

## *Curriculum Vitae*

**Eric F. Donaldson, Ph.D.**

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### **A. ADDRESSES**

<i>Work Address:</i>	<i>Phone numbers:</i>
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### **B. EDUCATION**

- 1. University of North Carolina, Chapel Hill, NC**  
Ph.D. 2008 Microbiology/Immunology
- 2. Montana State University, Bozeman, MT**  
B.S. 2001 Microbiology
- 3. Flathead Valley Community College, Kalispell, MT**  
A.A/A.S. 1999 Science

### **C. POSITIONS HELD**

- 1. University of North Carolina, Chapel Hill, NC**
  - Dept. of Epidemiology Research Assistant Professor Aug. 2009 to present  
Research Associate (post doc) Apr. 2008 to Jul 2009
  - Dept. of Microbiology and Immunology Research Assistant (student) 2003-2008
- 2. Montana State University, Bozeman, MT**
  - Department of Microbiology Bioinformatician II (Research technician) 2000-2003
  - College of Letters and Sciences Bioinformatics advisor 2002-2003
  - Department of Genetics Lab assistant 1999-2000
- 3. Bozeman Daily Chronicle**
  - Sports Department Sportswriter 2000-2001
- 4. Flathead Valley Community College**
  - Administrative Department Service Learning/  
AmeriCorps Coordinator 1998-1999

## D. RESEARCH EXPERIENCE

### 1. Research Assistant Professor

I am currently employed as a Research Assistant Professor in the Department of Epidemiology, working in the lab of Dr. Ralph Baric. I am funded by the NIAID to conduct a study looking at the viruses in bats and studying how viruses cross the species barrier to emerge into new populations. In addition, I am working with Dr. Baric to resurrect bat coronaviruses to determine the cross species transmission potential of a variety of novel coronaviruses identified in bats. I am also funded as a Gillings Innovative Lab through the Gillings School of Global Public Health to do a norovirus evolution study looking at the different genogroups and genotypes of this virus to determine how this virus persists in human populations; and using structural bioinformatics and evolution to guide computational design of candidate vaccine strains.

### 2. Research Associate/Postdoctoral Scholar

I worked in Dr. Ralph Baric's lab from April 2008 through July 2009 as a research associate studying viral evolution and protein structure, and rational design of candidate vaccine strains. Advisor: Dr. Ralph S. Baric.

### 3. Graduate Research Assistant

Doctoral Dissertation: Computational and molecular biology approaches to viral replication and pathogenesis. My thesis focused on the integration of bioinformatics and molecular biology to generate informed hypotheses about coronavirus replication and norovirus pathogenesis, and these hypotheses were tested empirically in the laboratory. Duration: Fall 2003 to spring 2008. Advisor: Dr. Ralph S. Baric.

### 4. Undergraduate Research Project

- a. Integrative Graduate Education and Research Traineeship Program "Identification of Retroviral Agents in the Human Genome". 2001. Advisor: Dr. Marcie McClure.
- b. Lab assistant in the wheat genetics lab. My project was to grind up wheat infected with Wheat Streak Mosaic Virus. Isolate virus and conduct ELISAs.

## E. LAB TRAININGS AND CERTIFICATIONS

### 1. Trainings

	<b>Date received</b>	<b>Renewal</b>
a. Lab Environment Training	07-08-2003	
b. Radiation Safety Training	09-01-2004	
c. Biological Safety Training Level 3-SARS	2004 to present	Annually
d. Blood borne Pathogen Training	2004 to present	Annually
e. Formaldehyde Use Training	12-21-2004	
f. Managing Lab Generated Hazardous Waste	07-08-2003	
g. Respirator Training	2004 to present	Annually
h. Mouse Handling Techniques	2007	

### 2. Certifications

- a. Certified to work under Biological Safety Level 3 (BSL3) conditions.

## F. TEACHING EXPERIENCE

### 1. Flathead Valley Community College Service Learning Program

- a. Tutored high school students in chemistry and anatomy/physiology for 1 year
- b. Tutored college students in calculus for one semester

## **2. Prudential Youth Leadership Institute**

- a. Served as camp counselor and service project mentor

## **3. Flathead Valley Community College AmeriCorps Program**

- a. Designed and participated in three annual weeklong leadership camps designed to teach leadership skills to at-risk youth from ages 13-18. I designed the curriculum and the program and arranged service projects for approximately 50 teenagers each year.

