteropus lylei) in Thailand. [illegible] 2020;15(1):38.

   c. Plipat T, Buathong R, **Wacharapluesadee S**, Siriarayapon P, Pittay[illegible] Kaewpom T, Petcharat S, Ponpinit T, Jumpasri J, Joyjinda Y, Rodpan A, Ghai S, Jittmittraphap A, Khongwichit S, Smith DR, Corman VM, Drosten C, Hemachudha T (2017). Imported case of Middle East respiratory syndrome coronavirus (MERS-CoV) infection from Oman to Thailand, June 2015. **Euro Surveill** 22(33):pii: 30598.

   d. **Wacharapluesadee S**, Duengkae P, Rodparn A, Kaewpom T, Maneeorn P, Kanch[illegible]saka B, Yingsakmongkon S, Sittidet[illegible] N, [illegible] Epstein JH, Daszak P, Oliv[illegible] P, Olival KJ, Blair PJ, Callahan MV and Hemach[illegible] Coronavirus in Bats from Eastern Thailand. **Virol J** 12(1):57.

2. **Research on N[illegible] prevalenc[illegible] bats.** Nipah virus outbreaks, pre[illegible] in [illegible]ailand's neighbouring country, Malaysia, and ongoi[illegible] Bangladesh have high [illegible] projects study the characterization of Ni[illegible] Virus (N[illegible]) [illegible] bats in Thailand. Our surveillance studies continue to analyze the drivers of their emergence, unde[illegible]tanding the[illegible] factors for spillover.
   a. **Wacharapluesa[illegible]** S, [illegible] Srongmongkol P, Kanchanasaka B, Hemachudha T (2[illegible]). Molecular chara[illegible] from Pteropus hypom[illegible] in Southern Thailand. **Virol J** 13(1):53
   b. **Wacharapluesad[illegible]** [illegible] Detection of Animal Viral Pat[illegible] Nipah Virus. CRC Press.
   c. **Wach[illegible]sadee S**, Ngamprasertwong T, Kaewpom T, Kattong P, Rodpana A, Wanghongsa S, Hemachudha T (2013). Genetic characterization of Nipah virus from Thai fruit bats (*Pteropus lylei*). **Asian Biomedicine** 7(6);813-819
   d. Breed AC, Meers J, Sendow I, Bossart KN, Bar[illegible], Smith I, [illegible] **[illegible]e S**, Wang L, Field HE (2013). The Distribution of Henipaviruses in Southeast Asia and Australasia: Is Wal[illegible] Nipah Viru[illegible]? **PLoS O[illegible]** [illegible]

3. **Rabies Neuropathogenesis, [illegible] and management.** The centre worked ma[illegible] molecu[illegible] analyses of rabies, including mutational effects, and designing primers to detect Thai [illegible] virus. I regula[illegible] organize workshops to teach labor[illegible] in the region on how to correctly collect [illegible] and test for rabies.
   a. Hemachudha T, Ugolini G, Sung[illegible], Laothamatas J, S[illegible] **Wacharapluesadee S** (2013). Human Rabies: neuropathogenesis, diagnosis and managem[illegible]ology 498-513.
   b. Shuangsh[illegible] N, Phukpattara[illegible] [illegible]nphap A, In[illegible] **Wacharapluesadee S**, Thorner PS, Hemachudha T (2013). Reduced viral burden in paralytic compared to furious canine rabies is ass[illegible]ated with prominent inflammation at the brainstem level. **BMC Vet Res** 14;9(1):3[illegible]
   c. Virojan[illegible] P, Khawplod P, Sawangvaree A, **Wacharapluesadee S**, Hemachudha T, Yamada K, Morimoto K, Nishizono A (2012). Molecular analysis of the m[illegible]tional effects of Thai street rabies virus with increa[illegible]
   d. Wilde H, Hemachudha T, **Wacharapluesadee S**, Lumlertdacha B, Tepsume[illegible] (2013). Rabies in Asia: The Classical Zoonosis. **Curr Top Microbi[illegible] Immun[illegible]** [illegible]:185-20[illegible].

4. **Investigating causes of enceph[illegible]tis.** More than 50% of patients presenting with [illegible] undiagnosed. Our centre has focused a lot of research into diagnosing fever of unknown origins (FUO). We study epid[illegible]ology, pathology and conduct surveillance studies into viral pathogens, and autoimmune diseases.
   a. Hemachudha P, **Wacharapluesadee S**, Buathong R, Petch[illegible] S, Bunprakob S, Ruchiseesarod C, Roeksom[illegible]n P, Hem[illegible] T (2019). [illegible] Infant. **Clin Med In[illegible] Case Rep** 12:1179547619835179.
   b. Phumee A, Bua[illegible], Boonserm R, [illegible]tayot P, Aungsananta N, Jittmittraphap A, Joyjinda Y, **Wacharapluesadee S**, Siriyasatien P (2019). Molecular Epide[illegible]ology and Genetic Diversity of Zika Virus from Field-Caught M[illegible]quitoes in Various Regions of [illegible]
   c. Phumee A, Chompoosri J, Intayot P, Bo[illegible]nserm R, Boonyasuppayakorn S, Buathong R, Thavara U, T[illegible] Joyjinda Y, **Wacharapluesadee S**, Siriyasatien P (2019). Vertical tr[illegible] of Zika virus in Culex quinquefasciat[illegible] Say and Aedes aeg[illegible] (L.) mo[illegible] Reports 9(1):5[illegible]

