BRIAN D. WEITZNER, PhD

Seattle, Washington

brian.weitzner@gmail.com phone: 856.316.8337

INDUSTRIAL EXPERIENCE

Senior Scientist — **Outpace Bio**
Computational and Structural Biology Lead — November 2020–Present

Senior Scientist — **Lyell Immunopharma**
Protein and Cell Engineering — January 2019–November 2020

RESEARCH EXPERIENCE

WRF Innovation Fellow — **Institute for Protein Design**
Adviser: Dr. David Baker — June 2016–December 2018

My work in the Baker Lab is focused on developing methods to enable computational *de novo* design of enzymes capable of catalyzing abiological chemical reactions. These methods will be put to the test in the lab to demonstrate their efficacy.

Postdoctoral Fellow — **Johns Hopkins University**
Adviser: Dr. Jeffrey J. Gray — March 2015–May 2016

During my postdoctoral year at Johns Hopkins I developed a new method for *de novo* CDR H3 loop structure prediction using structure-based constraints and fully incorporated it into Rosetta. Once this was in place, I determined a new set of best practices for computational antibody structure prediction and antibody–antigen docking and codified them in a protocols paper.

Graduate Research Assistant — **Johns Hopkins University**
Adviser: Dr. Jeffrey J. Gray — August 2009–March 2015

My studies focused on antibody structure prediction, namely accurate de novo modeling of the CDR H3 loop. I determined the weaknesses in existing structure prediction methods during a blind structure prediction challenge. To rectify these weaknesses, I performed statistical analyses of known structures of antibodies and non-antibody proteins to determine what governs the conformation of CDR H3 loops. Using the results from these analyses, I formulated a structure-based constraint that can be applied during de novo modeling to produce accurate models of CDR H3 loops. During this work I developed a new hypothesis regarding the functional utility of the C-terminal kink present in most antibody CDR H3 loops.

Undergraduate Research Assistant — Cornell University
Advisers: Dr. Matthew P. DeLisa & Dr. Jeffrey D. Varner — Nov. 2006–May 2009

I began a collaborative project between the DeLisa and Varner research groups with the aim of computa- tionally retargeting an E3 ubiquitin ligase. I performed in silico mutational and protein–protein docking studies. Loss of function predictions were successful, however full retargeting remains an open problem.

Undergraduate Research Assistant — Fox Chase Cancer Center
Adviser: Dr. Roland L. Dunbrack, Jr. — June 2005–August 2009

I studied dimerization motifs of cytosolic sulfotransferases by analyzing the unique interfaces in every available sulfotransferase crystal structure. I identified a small interface that had previously been shown to be biologically significant in every crystal structure, indicating the functional quaternary structure was contained in each crystal structure.

Howard Hughes Student Scientist — Fox Chase Cancer Center
Adviser: Dr. Roland L. Dunbrack, Jr. — September 2004–June 2005

As a high school student, I studied the agreement among quaternary structure assignments, namely the Protein Data Bank (PDB) and the Protein Quaternary Structure (PQS) server. The analysis showed that, at the time, neither server should be considered definitive, and instead both should be used.

EDUCATION

Johns Hopkins University — Baltimore, MD
PhD Chemical & Biomolecular Engineering — March 2015

Dissertation title: Next-generation antibody modeling

Cornell University — Ithaca, NY
BS Chem. & Biomol. Engineering, Minor Biomed. Eng., Cum Laude — May 2009

PUBLICATIONS

PEER-REVIEWED PUBLICATIONS

18. Le KH, Adolf-Bryfogle J, Klima JC, Lyskov S, Labonte JW, Bertolani S, Burman SSR, Leaver-Fay A, **Weitzner BD**, Maguire J, Rangan R, Adrianowycz MA, Alford RF, Adal A, Nance ML, Wu Y, Willis J, Kulp DW, Das R, Dunbrack RL, Schief W, Kuhlman B, Siegel JB, Gray JJ (2021) "PyRosetta Jupyter Notebooks Teach Biomolecular Structure Prediction and Design," The Biophysicist. 2(1), 108–122.