## **4. Montana State University**

- a. Served as a Teachers assistant for a one-semester undergraduate Microbiology course. Taught labs and corrected papers.
- b. Taught a two-hour seminar on Bioinformatics for faculty, staff and students.
- c. Mentored two faculty members, three graduate students, and several undergraduates in bioinformatics methods such as sequence retrieval and analysis, multiple alignments, phylogenetic trees, etc.

## **5. University of North Carolina**

- a. Tutored three students in Medical Microbiology
- b. Served as a lecture TA for the Medical Microbiology course
- c. Served as a lab instructor for the Medical Microbiology laboratory
- d. Tutored three faculty, three postdocs and multiple graduate students in the use of bioinformatics methods.
- e. Guest Lecturer                      Graduate course in Virology                      Emerging viruses                      09/29/08
- f. Guest Lecturer                      Graduate course in Virology                      Viral Evolution                      10/06/08
- g. Summer of 2010 I served as a mentor for an undergraduate student in the SOLAR program.
- h. During the fall semester of 2010 I served as mentor to four undergraduate students in the departments of biology, chemistry, and computer science.
- i. Spring 2011: Guest lecturer in Epidemiology of Infectious Diseases course, presenting lectures on Norovirus and West Nile Virus.

## **6. Lee County NC High School**

- a. 2009 DNA Day ambassador teaching high school students about the genetics of Cystic Fibrosis

## **G. TEACHER TRAININGS AND CERTIFICATIONS**

### **1. College Teaching Certificate Program**

- a. Training Initiative in Biomedical and Biological Sciences and the UNC Center for Teaching and Learning. Certificate completed in 2007. Topics covered: Curriculum design, learning styles and teaching styles, teaching with technology, interactive instruction, engaging students in scientific discussions, and designing collaborative learning experiences.

### **2. Tools for Teaching Evolution**

- a. National Evolutionary Synthesis Center (NESCent) Synergistic Evolutionary Learning consortium: Evolution in ACTION (SELECTION). Completed in 2008. Topics covered: SELECTION's Lessons from Darwin's Laboratory, Applications of the Tree of Life, Exploring HIV evolution Lab Activity, Single Nucleotide Polymorphisms, and Population Genetics lesson as presented by the BioQUEST Curriculum Consortium.

### 3. Structural Bioinformatics Apprenticeship Program

- a. UNC Structural Bioinformatics Core Facility. Apprenticeship completed in 2008. Topics covered: Databases and search tools, multiple sequence alignment, phylogenetics, protein domains and motifs, structural motifs, Hidden Markov Models, homology modeling, the protein database, X-ray crystallography, Nuclear Magnetic Resonance, PyMol, molecular dynamics, and molecular docking.

## H. MEMBERSHIPS

### 1. American Society of Virology

## I. RESEARCH SUPPORT

### 1. Current Support

#### a. ARRA grant (SERCEB)

U54-AI057157	PI: Donaldson	9/12/09 – 8/31/11
NIH/NIAID	\$301,000	10% FTE

#### *Metagenomic Analysis of the virome of Eastern North American Bats*

The major goals of this project are to define the virome of seven to ten different bat species that cohabitate in one roost in Maryland to determine the viral population of each and define the role of orthologous receptors to viral cross-species transmission.

#### b. University Research Council grant

ACCT: 3-10119	PI: Donaldson	12/01/2009 - 11/30/2011
UNC URC	\$4,724	0% FTE

#### *Adaptation of a Human Norovirus to Gnotobiotic Calves*

The major goals of this project are to deep sequence human norovirus passage populations at different intervals to determine the adaptations that allow the human virus to adapt to the gnotobiotic bovine and porcine model systems. Once this adaptation is characterized, we will use the information to generate an infectious clone of the virus to develop an animal model for norovirus infection.

#### c. Gillings Innovation Lab (GIL) grant

Gillings Innovation Lab	PI: Donaldson	07/01/10 – 06/31/12
UNC Public Health Foundation	\$79,681	10% FTE

#### *Structure-based “Super Antigen” Vaccines for the Prevention of Childhood Diarrhea*

The major goals of this proposal are to use structural bioinformatics and computational biology to generate “super antigen” VLPs as candidate vaccine strains against noroviruses and all RNA viruses.

