Valerie Daggett

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EDUCATION

Reed College

B.A. Chemistry

University of California, San Francisco

Ph.D. Pharmaceutical Chemistry with Irwin Kuntz and Peter Kollman

Stanford University

Structural Biology, Postdoctoral Fellow with Michael Levitt (2013 Chemistry Nobel Laureate)

PROFESSIONAL EXPERIENCE

University of Washington

Professor of Bioengineering (9/07- present) Director of the Biomolecular Structure and Design Program (7/07-6/10) **Professor of Medicinal Chemistry** (7/03-9/07) Adjunct Professor of Chemical Engineering (1/16-present) Adjunct Professor of Biochemistry (7/00-present) Adjunct Professor of Biomedical and Health Informatics (7/02-present) Adjunct Professor of Bioengineering (2/05-9/07) Member of Biomolecular Structure and Design Program, now called the Biological *Physics, Structure and Design Program* (9/96-present) Member of Molecular Biophysics Program (6/93-present) *Member of Neuroscience Program* (5/02-present) Member of the Biomedical and Health Informatics Program (6/00-present) Member of the Computational Molecular Biology Program (6/05-present) Member of Sackler Scholars Program Member of Center for Nanotechnology Affiliate Member of eScience Institute Associate Professor of Medicinal Chemistry (7/98-6/03) Assistant Professor of Medicinal Chemistry (1/93-6/98)

Lund University, Sweden

Lise Meitner Visiting Professorship, 2010 Lunds Tekniska Högskola and Faculty of Engineering, Biophysical Chemistry and Center for Molecular Protein Science. Host: Professor Mikael Akke

Cambridge University and Medical Research Council, UK

Visiting Professor, Chemistry Department and Center for Protein Engineering, 2002 Member of the Room, Gonville & Caius College Host: Sir Alan Fersht

Stanford University, Department of Structural Biology Staff Research Associate (4/92-1/93) Postdoctoral Fellow (6/90-3/92) Advisor: Professor Michael Levitt

University of California, S.F., Department of Pharmaceutical Chemistry

Physical Chemistry Teaching Assistant (9/86-5/87)
Physical Chemistry Tutor (9/88-12/88)
Graduate Student (9/85-6/90)
Advisors: Professors Irwin Kuntz and Peter Kollman

Triton Biosciences, Inc.

Consultant (9/88-9/89) General force field issues and generation of NMR structures.

Rutgers University, Department of Biochemistry and Microbiology

Research Assistant (12/83-9/85)

Development of 2-D electrophoresis methods to screen for the existence of dioxins in the blood of veterans exposed to Agent Orange.

Reed College, Chemistry Department

Senior Thesis Research (5/82-5/83). Deamidation of proteins and the possible effects of modification on protein folding.

HONORS AND FELLOWSHIPS

- College of Fellows, American Institute of Medical and Biological Engineering, elected 2017. Elected for outstanding contributions to protein engineering and design via the characterization of protein unfolding and structural changes linked to disease.
- Biophysical Society Fellow, 2011, Elected for technical innovations and improvements in the field of molecular dynamics simulation.
- US Department of Energy (DOE) Innovative and Novel Computational Impact on Theory and Experiment (INCITE) award for research in "Molecular Dynameomics." Award of 2 million CPU hours, 2005. (one of three awards in the country)

DOE National Research Energy Scientific Computing Center Award of >25 M hours since 2006.

Two papers from my group were in the 'Top 5' Downloads from the *Journal of Molecular Biology* in 2005.

National Academy of Sciences: Participated in the First Annual Japanese-American National Academy of Sciences' Frontiers of Science Symposium, August, 1998; Invited to participate in the National Academy of Sciences' Frontiers of Science Symposium, November, 1996 (I was unable to attend); Sackler NAS Colloquium, Frontiers in Bioinformatics: Unsolved Problems and Challenges, 2004, invited participant and session chair.

Young Investigator Award, Office of Naval Research (5/95-4/98), renewed as grant (1/99-12/01, 1/02-9/05, 10/05-9/08).

Invited to Office of Naval Research 50th Anniversary Symposium as a representative of work they are supporting, National Academy of Sciences, 1996.

Office of Naval Research, Two DURIP Equipment Awards (8/96-7/97 and 4/98-3/99).

FIRST Award, National Institutes of Health (8/95-7/00), renewed as R01 and still in effect

Co-PI on NIH Program Project Grant on Prion Diseases, Stanley Prusiner, P.D., Fred Cohen, co-P.I. (1/93-12/98).

American Health Assistance Foundation, Alzheimer's Disease Research Program, two awards (4/93-3/95, 4/95-3/97).

National Science Foundation, RPG Award (7/94-6/95).

Petroleum Research Fund, American Chemical Society, Grant (2/94-8/96).

Sandoz Foundation for Gerontological Research, Grant (5/94-5/95).

Jane Coffin Childs Foundation Postdoctoral Fellowship, (7/90-7/93).

Two separate fellowships from the Katherine McCormick Fund, Stanford University (10/90-10/91, 10/92-10/93).

National Institutes of Health Postdoctoral Fellowship (1990, declined).

Graduate Opportunity Fellowship, University of California, S.F. (9/85-9/86).

Coca Cola Academic Scholarship, Reed College, (9/79-6/81).

Oregon Scholar, Reed College, (9/79-5/83).

PROFESSIONAL ACTIVITIES AND SERVICE

Senior Editor of <i>Protein Engineering Design and Selection (PEDS)</i> with Alan Fersht (January
2004-present)
Editorial Boards (current): Biochemistry (2003-present), Structure (1995-present), Current
Opinion in Structural Biology (2012-present).
Board of Reviewing Editors of <i>eLife</i> , 2012 – 2015.
External Advisory Committee, Training Grant in Molecular and Cellular Biology, Washington
State University, 2012 – present.
Member of NIH Macromolecular Structure and Function B Study Section, July 2005 - 2008.
Contributing faculty member to 'Faculty of 1000 Biology', February 2005 – June 2007.
Co-Editor with Alan Fersht of Current Opinion in Structural Biology issue on Folding and
Binding, 2007 and 2009.
Elected Biophysical Society Council Member, 2007-2010.
Elected Vice-Chair (2015) and Chair (2017) Gordon Research Conference on Computational
Aspects of NMR.
Elected Chair of 2009 Cellular Osmoregulation Gordon Conference.Vice Chair 2007.
Chair of 2004 Biopolymers Gordon Conference.Vice Chair 2002.
Co-organizer of the 2002 Protein Society Meeting.
Editor of a 2003 volume on Protein Simulations for Advances in Protein Chemistry
Editorial Boards (past): Principal Editor for <i>TheScientificWorld</i> (2000-2001), Structural Biology
section of Biomed Central, electronic publications (2001-2003), Protein Science (1996-
1999, 2000-2003), Biomedical Computation Review (BCR) (2005-2014).
Participant/lecturer for Royal Society Discussion Meeting on New Science from High
Performance Computing, I represented Biomolecular Modeling (10/2001)
Elected to the Nominating Committee for the Protein Society (2000-2003)
Steering and Admissions Committees (1994-2002) and founding member of interdisciplinary
program for Biomolecular Structure and Design at U. of WA
Acting Director for Biomolecular Structure and Design Program, 7/99 – 6/00.

