Jordan R. Willis

Ph.D.

"Somewhere, something incredible is waiting to be known." –
Carl Sagan

Info

Born	July 20th, 1985 at Norfolk VA (USA)	Citizenship	USA
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Profile

Objective Computational and molecular biologist working in the area of human antibodies and vaccines

- 8 years experience with molecular biology
- 5 years experience with molecular modeling
- 5 years experience with cell culture and protein production
- 4 years experience with high-throughput sequencing and analysis

Education

2008-2014 **Ph.D. Chemical and Physical Biology**, *Vanderbilt University Medical Center*, Nashville, TN.

Rational Antibody Design: From Mechanisms of Specificity, to Novel Vaccine Strategies
Advisors: James E. Crowe, Jr., M.D., Jens Meiler, Ph.D.

2004-2008 **B.S. Chemistry**, *Northwest Missouri State University*, Maryville, MO.
GPA 3.9/4.0

2004-2008 **B.A. Molecular Biology**, *Northwest Missouri State University*, Maryville, MO.
GPA 3.9/4.0

Specialized Computational Skills

Languages	PYTHON, JAVA, C++, SQL, LaTeX, CSH, BASH
Platforms	Unix, Linux, Apple
Database	MySQL, MongoDB, SQLlite
Tools	TeXShop, Eclipse IDE, Netbeans IDE, SCONS, Git, SVN, Illustrator, Genious, Microsoft Office, IPython Notebook, Sublime Text

Specialized Experimental Skills

Dry-Lab   Molecular modeling

- Development and application of the software suite Rosetta
- Molecular mechanisms with software suite MOE and AMBER
- Molecular viewing and scripting, PyMOL, Chimera, and RasMol
- Bioinformatics resources and tools

Dry-Lab   Proteomics

- Protein structure prediction
- Molecular mechanisms with software suite MOE and AMBER
- Post-translational modifications
- Similarity search and alignments
- Phylogeny and evolution

Wet-Lab   Influenza and human immunodeficiency virus (HIV) applications

- HIV neutralization assays
- Virus-like particles and pseudovirion production
- Viral isolation and purification

Wet-Lab   Protein expression and purification

- Novel cloning strategies
- Novel Pufication strategies
- Cell culture and maintenance

Wet-Lab   Biophysical characterization

- Biolayer interferometry
- ELISA
- Isothermal titration calorimetry

Research Experience

2009-2014   **Graduate Research Assistant**, *Vanderbilt University Medical Center*, Nashville, TN.

My thesis involves using computational design to answer specific questions in viral HIV immunology, with a focus on antibody design. The computational work was accomplished in the Meiler laboratory while the experimental laboratory work was conducted in the Crowe laboratory. My thesis work can be divided into four parts:

1. Multi-state antibody design to interrogate mechanisms for antibody polyspecificity. How do antibodies use a limited sequence repertoire to bind many antigens?

2. Molecular mechanisms of CD4-binding site escape for HIV-1 gp120. How does gp120 escape neutralization by two CD4-binding site-specific, broadly neutralizing antibodies, VRC01 and b12? We used computational characterization, homology modeling, and biophysical characterization to test our hypothesis.

3. Determine how closely antibody sequences from HIV-naive individuals are to broadly neutralizing antibodies against HIV. Using computational modeling, high-throughput sequencing, and bioinformatics tools, we designed antibodies from HIV-naive donor sequence pools that mimic broadly neutralizing antibodies with exceptionally long HCDR3s.

4. Computational design of antibodies with increased neutralization breadth against diverse natural variants of the influenza hemagglutinin stem.

2007-2008 **Undergraduate Research Fellow**, *University of Missouri, Department of Chemistry*, Columbia, MO.
Lead optimization drug discovery of hypoxic-cell targeting molecules that treat tumors. Using the pharmacaphore Tirapazamine as a scaffold, I used combinatorial synthesis techniques to add organic groups and evaluate structural activity relationships.

Teaching Experience

2012 **Instructor - Rosetta teaching worksop**, *Vanderbilt University*, Nashville, TN.
Developed protocol, taught background and gave hands-on demonstration for design for Rosetta teaching workshop 2012

2011 **Instructor - Rosetta teaching worksop**, *Vanderbilt University*, Nashville, TN.
Developed protocol, taught background and gave hands-on demonstration for protein docking for Rosetta teaching workshop 2011

2007-2008 **Laboratory teaching assistant**, *Northwest Missouri State University*, Maryville, MO.
General Chemistry 1 and 2

2005-2007 **Tutor - Talent Development Center**, *Northwest Missouri State University*, Maryville, MO.
Tutored in the following subjects: Physics I and II, general chemistry, organic chemistry, analytical chemistry, physical chemistry, statistics, algebra, and calculus.