### 2. Pending Support

#### a. A multiple investigator R01 grant to the NIH

Proposal no: 11-1562 (R01)	PI: Ram Datar	07/01/11 – 06/30/16
NIH	\$555,000	15% FTE

*Development of Nanosensor Platform for SARS Diagnosis.* The goals of the proposal are to develop nanosensors that detect different coronaviruses and influenza viruses, and then test these under BSL3 conditions. The PI is a nanosensor expert with expertise in SARS-CoV, and we will provide computational biology support and testing of the system with samples.

### 3. Grants Under Preparation

#### a. A multiple investigator R01 grant to the National Science Foundation

Proposal type R01	PI: Donaldson	07/01/11 – 06/30/16
NSF	\$1,360,593	33% FTE

*Collaborative Research: Defining the Role of North American Bats in Virus Evolution and Dissemination within Various Habitats*

The major goals of this proposal are to determine the viral populations in different bat species that share a common habitat in the northeastern US, determine viral trafficking between bats and different vertebrates and invertebrates that share the same habitat, and develop computational tools to facilitate rapid response to cross species transmission events.

#### b. An R01 grant to the National Institutes of Health

Proposal type R01	PI: Donaldson	07/01/11 – 06/30/16
NIH	\$1,850,000	25% FTE

*Cross species emergence of coronaviruses from bats*

This work builds upon our ARRA grant, which allowed us to discover a novel Coronavirus in bats that is closely related to a human pathogen, human Coronavirus 229E. The major goals of the proposal are to characterize the coronaviruses found in bat species in the northeastern United States, by sequencing several bat fecal samples to determine the complete genomic sequences, isolate and/or synthetically resurrect these coronaviruses using in silico biology, and assess the ability of these viruses to emerge into the human host by using orthologous receptors and homologous innate immune factors such as interferon antagonists.

#### c. Team leader of Sequencing Team for DARPA Prophecy Grant

Three year collaborative grant (12 PIs)	PI: Marasco/Donaldson	04/01/11 – 03/31/14
Defense Advanced Research Projects Agency	\$1,760,000	25% FTE

*Studies of Coronavirus Evolution from the Molecular, Atomic and Computational Prospective.*

The major goals of the proposal are to characterize the coronavirus quasispecies using next generation sequencing to determine the variation of the population under normal in vitro conditions and in vivo conditions, and then under various selective pressures including monoclonal antibody neutralization and orthologous receptor switching to determine the evolutionary dynamics present in the population. These observations will then be used to determine which viral spike gene genotypes give rise to novel phenotypes that can be used to measure binding to the receptor and or the antibody or both. The ultimate goal of this high-risk grant is to provide an algorithm for predicting routes of coronavirus evolution in the future.

## J. PUBLICATIONS

1. Messer WB, Yount B, Hacker K, **Donaldson EF**, Wahala W, de Silva A, Baric R. Variable Neutralization Among Chimeric Genotype I-IV DENV3 E Glycoprotein Recombinant Viruses: Development of a Reverse Genetic System for Studying DENV-3 Strain Variation and Neutralization. 2010. (Manuscript submitted).
2. **Donaldson EF**, Haskew A, Gates JE, Huyhn J, and Frieman MB. Metagenomic Analysis of the Virome of three North American Bat Species: Viral Diversity Between Different Bat Species that Share a Common Habitat. *J Virol.* 2010 Dec;84(24):13004-18.
3. Lindesmith LC, **Donaldson EF**, and Baric RS. Demonstration of Norovirus GII.4 Strain Antigenic Drift. *J Virol.* 2010 Oct 27.