Member of the Biophysics Group at U. of WA since 1993, Selection Committee for Trainees for NIH Biophysics Training Grant, 1995, 1998, 1999, 2003.

Member of the Steering Committee, Molecular Biophysics Training Grant, U of WA (2002-2006) Member of the Biomedical and Health Informatics Program at U. of WA since 2000, Selection

Committee for Trainees and Admissions.

- Member of the Steering Committee, Computational Molecular Biology Program, U of WA (2013present)
- Manuscript reviews: Biochemistry, Biopolymers, Biophysical Journal, Journal of Molecular Biology, Proceedings of the National Academy of Sciences, Structure, Protein Engineering Design and Selection, Protein Science, Chemical Physics, Journal of Computational Physics, Nature Structural Biology, Nature, Journal of Biological Chemistry, International Journal of Quantum Chemistry, Journal of Computational Chemistry, Journal of Chemical Theory and Computation, Journal of Physical Chemistry, Journal of the American Chemical Society, Nature Methods, Royal Society of Chemistry: Chemical Science, Bioessays, plus others on an occasional basis.
- Professional Societies: American Chemical Society, Protein Society, Biophysical Society, International Society for Computational Biology.
- Special Programs Grant Reviews: National Institutes of Health; National Academy of Sciences/ National Research Council; Department of Energy; Research Corporation--A Foundation for the Advancement of Science; Medical Research Council, U.K., The Wellcome Trust, UK, Hereditary Disease Foundation, Biotechnology and Biological Sciences Research Council (BBSRC UK), Alzheimer's Association, and the European Research Council, plus other private and local foundations.
- Grant/Program Reviews NIH: Special Study Section Member for Project Site Visit, April 1997; Special Study Section Member for Human Genome RFA, July 1997; Special Study Section Member for Program Project Grant, March 2003; Ad hoc for BBCA, February 2003.
- Grant/Program Reviews DOE: Workshop addressing future of biological computations, July 2003 (could not attend), panel member to review INCITE proposals for 2007 (Nov. 2006).

External Reviewer for DOE Biofuel Center at Oak Ridge National Lab, October 2009.

- NSF Graduate Research Fellowship Program (GRFP) panelist 2017 (conflict), NSF and NIH requests for numerous grant proposal panels as ad hoc reviewer.
- BMES, Attended 2013 meeting as instructed by Chair. Co-Chair of session at 2013 annual meeting. On committee that reviewed abstracts and determined poster eligibility and chose platform talks for computational section for 2013 BMES Meeting.
- International Service Requests Grant and Program Reviews: Science Foundations of Ireland, the Netherlands, UK, EU, Sweden, Germany, Israel, Canada and others.
- Executive Advisory Committee for CCMB Training Grant at Washington State University, 2010present.

INVITED TALKS

Science in Medicine Seminar, UW, Seattle, WA, January 26, 2017

- CECAM Workshop: Challenges across Large-Scale Biomolecular and Polymer Simulations, Vienna, Austria, February 21-24, 2017
- Biophysics/Soft Matter Seminar Series, Physics Department, Simon Fraser University, Vancouver, Canada, March 29, 2017
- Nobel Foundation Symposium on Protein Folding: From Mechanisms to Impact on Cells, Stockholm, Sweden, June 11-14, 2017

- 2017 Colorado Protein Stability Conference, Breckenridge, CO July 18-20, 2017
- Protein Folding Symposium, Cambridge University, Cambridge, UK, September 4-7, 2017
- Chemistry Colloquium Series, New York University, NY, October 14, 2016
- Seminar, Graduate Program in Neuroscience, UW April 18, 2016
- Evolution of Cells, Genomes and Proteins, Singapore and Bintan, Indonesia, February 3-6, 2016
- 4th Prague Protein Spring Meeting, Prague, Czech Republic, May 5-8, 2016
- NII Shonan Meeting, Japan, September, 2016.
- University of California, Irvine, Department of Molecular Biology and Biochemistry, January 23, 2015.
- Swedish University, Stockholm, Seminar and Opponent for Swedish Doctoral Defense, April 17, 2015.
- Gordon Research Conference, Computational Aspects of NMR, Discussion Leader, June 7-12, 2015.
- CECAM Meeting, Biomolecules under Nonnatural Conditions, Stuttgart, March 9-13, 2014.
- Faraday Discussion Meeting, Royal Society of Chemistry, Macromolecular visualization and visual analytics, Nottingham, UK, May 7-9, 2014.
- Third Prague Protein Spring Meeting, Prague, Czech Republic, May 10-13, 2014.
- Oxford Biophysics Group, Oxford UK, May 2014.
- Bristol Chemistry Department, Bristol, UK May 2014.
- Canadian Chemistry Society Meeting, Vancouver, BC, June 1-5, 2014.
- ACS Regional Meeting, Missoula, MT, June 22-25, 2014.
- Lorne Protein Meeting, Lorne Australia, February 10-14, 2013.
- VIZBI 2013, International Meeting on Visualizing Biological Data, The Broad Institute of MIT and Harvard, March 20-22, 2013.
- Prion 2013, Banff, Canada, May 26-29, 2013.
- Gordon Research Conference on Computational Aspects of Biomolecular NMR, West Dover, Vermont, June 2-7, 2013
- Bioinformatics 2013, Society for Bioinformatics in northern European countries and the Polish Bioinformatics Society, Torun, Poland, June 26-29, 2013.
- BMES Meeting, Seattle, WA, Co-chair of a session of Bioinformatics, Computational and Systems Biology, September 25-28, 2013.
- Gibbs Conference, Illinois, October 5-8, 2013.
- 4th Latin American Protein Society Meeting, Puerto Varas, Chile, November 9-14, 2013.
- EMBO VIZBI workshop on Visualizing Biological Data, European Molecular Biology Laboratory, Heidelberg, Germany, March 7-9, 2012.
- 2nd Prague Protein Spring Meeting, Prague, Czech Republic, 5/3/12-5/6/12.
- Telluride Workshop on Protein Folding and Dynamics: From Experiment to Theory, Telluride, CO, 6/17/12-6/21/12 (unable to attend).
- BioVis 2012, The 2nd IEEE Symposium on Biological Data Visualization, Seattle, October 14-15, 2012.
- Neutron Dynamics Data Bank Workshop, Institut Laue, Grenoble, France, January 9-11, 2011.
- Cambridge Healthtech Institute's Inaugural Protein Data Integration and Interrogation Meeting as part of 10th Annual PepTalk Conference, San Diego, CA January 12-13, 2011.
- Computational Molecular Biology Seminar Series, UW, March 3, 2011.

US-Mexico Workshop in Biological Chemistry:Protein Folding, Misfolding and Design,

Universidad Nacional Autónoma de México, Mexico City, Mexico, March 18-21, 2011.