17. Guttman M, Padte NN, Huang Y, Yu J, Rocklin GJ, **Weitzner BD**, Scian M, Ho DD, Lee KK (2020) "The influence of proline isomerization on potency and stability of anti-HIV antibody 10E8," Sci. Rep. 10(1), 14313.

16. Koehler Leman J*, **Weitzner BD***, Lewis SM*, Adolf-Bryfogle J, Alam N, Alford RF, Aprahamian M, Baker D, Barlow KA, Barth P, Basanta B, Bender BJ, Blacklock K, Bonet J, Boyken SE, Bradley P, Bystroff C, Conway P, Cooper S, Correia BE, Coventry B, Das R, D JRM, DiMaio F, Dsilva L, Dunbrack R, Ford AS, Frenz B, Fu DY, Geniesse C, Goldschmidt L, Gowthaman R, Gray JJ, Gront D, Guffy S, Horowitz S, Huang P, Huber T, Jacobs TM, Jeliazkov JR, Johnson DK, Kappel K, Karanicolas J, Khakzad H, Khar KR, Khare SD, Khatib F, Khramushin A, King IC, Kleffner R, Koepnick B, Kortemme T, Kuenze G, Kuhlman B, Kuroda D, Labonte JW, Lai JK, Lapidoth G, Leaver-Fay A, Lindert S, Linsky T, London N, Lubin JH, Lyskov S, Maguire J, Malmström L, Marcos E, Marcu O, Marze NA, Meiler J, Moretti R, Mulligan VK, Nerli S, Norn C, Ó'Conchúir S, Ollikainen N, Ovchinnikov S, Pacella MS, Pan X, Park H, Pavlovicz RE, Pethe M, Pierce BG, Pilla KB, Raveh B, Renfrew PD, Burman SSR, Rubenstein A, Sauer MF, Scheck A, Schief W, Schueler-Furman O, Sedan Y, Sevy AM, Sgourakis NG, Shi L, Siegel JB, Silva D, Smith S, Song Y, Stein A, Szegedy M, Teets FD, Thyme SB, Wang RY, Watkins A, Zimmerman L, Bonneau R. (2020) "Macromolecular modeling and design in Rosetta: recent methods and frameworks," Nat. Methods. 17, 665–680.
(* equal contribution authors)

15. Koehler Leman J*, **Weitzner BD***, Renfrew PD, Lewis SM, Moretti R, Watkins AM, Mulligan VK, Lyskov S, Adolf-Bryfogle J, Labonte JW, Krys J, RosettaCommons Consortium, Bystroff C, Schief W, Gront D, Schueler-Furman O, Baker D, Bradley P, Dunbrack R, Kortemme T, Leaver-Fay A, Strauss CEM, Meiler J, Kuhlman B, Gray JJ, Bonneau R (2020) "Better together: Elements of successful scientific software development in a distributed collaborative community," PLoS Comput. Biol. 16(5): e1007507.
(* equal contribution authors)

14. **Weitzner BD***, Kipnis Y*, Daniel AG*, Hilvert D, Baker D (2019) "A computational method for design of connected catalytic networks in proteins," Protein Sci. 28: 2036–2041.
(* equal contribution authors)

13. Ford AS, **Weitzner BD**, Bahl CD (2019) "Integration of the Rosetta suite with the python software stack via reproducible packaging and core programming interfaces for distributed simulation," Protein Sci. 29: 43–51.

12. Silva DA*, Yu S*, Ulge U*, Spangler JB*, Jude KM, Labão−Almeida C, Ali L, Quijano−Rudio A, Ruterbusch M, Leung I, Biary T, Marcos E, Walkey CD, **Weitzner BD**, Carter L, Stewart L, Riddell S, Pepper M, Bernardes GJL, Dougan M, Garcia KC, Baker D (2019) "De novo design of potent and selective mimics of IL-2 and IL-15," Nature. 565(7738), 186–191.
(* equal contribution authors)

11. Adolf-Bryfogle J, Kalyuzhniy O, Kubitz M, **Weitzner BD**, Hu X, Adachi Y, Schief WR, Dunbrack RL, Jr (2018) "Rosetta Antibody Design (RAbD): A General Framework for Computational Antibody Design," PLoS Comput. Biol. 14(4): e1006112.