4. **Donaldson EF**, Long C, Yount B, Baric RS, and Sims, A. Mapping the determinants of HCoV-NL63 host range expansion via in vitro passage. 2010. *J Virol.* (Manuscript in preparation).
5. Krzysztof Pyrc, Amy C. Sims, Ronald Dijkman, Maarten Jebbink, Casey Long, Damon Deming, **Eric Donaldson**, Astrid Vabret, Ralph Baric, Lia van der Hoek and Raymond Pickles. Culturing the Unculturable: Human Coronavirus HKU1 Infects, Replicates, and Produces Progeny Virions in Human Ciliated Airway Epithelial Cell Cultures. *J Virol.* 2010 Aug 18.
6. **Donaldson EF**, Lindesmith LC, LoBue AD, and Baric, RS. Viral Shapeshifting: How Noroviruses Utilize Capsid Plasticity to Outwit the Human Immune Response. 2009. Invited review for *Nature Reviews Microbiology.* 2010 Mar;8(3):231-41.
7. Wahala W, **Donaldson EF**, Baric RS, and deSilva, AM. Differential neutralization of dengue virus type 3 by sero-type specific, envelope protein reactive antibodies. *PLoS Pathog.* 2010 Mar 19;6(3).
8. Sheahan T, Whitmore A, Rogers K, Ferris M, Rockx B, Funkhouser W, **Donaldson EF**, Collier M, Heise M, Davis N, Johnston R, and Baric RS. 2009. Successful vaccination Strategies that Protect Aged Mice from Lethal Influenza and Lethal Heterologous SARS-CoV Challenge. *J Virol.* 2010 Oct 27.
9. Lindesmith LC, **Donaldson E**, Leon J, Moe CL, Frelinger JA, Johnston RE, Weber DJ, Baric RS. Heterotypic humoral and cellular immune responses following Norwalk virus infection. *J VIROL.* 2010 FEB;84(4):1800-15.
10. Rockx B, **Donaldson EF**, Corti D, Sheahan TP, Lanzavecchia A and Baric RS. Escape from Human Monoclonal Antibody Neutralization in the Severe Acute Respiratory Syndrome Coronavirus Spike Glycoprotein. *J Infect Dis.* 2010 Mar 15;201(6):946-55.
11. Cannon JL, Lindesmith LC, **Donaldson EF**, Baric, R.S., and Vinjé J. Herd immunity to GII.4 noroviruses is supported by outbreak patient sera, 1985-2006. *J VIROL.* 2009 JUN;83(11):5363-74.
12. Miknis ZJ, **Donaldson EF**, Umland TC, Rimmer R, Baric, R.S., Schultz LW. SARS-CoV Nsp9 Dimerization is required for Viral Growth. *J VIROL.* 2009 APR;83(7):3007-18.
13. Becker M, Graham R, **Donaldson EF**, Rockx B, Sims AC, Sheahan TP, Burkett S, Pickles RJ, Baric, R.S. and Denison MR. Synthetic Reconstruction of an Infectious Bat SARS-like Coronavirus *Proc Natl Acad Sci USA.* 2008 Dec 16;105(50):19944-9.
14. Sheahan TP, Rockx B, **Donaldson EF**, Corti D, and Baric RS. The Plasticity of the SARS-CoV Spike Protein: Receptor Usage, Dependence, Evolution and Species Specificity of both Zoonotic and Human Tropic SARS-CoV. *J Virol.* 2008 Sep;82(17):8721-32.
15. **Donaldson EF**, Lindesmith LC, LoBue AD, and Baric RS. Norovirus Pathogenesis: Mechanisms of Persistence and Immune Evasion in Human Populations. *Immunol Rev.* 2008 Oct;225(1):190-211.
16. Sparks JS, **Donaldson EF**, Lu X, Baric, R.S., and Denison MR. A Novel Mutation in Murine Hepatitis Virus nsp5, the Viral 3C-like Proteinase, Causes Temperature-Sensitive Defects in Viral Growth and Protein Processing. *J Virol.* 2008 Jun;82(12):5999-6008.
17. **Donaldson EF**, Yount B, Sims AC, and Baric, R.S. Systematic Assembly of a Full-length Infectious Clone of Human Coronavirus NL63. 2008. *J Virol.* Dec;82(23):11948-57.