Frontiers in Macromolecular Simulations Symposium, Point Clear, Alabama, March 30-April 1, 2011.

- Gordon Research Conference on Computational Aspects of Biomolecular NMR, Il Ciocco, Italy, May 22-27, 2011.
- Dynamics, Function, and Design of Biological Macromolecules, Huenfeld, Germany, June 2-4, 2011.
- University of Toronto, September, 2011.
- International Biophysics Congress, Session on Protein Folding/Unfolding, Beijing, China, October, 2011.
- 3rd UW-KN Joint Symposium, South Korea, October, 2011.
- IFIP International Conference on Bioinformatics at SVNIT, Surat, India, March 25-28, 2010 (declined, conflict).
- First Prague Protein Spring Symposium, Prague, Czech Republic, May 6-9, 2010.
- Seminar, Biophysical Chemistry, Center for Molecular Protein Science, Lund University, May 12, 2010.
- Seminar, D.E. Shaw Research, New York, June 9, 2010.
- Telluride workshop in protein folding, Telluride, CO, June 21-25, 2010 (declined).
- Frontiers of Protein Science, Shanghai Institute of Materia Medica, Chinese Academy of Sciences, Shanghai, China, July 1 16, 2010.
- Symposium in honor of Alan Fersht, Cambridge, England, September 23-25, 2010.
- Advances in Amyloid Sciences: From Disease to Devices. Sandbjerg Estate (University of Aarhus), Denmark September 27-29, 2010.
- CECAM Workshop on Protein Folding Dynamics, Lausanne, Switzerland, October 4-7, 2010. Protein Folding Symposium, Rome, December 1-5, 2010.
- Other service travel: Biophysical Society Meeting to attend Council Meeting, February, 2010.
- Biophysical Society Professional opportunities for women (CPOW) Committee, Panel discussant, February 28 – March 4, 2009 (declined, conflict).
- PrPCANADA 2009 Canada's Prion Research Conference from March 1-3, 2009, in Edmonton, Alberta, Canada.
- Pittcon 2009, Novel Biospectroscopy for Amyloid Diseases, Chicago, March 8-13, 2009.
- Ions and Osmolytes, ACS meeting in Salt Lake City (declined, conflict).
- Seminar School of Molecular Biosciences, Washington State University, Pullman, WA, April 29 May 1, 2009.
- Seminar Instituto de Biotecnología, Cuernavaca, Mexico, March, 2009 (declined, conflict).
- Beijing Kavli Institute for Theoretical Physics program on protein function and Dynamics, July 1 – August 15, 2009 (declined, conflict).
- Biochemical Engineering XVI, Burlington, Vermont, July 5-9, 2009 (declined, conflict).
- U.S. Department of Energy Large Scale Computing and Storage Requirements for Biological and Environmental Research. A Joint ASCR/BER/NERSC Workshop, Rockville, MD, May 6-7, 2009 (declined, conflict).
- 8th MERCURY conference on undergraduate computational chemistry, Hamilton College, August 2-4, 2009.
- Beckman Institute 20th Anniversary Symposium, Computational Biology --- The Next Decade, Urbana, IL September 20-23, 2009.
- Workshop on scientific opportunities in advanced modeling and simulation at the extreme scales in the biological sciences, Macromolecules, Proteins and Protein Complexes session, Chicago, IL, August 17-19, 2009 (declined, conflict).
- The Center for Biomolecular Structure & Dynamics Seminar, Missoula, MT, October 29, 2009.
- Sixth Frontiers Symposium in Macromolecular Simulations here at Georgia Tech, November 16-17, 2009.

- Other Work Travel: Annual council meeting for Biophysical Society, February, 2009; DOE Site visit at Oak Ridge National Labs, October, 2009.
- Gordon Research Conference on Protein Folding, Ventura, CA, January 6-11, 2008.
- Prion Research Network of Canada, February 4-6, Toronto, March 8, Vancouver (declined, conflict)
- University of Oregon, Eugene, March 11, 2008.
- Fibrous Proteins: Transforming structural knowledge into new materials, Melbourne, Australia, March 31-April 4, 2008.
- American Chemical Society Meeting, New Orleans, April 6-10, 2008 (declined, conflict).
- Gordon Research Conference, Computational Aspects of Biomolecular NMR, Italy, May 18-23, 2008.
- Gordon Research Conference, Biopolymers, Rhode Island, June 8-13, 2008.
- EMBO Conference on Protein Modeling, Paris, July 1-8, 2008.
- Human Frontiers of Science Annual Meeting, Berlin, July 6-9, 2008 (declined, conflict).
- American Chemical Society Meeting, Philadelphia, August 17-21, 2008 (declined, conflict).
- 8th KIAS International conference on Protein Structure and Function scheduled on 10/9/2008-10/11/2008 in Seoul, Korea.
- Biomedical High Performance Computing Leadership Summit 2008, Boston MA, Oct. 6-7 (declined).
- Jane Coffin Childs Annual Meeting, Connecticut, October 17-19, 2008.
- Structural Biology Partnership, North Eastern Structural Symposium, University of Connecticut, October 11, 2008 (declined, conflict).
- International Workshop on Biomaterials for tissue engineering and Biotechnological Applications, IIT Kharagpur India, November 22 - 24, 2008 (declined, conflict).
- Other Work Travel: Annual editorial board meeting for *Biochemistry*, October 2008; Annual council meeting for Biophysical Society, February, 2008; NIH MSFB study section, February and June, 2008.
- Indiana University, Seminar Chemistry Department and School of Medicine, March, 2007.
- Albert Einstein College of Medicine, Yeshiva University, Seminar Biophysics Department, March, 2007.
- Gordon Research Conference on Osmoregulation, France, June, 2007, declined, conflict with NIH study section meeting.
- American Chemical Society Meeting, Boston, declined, conflict, August, 2007.
- 2007 Frontiers of Macromolecular Simulations, Atlanta, GA, Nov, 2007.
- University of California, San Francisco, Biochemistry Seminar Series, October 2007.

Stanford University, Seminar, September, 2007.

- Other Work Travel: Annual editorial board meeting for *Biochemistry*, October 2007; Annual council meeting for Biophysical Society, February, 2007; Three meetings a year for NIH study section.
- Gordon Research Conference on Protein Folding, Ventura, CA, January 8-13, 2006.
- Keystone Meeting on Structural Biology, Keystone, CO, January 29- February 3, 2006.
- DARPA's Control of Protein Conformation Workshop, Arlington, VA, February 16-17, 2006 (declined, conflict with NIH study section meeting).
- Computational/Experimental Approaches to Protein Defects in Human Disease, Rutgers University, April 20-21, 2006.
- International Symposium on Biomolecules: Proteins, DNA/RNA, and Their Interactions, Taipei, Taiwan, June 19-20, 2006.
- EMBO Practical Course on Biomolecular Simulation, Pasteur Institute, Paris, June 28 July 5, 2006.

University of Texas Medical Branch, Neurology Department, Protein Misfolding Seminar Series, Spring, 2006.

Protein Folding in the Cell, FASEB Conference, Vermont, July 29 – August 3, 2006.