10. **Weitzner BD***, Jeliazkov JR*, Lyskov S*, Marze N, Kuroda D, Frick R, Adolf-Bryfogle J, Biswas N, Dunbrack RL, Jr, Gray JJ (2017) "Modeling and docking antibody structures with Rosetta," Nat. Protoc. 12(2), 401–16.
(* equal contribution authors)

9. **Weitzner BD**, Gray JJ (2016) "Accurate structure prediction of CDR H3 loops enabled by a novel structure-based C-terminal constraint," J. Immunol. 198(1), 505–15.

8. Porter JR, **Weitzner BD**, Lange OF (2015) "A framework to simplify combined sampling modes in Rosetta," PLOS ONE 10(9): e0138220.

7. Alford RF*, Koehler Leman J*, **Weitzner BD**, Duran AM, Tilley DC, Elazar A, Gray JJ (2015) "An integrated framework advancing membrane protein modeling and design," PLoS Comput. Biol. 11(9): e1004398.
(* equal contribution authors)

6. **Weitzner BD**, Dunbrack RL, Jr, Gray JJ (2015) "The origin of CDR H3 structural diversity," Structure 23(2), 302–11.

5. **Weitzner BD***, Kuroda D*, Marze N, Xu J, Gray JJ (2014) "Blind prediction performance of RosettaAntibody 3.0: Grafting, relaxation, kinematic loop modeling, and full CDR optimization," Proteins 82(8), 1611–23.
(* equal contribution authors)

4. Lyskov S, Chou FC, Conchúir SÓ, Der BS, Drew K, Kuroda D, Xu J, **Weitzner BD**, Renfrew PD, Sripadeevong P, Borgo B, Havranek JJ, Kuhlman B, Kortemme T, Bonneau R, Gray JJ, Das R (2013) "Serverification of Molecular Modeling Applications: The Rosetta Online Server That Includes Everyone (ROSIE)," PLOS ONE 8(5): e63906.

3. Baugh EH, Lyskov S, **Weitzner BD**, Gray JJ (2011) "Real-time PyMOL visualization for Rosetta and PyRosetta," PLOS ONE 6(8): e21931.

2. Chaudhury S, Berrondo M, **Weitzner BD**, Muthu P, Bergman H, Gray JJ (2011) "Benchmarking and analysis of protein docking performance in Rosetta v3.2," PLOS ONE 6(8): e22477.

1. **Weitzner B**, Meehan T, Xu Q, Dunbrack R (2009) "An unusually small dimer interface is observed in all available crystal structures of cytosolic sulfotransferases," Proteins. 75(2), 1097–134.

NON-PEER-REVIEWED PUBLICATIONS AND CONTRIBUTIONS

5. Science Careers Staff (2017) "What career items are on your holiday wish list?" Science. doi:10.1126/science.caredit.aar5568.
(contributor)

4. Science Careers Staff (2017) "Scientists: What are you thankful for?" Science. doi:10.1126/science.caredit.aar5568.
(contributor)

3. UW_PostDoc_Union , r/Science (2017) "We're Forming a Postdoc Union at the University of Washington, Ask Us Anything!" The Winnower. 5: e150996.69034.

2. **Weitzner BD** (2017) "I am a United Academic Worker," Science. 358(6360), 266.

1. Bourne PE, Beran B, Bi C, Bluhm W, Dunbrack R, Prlic A, Quinn G, Rose P, Shah R, Tao W, **Weitzner B**, Yukich, B (2010) "Will Widgets and Semantic Tagging Change Computational Biology?" PLoS Comput. Biol. 6(2): e1000673.

INVITED SEMINARS AND TALKS

6. **Weitzner BD** (2018) "Best practices in collaborative software development: lessons learned in the Rosetta Commons" Institute for Disease Modeling, Bellevue, WA.

5. **Weitzner BD** (2016) "Computer-guided prediction and validation of antibody structures" Roundtable, America's Antibody Congress, San Diego, CA.