18. **Donaldson EF, Lindesmith LC\***, LoBue AD, Cannon JL, Vinje J, and Baric, R.S. Molecular Mechanisms Governing the Susceptibility and Persistence of Norovirus GII.4 Strains in Humans. 2008. PLoS Med. 2008 Feb;5(2):e31. \***Co-first authors.**
19. Rockx B, Corti D, **Donaldson EF**, Sheahan T, Stadler K, Lanzavecchia A, Baric R. Structural Basis for Potent Cross-Neutralizing Human Monoclonal Antibody Protection Against Lethal Human and Zoonotic SARS-CoV Challenge. J Virol. 2008 Apr;82(7):3220-35.
20. Rockx B, Sheahan TP, **Donaldson EF**, Sims AC, Harkema J, Heise M, Pickles RJ, and Baric RS. Synthetic Reconstruction of zoonotic and Early Human SARS-CoV isolates that Produce Fatal Disease in Senescent Mice. J Virol. 2007 Jul;81(14):7410-23.
21. Sheahan T, Rockx B, **Donaldson EF**, Sims A, Pickles R, Corti D, Baric R. Mechanisms of zoonotic severe acute respiratory syndrome coronavirus host range expansion in human airway epithelium. J Virol. 2008 Mar;82(5):2274-85.
22. **Donaldson EF**, Amy C. Sims, and Baric, R.S.. (2008). Systematic Assembly and Genetic Manipulation of the Mouse Hepatitis Virus A59 Genome. In Methods in Molecular Biology (vol. 454), SARS and Other Coronaviruses: Strategies and Protocols. Cavanagh, Dave, editor. The Humana Press Inc. Totowa, NJ, pp.
23. **Donaldson EF**, Sims AC, Graham R, Denison MR, and Baric, R.S. Murine Hepatitis Virus replicase protein nsp10 is a critical regulator of viral RNA synthesis. J Virol. 2007 Jun;81(12):6356-68.
24. **Donaldson EF**, Graham R, Sims AC, Denison MR, and Baric, R.S. Analysis of Murine Hepatitis Virus strain A59 temperature sensitive mutant TS-LA6 suggests that nsp10 plays a critical role in polyprotein processing. J Virol. 2007 Jul;81(13):7086-98.
25. Deming DJ, Sheahan TP, Yount BL, Davis N, Sims AC, West A, Heise M, Whitmore A, **Donaldson EF**, Curtis K, Johnston R, and Baric RS. Vaccine efficacy in senescent mice challenged with recombinant SARS-CoV bearing epidemic and zoonotic spike variants. PLoS Med. 2006 Dec;3(12):e525.
26. **Donaldson EF**, Deming DJ, Sims AC, and Baric, R.S. Mutational Analysis of MHV-A59 replicase protein nsp10. 2005. Proceedings of the Xth International Nidovirus Symposium
27. Sheahan TP, Sims AC, Deming DJ, **Donaldson EF**, Pickles RJ, and Baric RS. Construction and characterization of a civet cat like SARS-CoV. 2005. Proceedings of the Xth International Nidovirus Symposium
28. Baric RS, Sheahan TP, Deming DJ, **Donaldson EF**, Yount B, Sims AC, Roberts RS, Freeman M, and Rockx B. SARS CORONAVIRUS VACCINE DEVELOPMENT. 2005. Proceedings of the Xth International Nidovirus Symposium
29. McClure MA, Richardson HS, Clinton RA, Hepp CM, Crowther BA, **Donaldson EF**. Automated characterization of potentially active retroid agents in the human genome. Genomics. 2005 Apr;85(4):512-23.
30. McClure MA, **Donaldson EF**, Corro S. Potential multiple endonuclease functions and a ribonuclease H encoded in retroposon genomes. Virology. 2002 Apr 25;296(1):147-58.

## K. PRESENTATIONS

- 1. Bats and White-Nose Syndrome: Searching for clues in the bat virome.** NC Wildlife Resources Commission, December 8 2010, Jordan Lake, NC.
- 2. Computational Design of “Super Immunogen” Vaccines Against RNA Viruses.** Gillings School of Global Public Health Lunch with the Dean series. November 17, 2010, Chapel Hill, NC.
- 3. Mapping the Antigenic Determinants of GII.4 Norovirus Escape from Herd Immunity.** 4th International Calicivirus Meeting, Santa Cruz, Chile, October 18, 2010.
- 4. Bats and White-Nose Syndrome: Searching for clues in the bat virome.** NC Wildlife Resources Commission, September 2010, New Hills, NC.
- 5. The Bat Virome: Understanding the role of viral trafficking between different bat species.** American Society for Virology, July 2010, Bozeman, MT.
- 6. Metagenomics and *In Silico* Design: Using high throughput approaches to counter emerging viruses.** University of Florida, July 2010, Gainesville, FL.
- 7. Exploring the Intersection of Viral Cross Species Transmission and Bat Ecology.** Presentation given at the National Regional Centers of Excellence meeting, April 11-15, 2010, Las Vegas, NV.
- 8. Bats and Viral Ecology: Defining the Viromes of North American Bats.** Seminar at University of Maryland Center for Environmental Science Appalachian Laboratory, May 6, 2010, Frostburg, MD.
- 9. The Bat Virome: Understanding the Role of Viral Trafficking Between Different Bat Species.** Presentation to be given at the American Society for Virology Conference, July 17 – 21, 2010, Bozeman, MT.
- 10. Toward the Development of Animal Models for HCoV-NL63.** Presentation given at the American Society of Virology, July 2009, Vancouver, British Columbia.
- 11. Characterization of NL63 Infectious Clone Expressing the Reporter Gene, GFP.** Presentation given at the American Society for Virology 2008, Rochester, NY
- 12. Mapping the molecular determinants of norovirus genotype GII.4 evolution over 20 years.** Presentation given at the American Society for Virology, July 2007, Corvallis, OR.
- 13. Mutational Analysis of MHV-A59 replicase protein nsp10.** American Society for Virology, July 2006, Madison, WI.
- 14. Mutational Analysis of MHV-A59 replicase protein p15 (nsp10).** Xth International Nidovirus Symposium, June 2005. Colorado Springs, CO.