American Chemical Society Meeting, Alfred Bader Award Symposium, Award recipient Alan Fersht, San Francisco, CA, September 10-14, 2006.

CECAM workshop on Protein folding and misfolding: Bringing theory close to experiment, Lyon, Paris, September 26-29, 2006.

7th Congress of the World Association of Theoretically Oriented Chemists, Cape Town, South Africa, 16-21 January, 2005.

- Biophysical Society Annual Meeting, Chair and Speaker, Symposium on Protein Folding: Theory, Experiment and Design, Long Beach, CA, February 12-16, 2005.
- Science Forum Colloquium, University of Washington, March 4, 2005.
- Biophysical Aspects of Protein and Peptide Aggregation: Experiment and Theory, American Chemical Society Meeting Symposium, San Diego, March 13-17, 2005.
- Cornell Biophysics Colloquia Series, Cornell University, NY, March 30, 2005.
- Mayo Clinic, Biochemistry Seminar Series, Minnesota, April 5, 2005.
- Flexibility in Biomolecules Workshop, Tempe Arizona, May 2005 (declined, conflict)
- Instituto de Biocomputacion y Fisica de Sistemas Complejos, Universidad de Zaragoza, BIFI Colloquia, April 25-28, 2005.
- Symposium on Protein Folding, Dynamics and Function, Peking University, Beijing, China, 4-7 July 2005.
- Gordon Conference on Cellular Osmoregulation: Sensors, Transducers and Regulators, Salve Regina College in Newport RI, August 7-12.
- Telluride Summer Research Workshop on "Vibrational dynamics of biological molecules", August 13-20, 2005 in Telluride, CO (declined, conflict).
- XX Congress of the International Union of Crystallography, Florence, Italy, August 23-31, 2005. (not attending, conflict)
- CECAM workshop on 'Multiscale Modeling of Macromolecule/Membrane Interactions' in Lyon, France, August 29-31, 2005 (conflict, unable to attend).
- Spetsai Summer School, Protein Misfolding, Protein Modification and Age-Related Diseases, Spetses Island, Greece, 5-15 September 2005.
- International Molecular Graphics and Modelling Society (MGMS) Meeting, Biomolecular Simulations - from Prediction to Practice, Dublin, Ireland 11th-14th September 2005. (not attending, conflict)
- International Bunsen Discussion Meeting, 'Mechanically Induced Chemistry: Theory and Experiment', Tutzing near Munich, October 3 6, 2005 (not attending, conflict).
- Center for Computational Biology Seminar series at Washington University, St Louis, 7 October 2005.
- Prion 2005---Between fundamentals and society's needs. German TSE Research Platform, Dusseldorf, Germany, October 19-21, 2005.
- Gordon Research Conference, Protein Folding Dynamics, Discussion Leader, Ventura, CA January 2004.
- Gordon Research Conference, Computational Aspects of Biomolecular NMR, January 2004 (conflict, declined)
- Southwestern Medical Center at Dallas, Molecular Biophysics Graduate Program Seminar Series, February 2004.
- Annual Suddath Symposium, Computational Biology, Georgia Institute of Technology, March, 2004.

- Isaac Newton Workshop 2004, Statistical Mechanics of Molecular and Cellular Biological Systems, Cambridge, UK, Spring 2004 (declined, conflict).
- Materials Research Society, Proteins as Materials, San Francisco, April 2004 (conflict, declined)
- Keystone Symposium, Frontiers in Structural Biology, Snowbird, Utah, April 2004 (conflict, declined)
- University of Maryland, College Park, Biochemistry Department, Student-selected speaker, May 2004.
- The Role of Theory in Biological Physics and Materials NSF Workshop, Tempe Arizona, May 2004 (declined, conflict)
- 91st Statistical Mechanics Conference, Rutgers University, May 2004 (declined, conflict)
- Dubrovnik 2004 Conference, From Solid State to Biophysics III, Dubrovnik, Croatia, June 2004. (declined, conflict)
- Elastin 2004, Third European Symposium, Manchester, UK, June 2004 (declined, conflict)
- FASEB Meeting on Folding in the Cell, Vermont, July 2004.
- Gordon Research Conference on Water and Aqueous Systems, New Hampshire, August 2004 (declined due to conflict)
- Hereditary Disease Foundation Meeting, Panel Member regarding structural properties of polyglutamine, Boston, MA, August, 2004.
- Yale University, MB&B Seminar Series, September 2004.
- VIP Scientific Forum of the International Internet, Processing, Systems for e-education/e-business, and Interdisciplinaries -2004 PESCARA Conference, Italy, July 2004 (declined, conflict)
- Congress on Tilted Peptides, Namur, Belgium, October 2004.
- Sackler Colloquia of the National Academy of Sciences, Frontiers in Bioinformatics: Unsolved Problems and Challenges, Irvine CA, October 2004. Session Chair.
- Protein Folding and Misfolding in Alzheimer's Disease, Satellite symposium of the Society for Neuroscience, organized by Elsevier and Neurobiology of Aging, October, 2004 (declined due to conflict)
- Karolinska Institute, Huddinge, Sweden, Seminar and external examiner for a dissertation, November, 2004.
- American Chemical Society Meeting, March 2003 (conflict, declined).

University of Pennsylvania, April 2003.

University of Arizona, April 2003.

Birthday Symposium for Alan Fersht, Cambridge University, April 2003.

- Johns Hopkins University, Spring 2003 (conflict, postponed)
- State University of New York, Spring 2003 (conflict, postponed)
- 19th International Congress of Biochemistry and Molecular Biology, Toronto, Canada, July 2003 (changed to Montreal, October 2003 because of SARS).
- DOE Symposium on Protein Folding and Structure Prediction, July 2003 (did not attend)
- CECAM Meeting, France, September 2003.
- Seoul Korea, September 2003 (declined, conflict)
- Duke University, November 2003.
- New York University, November 2003.
- 40th Anniversary Symposium of the Chinese University of Hong Kong, Hong Kong, China, December 2003.
- NSF Meeting on Folding, Function and Funnels, Co-sponsored by the US and Japanese National Science Foundations, Hawaii, January 2002.
- Gordon Conference, Protein Dynamics and Folding, Ventura, CA, January 2002.
- Program in Mathematics and Molecular Biology, Symposium on Modeling across the Scales-Atoms to Organisms, Santa Fe, NM, January 2002 (conflict, I had to decline).

Satellite Meeting of the Biophysical Society to honor Peter Kollman, San Francisco, February 2002.