4. **Weitzner BD**, Gray JJ (2015) "Next-generation antibody modeling" Seminar, Institute for Cellular and Molecular Biology, University of Texas at Austin, Austin, TX.

3. **Weitzner BD**, Gray JJ (2014) "Next-generation antibody modeling" Seminar, Center for Biomolecular Structure and Dynamics, University of Montana, Missoula, MT.

2. **Weitzner BD**, Dunbrack RL, Gray JJ (2014) "The origin of CDR H3 structural diversity" Vortrag, Fakultät für Chemie, Technische Universität München, Munich, Germany.

1. **Weitzner BD**, Gray JJ (2013) "Computational structure prediction, docking and design of antibodies" IBC Antibody Engineering and Therapeutics, Huntington Beach, CA. (delivered on behalf of JJG during his paternity leave)

CONFERENCE CONTRIBUTIONS

TALKS

7. **Weitzner BD**, Gray JJ (2015) "Producing physically realistic structural models with Rosetta-Antibody" America's Antibody Congress, San Diego, CA.

6. **Weitzner BD**, Kuroda D, Marze N, Xu J, Gray JJ (2013) "Benchmarking RosettaAntibody: Antibody Modeling Assessment II" Antibody Engineering and Therapeutics Conference, Huntington Beach, CA.

5. **Weitzner BD**, Roland RL, Gray JJ (2013) "Kinked CDR H3-like loops are common" AIChE Annual Conference, San Francisco, CA

4. **Weitzner BD**, Dunbrack RL, Gray JJ (2013) "Antibodies are proteins too!" Rosetta Conference, Leavenworth, WA.

3. Lyskov S, **Weitzner BD**, Gray JJ (2011) "PyRosetta 2.0: I can make a new score term in 6 lines!" Rosetta Conference, Leavenworth, WA.

2. **Weitzner BD**, Leaver-Fay A, Kulp D, Lyskov S (2010) "Using PyRosetta for research" Rosetta Conference, Leavenworth, WA. [workshop]

1. **Weitzner BD**, Baugh EH, Gray JJ (2010) "PyMOL–PyRosetta Integration" Rosetta Conference, Leavenworth, WA.

POSTERS

8. **Weitzner BD**, Kipnis Y, Daniel AG, Macdonald D, Baker D (2018) "*De novo* generation of fully-connected enzyme active sites" Rosetta Conference, Leavenworth, WA.

7. **Weitzner BD**, Baker D (2017) "Terminal disulfide bond to stabilize TIM $(\beta/\alpha)_8$ barrels" Rosetta Conference, Leavenworth, WA.

6. **Weitzner BD**, Gray JJ (2016) "Accurate structure prediction of CDR H3 loops enabled by a structure-based C-terminal constraint in Rosetta" AIChE Annual Conference, San Francisco, CA.

5. **Weitzner BD**, Dunbrack RL, Gray JJ (2015) "*De novo* CDR-H3 loop structure prediction using a structurally derived kink constraint" Rosetta Conference, Leavenworth, WA.

4. **Weitzner BD**, Dunbrack RL,Gray JJ (2015) "The origin of CDR H3 Structural Diversity" Biophysical Society Meeting, Baltimore, MD.

3. **Weitzner BD**, Dunbrack RL, Gray JJ (2014) "CDR H3 loop prediction" Rosetta Conference, Leavenworth, WA.

2. **Weitzner BD**, Dunbrack RL, Gray JJ (2012) "Are CDR H3 loops special?" Rosetta Conference, Leavenworth, WA.

1. **Weitzner BD**, Dunbrack RL, Gray JJ (2011) "Accessing the conformation space of long CDR H3 loops through β-turn detection" Rosetta Conference, Leavenworth, WA.