4. Satjanadumrong J, Robinson MT, Hughes T, Blacksell SD (2019). Distribution and Ecological Drivers of [illegible]

B. Positions and Honors

Positions and Employment

2004	Expedition Leader, Tropical Forest Project Malaysia, Coral Cay Conservation
2005 -07	Field Officer, Malaysia, EcoHealth Alliance
2007 -	Project Coordinator Malaysia, EcoHealth [illegible]
2010 -	PREDICT Country Coordinator Malaysia
[illegible]	[illegible]

Other Experience and Professional Memberships

[illegible]	Lead, Community Education Program, [illegible]
2005	Member, The Henipavirus Ecology [illegible] Group
2006	Lead, Community Education Program, Bat Ecology, Tioman Island, Malaysia
2008	Recipient, Scholarship to attend the International Ecology & Health Forum, Merida, Mexico
2008 -	Reviewer, *EcoHealth* Journal
2010	Member, Philippine government/Food and Agriculture Organization of the United Nations mission to investigate Philippine bats as a possible reservoir of Reston Ebolavirus
2014	Invited Presenter, Disease Ecology, UN Special [illegible]

C. Contributions to Science

1. Surveillance for emerging viruses in Southeast Asia

As project [illegible] in Malaysia for EcoHealth Alliance [illegible] have designed and led field programs that underpin advances in our understanding of wildlife-origin zoonoses (e.g. Macaques and Herpes B), risk factors for emergence (e.g. Nipah virus in fruit bats), the distribution of viruses (e.g. Ebola virus in the Philippines). Through the PREDICT project I currently [illegible] found 71 novel viruses and 26 known viruses in wildlife reservoirs, livestock and humans. I have [illegible] develop laboratory and personnel capacity for disease surveillance at the Department of Wildlife and National Parks (DWNP), Department of Ve[illegible] and Ministry of H[illegible] individuals from government partners, local universities and NGOs in surveillance [illegible] techniques including sharing SOPs and protocols. In collaboration with Sabah Wildlife Department I established the Wildlife Health, Genetic and Forensic Laboratory that has all the equipment necessary to store samples, run extractions, PCR and analysis on biological samples for disease surveillance. The lab is used to screen samples for the PREDICT and to generate PCR and serological data for EcoHealth Alliance. I also establish the new molecular zoonosis laboratories at the DWNP's National Wildlife Forensic Laboratory. The lab is used to screen samples for the PREDICT & DTRA projects and to generate PCR and serological data for EcoHealth Alliance.

a. Ep[illegible] SA, Basir MM, Field HE & Daszak P (2009). *Pteropus vampyrus*, a [illegible] multina[illegible] home-range and a need for regional management. Journal of Applied Ecology [illegible] 1002.

b. Halpin K, Hyatt AD, Fogarty R, Middleton D, Bingham J, Epstein JH, Sohayati AR, Hughes T, Smith C, Field HE, Daszak P (2011). Pteropid bats are confirmed as the reservoir [illegible] henipaviruses: A comprehensive experimental study of virus transmission. **Am J Trop Med Hyg** 85: [illegible]

c. Rahman SA, Hassan L, Epstein JH, [illegible] ZC, Yatim AM, Hassan SS, Field HE, **Hughes T**, Westrum J, [illegible], Daszak P, Henipavirus Ecology Research Group (2013). Risk factors for Nipah virus infection among pteropid bats, Peninsular Malaysia. **EID** 19: 51-60.

d. Lee M-H, Rostal MK, **Hughes T**, Sitam F, Lee C-Y, [illegible] N, Epstein JH. D[illegible] 2011. **EID** 21(7):1107-1113.

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

DTRA Epstein (PI) 05/01/17 – 4/30/22
Serological Biosurveillance for Spillover of Henipaviruses and Filovi[illegible]es at Agricultural and Hunting Human-Animal Interfaces in Pen[illegible]
Role: Co-PI

USA[illegible] Mazet (PI) [illegible]
PREDICT-2
The goal of [illegible]
characterize human risk behavior; analy[illegible]
Role: Country Coordinator Malaysia

Completed Research Support

USAID 1414374 (RDMA, Thailand) [illegible]
Infectious Disease E[illegible]ergence and Economics of Altered La[illegible]
The go[illegible] this cooperative agreemen[illegible]s to analyze how land use change affects disease [illegible] in SE Asia, and how ec[illegible] disease can be used t[illegible]
Role: Deputy Chief of Party