- 42nd Sanibel Symposium, Saint Augustine, FL, February-March 2002.
- Lise Meitner Symposium, University of Lund, Sweden, Sponsored by the Nobel Committee for Chemistry, Organized in response to media discussions in Sweden regarding the lack of women laureates, March 2002.
- Annual American Chemical Society Meeting, Award Symposium for Tack Kuntz, Computers in Chemistry Award, Orlando, Florida, April 2002.
- Western Washington University, Chemistry Department Seminar Series, Bellingham, WA, April 2002.
- University of California, Santa Cruz, April 2002.
- CECAM Workshop on Protein Dynamics, Lyon, France, May 2002 (declined, conflict with teaching).
- Hereditary Disease Foundation workshop on Structural Studies of Huntingtin, Dedicated to the memory of Max Perutz, May, 2002.
- Javits Meeting on Prion Diseases, San Francisco, CA, May 2002.
- Department of Environment, Food and Rural Affairs, Transmissible Spongiform Encephalopathy Research Unit, UK, Workshop to discuss BSE and other TSE diagnostics, London, England, May 2002 (declined, conflict).
- Biopolymers Gordon Conference, Rhode Island, June 2002.
- FASEB Meeting on Folding in the Cell, Vermont, July 2002.
- Center for Biologically Inspired Materials and Materials Systems, Duke University, 2002 (conflict).
- Structural Informatics Symposium, Georgia State University, Fall, 2002 (declined, conflict)
- ACS Meeting, Symposium on Energy Landscapes of Proteins, Glasses and Clusters, San Diego, April 2001.
- Javits Meeting on Prion Diseases, San Francisco, CA, May 2001.
- International Center for Theoretical Physics, Protein Folding, Structure and Design, Trieste, Italy, June 2001 (conflict, I had to decline).
- Proteins Gordon Conference, New Hampshire, June 2001.
- Telluride Summer Workshop on Conformational Dynamics in Proteins, August 2001 (conflict, I had to decline)
- Protein Society Meeting, Philadephia, PA, July 2001.
- University of California, Berkeley, Structural Biology Seminar Series, September 2001.
- Royal Society Discussion Meeting: New Science from High Performance Computing, London, England, October 2001.
- Novartis Foundation Discussion Meeting on Biological Computing, London, England, October 2001.
- The Lorne Conference on Protein Structure and Function, Lorne, Australia, Organized by Richard Simpson, February 2000.
- Sydney Protein Structure Group, Sydney, Australia, Organized by Brett Church, February 2000. 5th Johns Hopkins Protein Folding Meeting, Coolfont, WV, March 2000.
- European Biochemical Society Symposium, From Protein Folding to New Enzymes, Leeds, England, Organized by Sheena Radford and Alan Berry, April 2000.
- Ettore Majorana Center International Summer School of Biophysics: Structural Biology, Sicily, Italy, Organized by Vincent Torre and Antonino Cattaneo, May 2000. Meeting cancelled by NATO.
- Biopolymers Gordon Conference, Co-organized by Peter Kollman, Rhode Island, June 2000.

- Interdisciplinary Workshop on Protein Flexibility and Folding, sponsored by Michigan State University, August 2000.
- Martinsrieder Symposium 2000, Munich, Germany, Organized by Wolfgang Baumeister, Ulrich Hartl, the Max Planck Institute, October 2000.
- Hereditary Disease Foundation workshop on Structural Studies of Huntingtin, December, 2000.
- University of Wisconsin, Madison, Molecular Biophysics Seminar Series, Organized by the Training Grant Students, January 1999.
- 24th Taniguchi International Symposium, Old and New Views of Protein Folding, Tokyo, Japan, Organized by Kunihiro Kuwajima, March 1999.
- Research Development Corporation of Japan, Simulations of Biological Functions---Computational Biology, Tokyo, Japan, Organized by Nobuhiro Go and Shigeo Ihara, March 1999.
- NIH Meeting on Opportunities in Molecular Biomedicine in the Era of Pentaflop Computing, Organized by Klaus Schulten, March 1999. Unable to attend.
- University of Illinois, Urbana-Champaign, Theoretical Biophysics Seminar Series, Organized by Klaus Schulten, March 1999.
- Tri-institutional Structural Biology Seminar Series, Rockefeller University, Sloan-Kettering Institute and the Weill Medical College of Cornell University, Organized by Andrej Sali, September 1999
- European Molecular Biology Organization Workshop: Protein Folding and Misfolding Inside and Outside the Cell, Oxford, U.K., Organized by Chris Dobson, March 1998.
- University of Cambridge, Chemistry Department, Two seminars, Organized by Alan Fersht, March 1998.
- University of California, San Francisco, Department of Pharmaceutical Chemistry, Organized by Vladimir Basus and Lucy Waskell, June 1998.
- University of Iowa, Biochemistry Departmental Seminar Series, Organized by Ken Murphy, October, 1998.
- Javits Meeting on Prion Diseases, San Francisco, Organized by Stanley Prusiner, November, 1998.
- Johns Hopkins Meeting on Protein Folding, Coolfont, WV, Organized by Bob Matthews, March 1997.
- University of California, San Francisco, Organized by Peter Kollman, Biophysics Seminar Series, May 1997.
- Javits Meeting on Prion Diseases, San Francisco, Organized by Stanley Prusiner, May 1997.
- Annual Meeting of the Protein Society, Boston, Organized by David Eisenberg, July 1997.
- Spetsai Summer School on Molecular and Cellular Biology: Biomolecular Recognition, Spetsai, Greece, Organized by Alan Fersht, September, 1997.
- Javits Meeting on Prion Diseases, San Francisco, Organized by Stanley Prusiner, April, 1996.
- Western Washington University, Chemistry Department Seminar Series, Organized by Mark Bussell, May 1996.
- University of Minnesota, Biochemistry Department Seminar Series, Organized by Clare Woodward, June 1996.
- NEC Princeton Lectures on Biophysics, Organized by Bill Bialek, June, 1996.
- American Chemical Society Meeting: 2 separate talks in the Computers in Chemistry Division. Organized by Alex Tropsha, August 1996, Florida.
- University of California, Berkeley, Structural Biology Seminar Series, Chemistry Department and the Department of Cellular and Molecular Biology, Organized by Susan Marqusee, October 1996.
- Ohio State University, Physics Department Seminar Series, November 1996.

American Chemical Society Meeting: Invited to give two talks: Physical Chemistry Division and in the Division of Computers in Chemistry, Anaheim, CA, Organized by Laura Lerner and Peter Kollman, April, 1995,

- Symposium of the European Network on Protein Folding and Stability, San Feliou, Spain, Organized by Rainer Jaenicke, April, 1995.
- Javits Meeting on Prion Diseases, San Francisco, Organized by Stanley Prusiner, May 1995.
- Aspen Center for Physics, Workshop on Statistical Mechanics and Protein Structure, Organized by Ron Elber, August 1994.

Fairchild Symposium November, 1994, San Francisco, CA. Symposium on Prion Diseases.

International Society of Biochemists and Biophysicists, Asilomar, Organized by Peter Kollman, December 1993.

OTHER WORK EXPERIENCE/ACTIVITIES

Alumni representative for Reed College Admissions Office (9/85-1993).

- Volunteer teacher, Science Education Partnership (1/89-6/90). This was a partnership between scientists at U.C.S.F. and local high school teachers.
- Other seasonal employment includes: escorting orphans from Latin America to Scandinavia for the Swedish Center for International Child Welfare; and 3 years as a professional downhill ski instructor. Also, I was in a Warren Miller ski movie, 1980.