## L. POSTER PRESENTATIONS

1. Characterizing Viral Genomes in North American Bats. Moore, CJ, Baric, RS, and Donaldson, E.F. Annual Biomedical Research Conference for Minority Students in Charlotte, NC, November 11, 2010.
2. Metagenomic Analysis of the Virome of Eastern North American Bats. Bats and Emerging Viral Diseases conference, October 2009, Washington, DC.
3. Mapping the Molecular Determinants of Norovirus GII.4 Evolution Over 20 Years. Calicivirus Meeting, November 2007, Cancun, Mexico.
4. Evolution in Receptor Binding Site 2 May Direct the Emergence of Novel Norovirus GII.4 strains. May 26-30, 2007. RNA Plus Strand Meeting. Washington, DC.
5. Identification and characterization of Retroviral Agents in the Human Genome, Summer 2002, Intelligent Systems for Molecular Biology Conference, Ontario Canada.
6. Identification of Retroviral Agents in the Human Genome, Jan. 2002, Pacific Symposium of Biocomputing, Lihue, Kauai, Hawaii, USA.

## M. ADDITIONAL ABSTRACTS

1. Developing Human Coronavirus Vaccine Vectors: Mechanisms for Attenuating Genomes and Expressing Stable Foreign Antigens. Amy Sims, **Eric Donaldson**, Boyd Yount, Jr., Casey Long, Raymond Pickles, and Ralph Baric. Presented at the 2009 American Society for Virology Conference, Vancouver, BC Canada.
2. Derivation and Characterization of a Panel of Recombinant DEN3 E Variants using reverse genetics. Bill Messer, Boyd Yount, **Eric Donaldson**, Kari Hacker, Aravinda deSilva, and Ralph Baric. Presented at the 2009 American Society for Virology Conference, Vancouver, BC Canada.
3. Determination of the co-evolution of the GII.3 and GII.4 genocusters of Norovirus. Jen Cannon, **Eric Donaldson**, Ralph Baric, and Jan Vinje. Presented as a talk at the 2008 American Society for Virology Conference, Rochester, NY.
4. A Novel Temperature-Sensitive Mutation in the Murine Hepatitis Virus nsp5-3CLpro Causes Defects in Viral Growth and nsp5 Protein Processing. Mark R. Denison, **Eric F. Donaldson**, Xiaotao Lu, Ralph S. Baric, and Jennifer S. Sparks. Presented as a talk at the 2008 American Society for Virology Conference, Rochester, NY.
5. Recovery And Growth Of A Bat Sars-Like Coronavirus. M.M. Becker, R.L. Graham, **E.F. Donaldson**, X.T. Lu, R.S. Baric, and M.R. Denison. 2008 South East Regional Virology Conference, Atlanta, GA.
6. Dimerization and RNA binding by SARS-CoV Non-structural protein 9. Zachary J. Miknis, Wendy Franke, **Eric F. Donaldson**, Ralph S. Baric, Timothy C. Umland, L. Wayne Schultz. Poster presented at the 2007 RNA Plus Strand Meeting held in Washington, D.C.

## N. REFERENCES

**1. Ralph S. Baric, Ph.D.**

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