



Jordan R. Willis

Ph.D.

Info

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

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

- 11 years experience with molecular biology
- 8 years experience with molecular modeling
- 8 years experience with computation and big data
- 7 years experience with cell culture and protein production
- 7 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, L^AT_EX, BASH, HTML, Javascript

Database Spark, Hadoop, MySQL, MongoDB, SQLite

Tools VIM, Jupyter Notebook, Git, Illustrator, Geneious, Microsoft Office, oh-my-zsh

Specialized Experimental Skills

Dry-Lab Molecular modeling and Big Data Processing

- Development and application of the software suite Rosetta
- GUI and Web development with Python
- Big data analytics with Python
- Protein structure prediction
- Post-translational modifications
- Similarity search and alignments
- Phylogeny and evolution

Wet-Lab Protein production and analysis

- HIV neutralization assays
- Virus-like particles and pseudovirion production
- Mammalian library display and preparation
- Cell sorting

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- Biophysical characterization of protein-protein interactions - ELISA, SPR, and Octet
- Amplicon library preparation for High-throughput sequencing

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-naïve individuals are to broadly neutralizing antibodies against HIV. Using computational modeling, high-throughput sequencing, and bioinformatics tools, I designed antibodies from HIV-naïve 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 pharmacophore Tirapazamine as a scaffold, I used combinatorial synthesis techniques to add organic groups and evaluate structural activity relationships.

Teaching Experience

2012 **Instructor - Rosetta teaching workshop**, *Vanderbilt University*, Nashville, TN.

Developed protocol, taught background and gave hands-on demonstration for design for Rosetta teaching workshop 2012

2011 **Instructor - Rosetta teaching workshop**, *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

- 2014- Ragon Institute Fellow
- 2007-2008 NIH 5 T23 AI060571 HIV/AIDS Research Training Program
- 2010-2011 Steven's Research Scholarship, University of Missouri
- 2007-2008 Mary Marie Smith Chemistry Scholarship, Northwest Missouri State University
- 2006-2007 J. Gordon Strong Chemistry Scholarship, Northwest Missouri State University
- 2004-2008 Tower Scholar, Northwest Missouri State University

Travel Awards

- 2012 Keystone HIV Vaccine Symposium Scholarship
- 2012 Chemical and Physical Biology Travel Award
- 2011 IBC Antibody Engineering Symposium Scholarship

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 determining 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 Preparation

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

James E. Crowe Jr., M.D.

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