PUBLICATIONS

Total > 250 publications

(>17,700 citations, h-index = 70, Google Scholar)

- V. Daggett, Protein Degradation: The Role of Mixed-Function Oxidases, *Pharmaceutical Research* 4: 278-284, 1987.
- P. Kollman, S. Rao, F. Brown, V. Daggett, G. Seibel and U.C. Singh. Free Energy Perturbation Methods Can Give Exciting Insights Into the Effect of Site-Specific Mutants on Both Binding and Catalysis: Applications to Subtilisin, Trypsin and Triose Phosphate Isomerase and the Description of a Free Energy Component Analysis. In *Protein Structure, Folding and Design* 2, D. Oxender, ed., A. Liss & Co., 215-225, 1987.
- V. Daggett, P.A. Kollman, and I.D. Kuntz, Molecular Dynamics Simulations of Small Peptides, Conference Proceedings for the Fourth International Conference on Supercomputing II: 348-356, 1989.
- V. Daggett, P.A. Kollman and I.D. Kuntz, Free Energy Perturbation Calculations of Charge Interactions with the Helix Dipole, *Chemica Scripta* **29A**: 205-215, 1989.
- V. Daggett, F. Brown, and P. Kollman, Free Energy Component Analysis: A Study of the Glu 165 → Asp 165 Mutation in Triose Phosphate Isomerase, J. Am. Chem. Soc. 111: 8247-8256, 1989.
- L.A. Williams, K. Kirshenbaum, V. Daggett, C. Sorace, and P.C. Kahn, Two-Dimensional Electrophoresis of Liver Microsomal Proteins from Rats Treated with 2,3,7,8-tetrachloro-dibenzo dioxin, 3-methyl cholanthrene and phenobarbital, *Chemosphere* 18: 947-954, 1989.
- V. Daggett and P.A. Kollman, Molecular Dynamics Simulations of Active Site Mutants of Triosephosphate Isomerase, *Protein Engineering* **3**: 677-690, 1990.
- V. Daggett, P.A. Kollman, and I.D. Kuntz, Molecular Dynamics Simulations of Small Peptides: Dependence on Dielectric Model and pH, *Biopolymers* **31**: 285-304, 1991.
- V. Daggett, P.A. Kollman, and I.D. Kuntz, A Molecular Dynamics Simulation of Polyalanine: An Analysis of Equilibrium Motions and Helix-Coil Transitions, *Biopolymers* 31: 1115-1134, 1991.

- P. Kollman, V. Daggett, and L. Dang, The Application of Computational Methods to the Study of Enzyme Catalysis by Triose Phosphate Isomerase and Stabilities of variants of Bacteriophage T4 Lysozyme, in *The Ciba Foundation Symposium Series*, Wiley Press, Chichester, 161: 91-107,1991.
- S. Schröder, V. Daggett, and P.A. Kollman, A Comparison of the AMI and PM3 Semiempirical Models for Calculation of the Catalytic Properties of the Serine Proteases, J. Am. Chem. Soc. 113: 8922-8925,1991.
- Daggett, V., Schröder, S. and P.A. Kollman, The Catalytic Pathway in Trypsin: Classical and Quantum Mechanical Calculations, J. Am. Chem. Soc. 113: 8926-8935, 1991.
- **Daggett V.** and M. Levitt, A Molecular Dynamics Simulation of the C-Terminal Fragment of the L7/L12 Ribosomal Protein in Solution, *Chemical Physics*, **158**: 501-512,1991.
- V. Daggett and M. Levitt, Molecular Dynamics Simulations of Helix Denaturation, *J. Mol. Biol.*, 223: 1121-1138, 1992.
- V. Daggett and M. Levitt, A Model of the Molten Globule State from Molecular Dynamics Simulations, Proc. Natl. Acad. Sci. USA, 89: 5142-5146, 1992.
- V. Daggett and P.A. Kollman, The Use of Theoretical Methods in Protein Engineering, in *Protein Engineering: A Practical Approach*, A. Rees, M.J. Sternberg, and R. Wetzel, Eds., Oxford University Press, Chapter 6: 143-163, 1992.
- V. Daggett, A Model for the Molten Globule State of CTF Generated Using Molecular Dynamics, in *Techniques in Protein Chemistry IV*, R.H. Angeletti, Ed., Academic Press, 525-532, 1993.
- V. Daggett and M. Levitt, Realistic Simulation of Native Protein Dynamics in Solution and Beyond, *Ann. Rev. of Biophys. and Biomol. Struct.* 22: 353-380, 1993.
- V. Daggett and M. Levitt, Protein Unfolding Pathways Explored through Molecular Dynamics Simulations, J. Mol. Biol. 232: 600-619, 1993.
- V. Daggett and M. Levitt., Protein folding/unfolding dynamics. *Current Opinion in Structural Biology*.
 4(2): 291-295, 1994.
- A. Li and **V. Daggett**. Characterization of the Transition State of Protein Unfolding Using Molecular Dynamics: Chymotrypsin Inhibitor 2, *Proc. Natl. Acad. Sci. USA*, **91**: 10430-10434, 1994.
- M. Levitt, M. Hirshberg, R. Sharon, and V. Daggett, Potential Energy Function and Parameters for Simulations of the Molecular Dynamics of Proteins and Nucleic Acids in Solution, *Computer Physics Commun.* 91: 215-231, 1995.
- D.O.V. Alonso and V. Daggett, Molecular Dynamics Simulations of Protein Unfolding and Limited Refolding: Characterization of Partially Unfolded States of Ubiquitin in Methanol and in Pure Water, J. Mol. Biol., 247: 501-520, 1995.
- Kirshenbaum, K. and **V. Daggett,** pH Dependent Conformations of the Amyloid β (1-28) Peptide Fragment Explored Using Molecular Dynamics, *Biochemistry*, **34**: 7629-7639, 1995.
- Kirshenbaum, K. and V. Daggett, Sequence Effects on the Conformational Properties of the β (1-28) Amyloid Peptide Fragment: Testing a Proposed Mechanism for $\alpha \rightarrow \beta$ Transitions, *Biochemistry*, **34**: 7640-7647, 1995.
- Kazmirski, S., D.O.V. Alonso, F.E. Cohen, S. Prusiner and V. Daggett. Theoretical Studies of Sequence Effects on the Conformational Properties of a Fragment of the Prion Protein: Implications for Scrapie Formation. *Chemistry & Biology*, 2: 305-315, 1995.
- Storch, E. and V. Daggett, Molecular Dynamics Simulations of Cytochrome b₅: Implications for Protein-Protein Recognition, *Biochemistry*, 34: 9682-9693, 1995.