SELECTED HONORS AND AWARDS

Washington Research Foundation Innovation Fellowship	2016
RosettaCon XIII Best Poster Award	2015
JHU ChemBE Department Graduate Student Award	2015
Rosetta Service Award: Instructor at 1st Rosetta Boot Camp	2013
Rosetta Service Award: Transitioned Rosetta to a new VCS	2013
American Institute of Chemists Student Award	2009
1st place National AIChE Car Competition	2008
Howard Hughes Medical Institute Student Scientist	2004–2005
Eagle Scout	2003

FUNDING

1. Awarded a Washington Research Foundation Innovation Postdoctoral Fellowship 6/1/2016–11/15/2018, funds 100% of salary, benefits and includes a budget for research expenses.

2. Contributed to and secured NIH 5R01-GM078221, "Prediction of the structure of therapeutic antibodies with their antigens," 9/1/2012–8/31/2016, $1,241,054 ($821,600 direct). Specifically responsible for the development of Aim 1: Improve prediction of long, hypervariable CDR H3 loops.

   Work toward this aim led to four first-author publications: (1) "The origin of CDR H3 structural diversity" with RLD, and JJG; (2) "Blind prediction performance of RosettaAntibody 3.0: Grafting, relaxation, kinematic loop modeling, and full CDR optimization" with DK, NM, JX, and JJG; (3) "Accurate structure prediction of CDR H3 loops enabled by a novel structure-based C-terminal constraint" with JJG; and (4) "Modeling and docking antibody structures with Rosetta" with JJR, SL, NM, DK, RF, JA, NB, RLD, and JJG.

TEACHING EXPERIENCE

Guest Lecturer, Engl 182 — **University of Washington**
Multimodal Composition — Fall 2017

This course introduces the study and practice of strategies and skills for effective writing and argument in various situations, disciplines, and genres with an explicit focus on how multimodal elements of writing work together to produce meaning. My lecture focused on how rhetorical appeals are used in various scientific disciplines, ways in which the scientific record incorporates subjectivity, and how to critique scientific writing.

Co-Instructor, Rosetta Boot Camp — **Carborro, NC**
An intense week-long crash course to developing in Rosetta — Fall 2017

This course is aimed at introducing the computer science concepts and architecture of Rosetta to graduate students and postdocs who have recently joined labs that develop Rosetta. After this week-long course, students should be able to use Rosetta to solve specific structure prediction and design problems as well as develop new methods tailored to a specific problem. I delivered six lectures and guided lab sessions.

Guest Lecturer, ChemBE 414/614 — **Johns Hopkins University**
Computational Protein Structure Prediction and Design — Fall 2014

This course is aimed at introducing the fundamental concepts in protein structure, biophysics, optimization and informatics that have enabled the breakthroughs in computational structure prediction and design to advanced seniors and interested graduate students. My role in this course was delivering a lecture on side-chain conformations, optimization and libraries. All course lectures are available on YouTube.

Co-Instructor, Rosetta Boot Camp — **Chapel Hill, NC**
An intense week-long crash course to developing in Rosetta — Spring 2013

This course is aimed at introducing the computer science concepts and architecture of Rosetta to graduate students and postdocs who have recently joined labs that develop Rosetta. After this week-long course, students should be able to use Rosetta to solve specific structure prediction and design problems as well as develop new methods tailored to a specific problem. I delivered three lectures and guided lab sessions. All course lectures are available on YouTube.

Co-Instructor, ChemBE 418 — Johns Hopkins University
Projects in the Design of a Chemical Car — Fall 2011

Undergraduate students work in small groups over the course of the semester to design and build a chemically powered vehicle that will compete with other college teams at the American Institute of Chemical Engineers (AIChE) Regional Conference. The students must design and construct the chassis as well as chemically powered propulsion and break mechanisms within the constraints of the competition. In addition, students will give oral presentation, write reports, and do thorough safety analysis of their prototypes. My role as a co-instructor was to challenge the students' designs, assist them in organizing their experiments and keeping on schedule to successfully construct their car.

Teaching Assistant, ChemBE 409 — Johns Hopkins Univeristy
Modeling, Dynamics and Control of Chem. and Biol. Systems — Fall 2010

This course introduces the modeling, dynamics, and control concepts necessary for the unsteady state analysis of biomolecular and chemical processes to seniors in the Chemical & Biomolecular Engineering program. Model construction for biomolecular and cellular systems including pharmacokinetic model- ing, biomolecular modeling using the central dogma of biology/control of gene expression, large scale biosimulation. I held office hours, proctored exams, ran a lab assignment and assisted students with model analysis using Matlab.