Honors and Awards

Research and Scholarly Awards

2007-2008 NIH 5 T23 AI060571 HIV/AIDS Research Training Program

2010-2011 Steven's Research Scholarship, University of Missouri - $4,800

2007-2008 Mary Marie Smith Chemistry Scholarship, Northwest Missouri State University, $4,850/year

2006-2007 J. Gordon Strong Chemistry Scholarship, Northwest Missouri State University, $2,450/year

2004-2008 Tower Scholar, Northwest Missouri State University, $1,500/year

Travel Awards

2012 Keystone HIV Vaccine Symposium Scholarship

2012 Chemical and Physical Biology Travel Award

2011 IBC Antibody Engineering Symposium Scholarship

Recent Assigned Trainees

2013 Alex Sevy, Graduate student - Crowe laboratory

2013 Albert Cisneros, Graduate student - Crowe laboratory

2012 Martha Wall, Graduate student - Young laboratory

2012 Katherine Bradley, MPH student - University of California, Berkeley

2011 Jessica Finn, Graduate student - Crowe laboratory

2011 Mason Sanders, Summer undergraduate research intern

2010 Katherine Nichols, Graduate student - Kalams laboratory

Memberships

2004-2008	American Society of Collegiate Scholars
2006-2010	American Chemical Society
2008	Tri-Beta biology honor society

Abstracts and Presentations

2013 **Willis JR**, Crowe JE, Meiler J. Broadly neutralizing antibodies to HIV in HIV-naïve donor populations. The broadly neutralizing antibody problem. Chemical and Physical Biology Symposium, Vanderbilt University

2013 Finn JA, Nannemann, DP, **Willis JR**, Crowe JE, Meiler J. *De novo* modeling of antibody CDRH3 loops with constraints. RosettaCon

2012 **Willis JR**, Briney BS, Meiler J, Crowe JE. Potential paradigm shifts in HIV vaccine design using ultra high-throughput sequencing and antibody modeling. Chemical and Physical Biology Symposium

2012 Briney BS, **Willis JR**, Crowe JE. Somatic hypermutation-associated insertions and deletions reveal regions of antibody structural plasticity. Keystone symposium on HIV Vaccines

2012 Finn JA, **Willis JR**, Briney, BS, Crowe JE, Meiler J. Structural prediction of long complementarity determining region 3 loops. RosettaCon

2012 **Willis JR**, Briney BS, Meiler J, Crowe JE. Structure analysis of healthy donor repertoire confers sequences that match long complementarity deterring regions of broadly neutralizing antibodies. Keystone Symposium on HIV Vaccines

2011 Briney BS, **Willis JR**, Crowe JE. Genetic and functional analysis of the human anti-HIV antibody repertoire. Keystone Symposium on HIV Vaccines

2011 **Willis JR**, Crowe, JE, Meiler J. Multi-state design of antibody-antigen interactions confers conformational flexibility. RosettaCon

2011 Briney BS, **Willis JR**, Crowe JE. Genetic origin of long HCDR3s in the circulating antibody repertoire. IBC Life Sciences - Antibody Engineering & Therapeutics

2011 **Willis JR**, Crowe, JE, Meiler J. Structural basis for development of broadly neutralizing antibodies to HIV using computational predictions. Chemical and Physical Biology Symposium.

2011 **Willis JR**, Briney, BS, Crowe, JE, Meiler J. Antibody design infers optimal sequences for binding breadth and affinity maturation. IBC Life Sciences - Antibody Engineering & Therapeutics

2010 **Willis JR**, Crowe, JE, Meiler J. Constrained design of broadly neutralizing HIV antibody-antigen interactions. RosettaCon

2009 **Willis JR**, Meiler, J, Crowe JE. HIV gp160 targeted broadly neutralizing antibodies - modeling and design. RosettaCon

Research Publications

2011 Joyner AS, **Willis JR**, Crowe JE, Aiken C. Maturation-induced cloaking of neutralization epitopes on HIV-1 particles. *PLoS Pathog* **7(9)**: e1002234

2012   Briney BS, **Willis JR**, Crowe JE. Human peripheral blood antibodies with long HCDR3s are established primarily at original recombination using a limited subset of germline genes. *PLoS One* **7(5)**: e36750

2012   Briney BS, **Willis JR**, McKinney BA, Crowe JE. High-throughput antibody sequencing reveals genetic evidence of global regulation of the naïve and memory repertoires that extends across individuals. *Genes and Immunity* **13(6)**: 469-473

2012   Briney BS, **Willis JR**, Crowe JE. Location and length distribution of somatic hypermutation-associated DNA insertions and deletions reveals regions of antibody structural plasticity. *Genes and Immunity* **13(7)**: 523-529

2012   Briney BS, **Willis JR**, Hicar MD, Thomas JW, Crowe JE. Frequency and genetic characterization of V(DD)J recombinants in the human peripheral blood antibody repertoire. *Immunology* **131(1)**: 56-64

2013   **Willis JR**, Combs SA, DeLuca SL, DeLuca SH, Lemmon GH, Nguyen ED, Sheehan JH, Nannemann DP, Meiler J. Comparative modeling and small-molecule ligand docking in Rosetta. *Nature Protocols* **8(7)**: 1277-1298

2013   **Willis JR**, Briney BS, DeLuca, SL, Crowe JE, Meiler J. Human germline antibody gene segments encode polyspecific antibodies. *PLoS Computational Biology* **9**: e10030AA45L

In Submission or Preperation

Briney BS,**Willis JR**, Finn JA, McKinney BA, Crowe JE. Tissue-specific expressed antibody variable gene repertoires. Submitted. *PLoS One*

Willis JR, Sapparapu G, Singh V, King HG, Lebranche CC, Montefiori DC, Meiler J, Crowe JE. Redesigned PG9 variant monoclonal antibodies that exhibit enhanced HIV neutralizing potency and breadth. Submitted. *Nature Medicine*

Willis JR, Finn JA, Briney BS, Sapparapu G, King HG, Singh V, Lebranche CC, Montefiori DC, Meiler J, Crowe JE. HIV neutralizing heavy chain complementarity determining region 3 loops from HIV-naïve donors. In preparation

Willis JR, Crowe JE. PyIg - An open source graphical interface for analysis of high throughput sequencing of T-cell receptors and immunoglobulins. In preparation

References

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