- Li, A. and V. Daggett. Investigation of The Solution Structure of Chymotrypsin Inhibitor 2 Using Molecular Dynamics: Comparison to X-ray and NMR Data, *Protein Engineering*, 8: 1117-1128, 1995.
- Li, A.and V. Daggett. Identification and Characterization of the Unfolding Transition State of Chymotrypsin Inhibitor 2 by Molecular Dynamics Simulations, *J. Mol. Biol.*, **257**: 412-429, 1996.
- Daggett, V., A. Li, L.S. Itzhaki, D.E. Otzen and A.R. Fersht. Structure of the Transition State for Folding of a Protein Derived from Experiment and Simulation. J. Mol. Biol., 257: 430-440, 1996.
- K.E. Laidig and V. Daggett. Testing the Modified Hydration-Shell Hydrogen-Bond Model of Hydrophobic Effects using Molecular Dynamics Simulation, J. Phys. Chem. 100:5616-5619, 1996.
- S. Kazmirski, D.O.V. Alonso, F.E. Cohen, S. Prusiner and V. Daggett. The Conformational Consequences of Mutations to the H1 Helix of the Prion Protein. In *Techniques in Protein Chemistry VII*, Academic Press, 469-477, 1996.
- K.E. Laidig and V. Daggett. Molecular Dynamics Simulations of Apocytochrome b₅₆₂: The Highly Ordered Limit of Molten Globules, *Folding & Design*, 1: 335-346, 1996.
- E. Storch and V. Daggett, The Structural Consequences of Heme Removal: Molecular Dynamics Simulations of Rat and Bovine Apocytochrome b₅, *Biochemistry*, **35**: 11596-11604, 1996.
- P.M. Harrison, P. Bamborough, V. Daggett, S.B. Prusiner, and F.E. Cohen. The Prion Folding Problem, *Curr. Opin. Struct. Biol.*, 7:53-59, 1997.
- M. Levitt, M. Hirshberg, R. Sharon, K.E. Laidig, and V. Daggett, Calibration and Testing of a Water Model for Simulation of the Molecular Dynamics of Proteins and Nucleic Acids in Solution, J. Phys. Chem., 101: 5051-5061, 1997.
- S.L. Kazmirski and V. Daggett. Protein Dynamics: A Theoretical Perspective. In Advances in Molecular and Cellular Biology, JAI Press, Inc., Greenwich, CT. N.M. Allewell and C.K. Woodward, Eds., Volume 22B Protein Structural Biology in Biomedical Research, 339-390 1997.
- C.J. Bond, K. Wong, J. Clarke, A.R. Fersht and **V. Daggett**, Characterization of Residual Structure in the Thermally Denatured State of Barnase by Simulation and Experiment: Description of the Folding Pathway, *Proc. Natl. Acad. Sci. USA.*, **94**: 13409-13413, 1997.
- S. DeArmond, H. Sanchez, F. Yehiely, Y. Qiu, A. Ninchak-Casey, V. Daggett, A.N. Paminano-Camerino, J. Cayetano, M. Rogers, D. Groth, M. Torchia, P. Tremblay, M.R. Scott, F.E. Cohen and S. Prusiner. Selective Neuronal Targeting in Prion Disease, *Neuron*, 19: 1337-1348, 1997.
- Li, A. & V. Daggett. Molecular Dynamics Simulation of the Unfolding of Barnase: Characterization of the Major Intermediate. *J. Mol. Biol.*, **275**: 677-694, 1998.
- Li, Z., Laidig, K.E. & V. Daggett, Conformational Search Using a Molecular Dynamics-Minimization Procedure: Applications to Clusters of Coulombic Charges, Lennard-Jones Particles and Water. J. Comp. Chem., 19: 60-70, 1998.
- Alonso, D.O.V. & V. Daggett, Molecular Dynamics Simulations of Hydrophobic Collapse of Ubiquitin, *Prot. Sci.*, 7, 860-874, 1998.
- Kazmirski, S.L. & V. Daggett. Simulation of the Structural and Dynamic Properties of Unfolded Proteins: The "Molten Coil" State of Bovine Pancreatic Trypsin Inhibitor, J. Mol. Biol., 277, 487-506, 1998.
- Ladurner, A.G., Itzhaki, L.S., Daggett, V. & A.R. Fersht, Synergy Between Simulation and Experiment in Describing the Energy Landscape of Protein Folding, *Proc. Natl. Acad. Sci. USA*, 95, 8473-8478, 1998.
- Daggett, V., Structure-Function Aspects of Prion Proteins, Curr. Opin. Biotech., 9, 359-365, 1998.

- Wong, K.B. & V. Daggett, Barstar Has A Highly Dynamic Hydrophobic Core: Evidence From Molecular Dynamics Simulation And NMR Relaxation Data, *Biochemistry*, 37, 11182-11192, 1998.
- Laidig, K.E., Gainer, J.L. & V. Daggett. Altering Diffusivity in Biological Solutions Through Modification of Solution Structure and Dynamics, *J. Am. Chem. Soc.*, **120**, 9394-9395, 1998.
- Kazmirski, S. & V. Daggett, Non-Native Interactions in Protein Folding Intermediates: Molecular Dynamics Simulations of Hen Lysozyme, *J. Mol. Biol.*, **284**, 793-806, 1998.
- Laidig, K.E. & V. Daggett. Protein Modeling: Folding ↔ Unfolding Dynamics, in Volume 3 of the Encyclopedia of Computational Chemistry, Simulations of Biological Systems Section, P.v.R. Schleyer, N.L. Allinger, T. Clark, J. Gasteiger, P.A. Kollman, H.F. Schaefer III, P.R. Schreiner (Eds), John Wiley & Sons Ltd., Chichester, pp. 2211-2220, 1998.
- **Daggett**, V., Li, A., & A.R. Fersht, A Combined Molecular Dynamics and Φ-Value Analysis of Structure-Reactivity Relationships in the Transition State and Unfolding Pathway of Barnase: The Structural Basis of Hammond and Anti-Hammond Effects, *J. Am. Chem. Soc.*, **120**, 12740-12754, 1998.
- Storch, E.M., Daggett, V., and Atkins, W.M., Engineering Out Motion: Introduction of a *De Novo* Disulfide Bond and a Salt Bridge Designed to Close a Dynamic Cleft on the Surface of Cytochrome b₅, *Biochemistry*, 38, 5054-5064, 1999.
- Storch, E.M., Grinstead, J.S., Campbell, A.P., Daggett, V., and Atkins, W.M., Engineering Out Motion: A Surface Disulfide Bond Alters the Mobility of Trp 22 in Cytochrome b₅ as Probed by Time-Resolved Fluorescence and ¹H-NMR Experiments, *Biochemistry*, 38, 5065-5075, 1999.
- Kazmirski, S., Li, A. & V. Daggett, Analysis Methods for Comparison of Molecular Dynamics Trajectories: Applications to Protein Unfolding Pathways and Denatured Ensembles, J. Mol. Biol., 290: 283-304, 1999.
- Fulton, K.F., Main, E.R.G., **Daggett, V.** & S.E. Jackson, Mapping the Interactions Present in the Transition State for Folding/Unfolding of FKBP12, *J. Mol. Biol.*, **291**, 445-461, 1999.
- DeArmond, S., Qiu, Y., Sanchez, H., Spilman, P.R., Ninchak-Casey, A., Alonso, D.O.V., & V. Daggett, PrP^c Glycoform Heterogeneity as a Function of Brain Region: Implications for Selective Targeting of Neurons by Prion Strains. J. Neuropath. Exp. Neurology, 58, 1000-1009, 1999.
- Alonso, D.O.V., Alm, E. & **V. Daggett**, Characterization of the Unfolding Pathway of the Cell Cycle Protein P13suc1: Implications for Domain Swapping, *Structure*, **8**, 101-110, 2000.
- Alonso, D.O.V. & **V. Daggett**, Staphylococcal Protein A: Unfolding Pathways, Unfolded States, and Differences between the B and E Domains. *Proc. Natl. Acad. Sci. USA*, **97**, 133-138, 2000
- Wong, K.B., Clarke, J., Bond, C.J., Neira, J.L., Freund, S.M.V., Fersht, A.R.F. & V. Daggett, Towards a Complete Description of the Structural and Dynamic Properties of the Denatured State of Barnase and the Role of Residual Structure in Folding, J. Mol. Biol., 296, 1257-1282, 2000.
- Daggett, V., Long Timescale Simulations, Curr. Opin. Struct. Biol., 10, 160-164, 2000.
- Hom, K., Wolfe, G., Ma, Q-F, Zhang, H., E.M. Storch, V. Daggett, Basus, V.J., L. Waskell, NMR Studies of the Association of Cytochrome b₅ with Cytochrome c, *Biochemistry*, 39, 14025-14039, 2000.
- Mayor, U., Johnson, C.M., Daggett, V. and A.R. Fersht, Protein Folding and Unfolding in Microseconds to Nanoseconds by Experiment and Simulation, *Proc. Natl. Acad. Sci. USA*, 97, 13518-13522, 2000.
- Daggett, V., Molecular Dynamics Simulations of Protein Unfolding/Folding, In *Protein Structure*, Stability and Folding, Kenneth Murphy, Editor, Humana Press, New Jersey, 168, 215-247, 2000.