Teaching Assistant, ChemBE 414/614 — Johns Hopkins University
Computational Protein Structure Prediction and Design — Spring 2010

This course is aimed at introducing the fundamental concepts in protein structure, biophysics, optimization and informatics that have enabled the breakthroughs in computational structure prediction and design to advanced seniors and interested graduate students. My role in this course was running the weekly laboratory sessions as well as grading homework assignments.

Teaching Assistant, ChemE 3900 — Cornell University
Chemical Kinetics and Reactor Design — Spring 2009

This course is aimed at junior-level undergraduates to introduce the study of chemical reaction kinetics and principles of reactor design for chemical processes. The students develop a molecular-level understanding of chemical reaction kinetics, practical approaches to modeling complex reactions, and the ability to construct mathematical models to predict system behavior from first principles. With these tools in hand, the students learn to optimize reactor design with regard to multiple performance criteria. My role in this course was presenting problems along with solutions in weekly recitation sessions.

Teaching Assistant, ChemE 1120 — Cornell University
Introduction to Chemical Engineering — Fall 2008

This course introduces freshman undergraduate students to design strategies for contemporary chemical and biomolecular engineering. Methods for analyzing designs, mathematical modeling, empirical analysis by graphics, and dynamic scaling through dimensional analysis are also covered in the context of assessing product quality, economics, safety, and environmental issues. My role in this course was grading assignments and presenting problems along with solutions in weekly recitation sessions.

SCIENTIFIC LEADERSHIP

Elected Member of Bargaining Committee, UAW Local 4121 — 2018
Negotiated the first contract for University of Washington Postdocs. Required gaining detailed knowledge of the financial operations of a large university as well as negotiation and leadership skills.

Rosetta Commons Diversity and Inclusivity Committee — 2018
Collaboratively developed diversity and inclusivity policies and programs within the Rosetta Commns and for the annual Rosetta Conference.

Recruiter, Grace Hopper Celebration — 2017
Helmed a booth at the Grace Hopper Celebration of Women in Computing with the aim of recruiting talented undergraduates, prospective graduate students, and postdoctoral candidates with a background in computer science to apply for the NSF-funded Rosetta REU Site program, or positions in Rosetta-focused labs around the world.

Developed RosettaCon Code of Conduct — 2014
Led the development and implementation of Code of Conduct for RosettaCon to promote diversity. Served on the incident reporting panel 2014–2015.

Rosetta Boot Camp, Course Co-director — 2013
Identified need for training graduate students and postdocs. Helped developed curriculum to introduce students to Rosetta.

Undergraduate Research Mentor — 2012–2014
Mentor to four undergraduate researchers in the Gray Lab

Organizer, Rosetta Developer Meeting — 2012
Arranged the program, travel, lodging and meals

ACTIVITIES AND OUTREACH

Volunteer, Science at the Market — 2017
Booth at the U-District farmers market to discuss science with community members

Judge, Mount Royal Middle School Science Fair 2015
Evaluated middle school students' projects based on understanding and use of scientific thought

Volunteer, STEM Achievement in Baltimore Elem. Schools 2013–2015
Monthly visits to a Baltimore City elementary school to facilitate learning STEM skills

Runner, Baltimore Marathon 2012

Member, Extreme Rosetta Workshop (XRW) Team 2010–2011
A small team of developers gathered to overhaul the structure of the Rosetta source code

Volunteer at the Ricky Myers Day of Service Fall 2010
A city-wide day of service to clean parks, plant gardens, repair homes and more

Member, JHU ChemBE Department STEM outreach group 2009–2013
Visits to a Baltimore Recreation Center to teach STEM through demonstrations and activities

Captain of the AIChE Car Team, Cornell University 2008–2009
Leader of the team, organized various sub-groups and kept the project on schedule

Member of the AIChE Car Team, Cornell University 2006–2008
A project team that builds a shoe box-sized car that is powered and stopped by chemical reactions