- **Daggett, V.** & A.R. Fersht, Transition States in Protein Folding, In *Mechanisms of Protein Folding*, Second Edition, Frontiers in Molecular Biology Series, Roger H. Pain, Editor, Oxford University Press, Oxford, U.K., Chapter 7, 175-211, 2000.
- Clarke, J., Hounslow, A.M., Bond, C.J., Fersht, A.R. & **Daggett, V.**, The Effects of Disulfide Bonds on the Denatured State of Barnase, *Protein Science*, **9**, 2394-2404, 2000.
- Li, B., Alonso, D.O.V. and V. Daggett, The Molecular Basis for the Inverse Temperature Transition of Elastin. J. Mol. Biol., 305, 581-592, 2001.
- Daggett, V., Validation of Protein-Unfolding Transition States Identified in Molecular Dynamics Simulations, In *From Protein Folding to New Enzymes*, A. Berry and S.E. Radford, Editors, Portland Press, London, Biochemical Society Symposium 68, 89-93, 2001.
- Alonso, D.O.V. and Daggett, V., Simulations and Computational Analyses of Prion Protein Conformations, In *Prion Proteins*, Byron Caughey, Editor, *Adv. Prot. Chem.*, Vol. 57, Academic Press, San Diego, 107-137, 2001.
- Pan, Y. and V. Daggett, Direct comparison of experimental and calculated folding free energies for hydrophobic deletion mutants of chymotrypsin inhibitor 2: Free energy perturbation calculations using transition and denatured states from molecular dynamics simulations of unfolding. *Biochemistry* 40, 2723-2731, 2001.
- Li, B., Alonso, D.O.V., Bennion, B.J., and **Daggett, V**., Hydrophobic Hydration is an Important Source of Elasticity in Elastin-Based Biopolymers, *J. Am. Chem. Soc.*, **123**, 11991-11998, 2001.
- Alonso, D.O.V., DeArmond, S., Cohen, F., and **Daggett, V**., Mapping the Early Steps in the Conversion of the Prion Protein, *Proc. Natl. Acad. Sci. USA*, **98**, 2985-2989, 2001.
- Kazmirski, S.L., Wong, K.B., Freund, S.M.V., Tan, Y.J., Fersht, A.R., and Daggett, V., Protein Folding from a Highly Disordered Denatured State: The Folding Pathway of Chymotrypsin Inhibitor 2 at Atomic Resolution, *Proc. Natl. Acad. Sci. USA*, 98, 4349-4354, 2001.
- Ramamurthy, V., Tucker, C., Wilkie, S.E., Daggett, V., Hunt, D.M. and J.B. Hurley, Interactions within the Coiled-coil Domain of RetGC-1 Guanylyl Cyclase are Optimized for Regulation Rather than for High Affinity, J. Biol. Chem., 276, 26218-26229, 2001.
- Best, R.B., Li, B., Steward, A., **Daggett, V**. and Clarke, J. Can Non-Mechanical Proteins Withstand Force? Stretching Barnase by AFM and MD Simulation. *Biophys. J.*, **81**, 2344-2356, 2001.
- Main, E.R.G., Fulton, K.F., Daggett, V., and Jackson, S.E., A Comparison of Experimental and Computational Methods for Mapping the Interactions Present in the Transition State for Folding of FKBP12, J. Biol. Phys., 27, 99-117, 2001.
- Ferguson, N., Pires, J.R., Toepert, F., Johnson, C.J., Pan, Y.P., Volkmer-Engert, R., Schneider-Mergener, J., Daggett, V., Oschkinat, H. and A.R. Fersht, Using Flexible Loop Mimetics to Extend Φ-value Analysis to Secondary Structure Interactions, *Proc. Natl. Acad. Sci. USA*, 98, 13008-13013, 2001.
- Kazmirski, S.L., Isaacson, R.L., An, C., Buckle, A., Johnson, C.M., Daggett, V. and A.R. Fersht, Pinpointing the Cause of Familial Amyloidosis—Finnish Type (FAF): Identification of a Metal Binding Site in the Crystal Structure of Human Gelsolin Domain 2, *Nat. Struct. Biol.*, 9(2), 112-116, 2002.
- Zou, Q., Bennion, B.J., Daggett, V. & Murphy, K.P. The Molecular Mechanism of Stabilization of Proteins by TMAO and its Ability to Counteract the Effects of Urea. J. Am. Chem. Soc., 124, 1192-1202, 2002.
- Fersht, A.R. and **Daggett**, V., Protein Folding and Unfolding at Atomic Resolution, *Cell*, **108**, 573-582, 2002.
- Daggett, V., Molecular Dynamics Simulations of the Protein Unfolding/Folding Reaction, Acc. Chem. Res., 35, 422-429, 2002.

- Alonso, D.O.V., An, C. and Daggett, V. Simulations of Biomolecules: Characterization of the Early Steps in the pH-Induced Conformational Conversion of the Hamster, Bovine, and Human Forms of the Prion Protein. *Phil. Tran. Roy. Soc.*, 360, 1165-1178, 2002.
- De Jong, D., Alonso, D.O.V., Riley, R. and **Daggett, V.**, Probing the Energy Landscape of Protein Folding/Unfolding Transition States, *J. Mol. Biol.*, **319**, 229-242, 2002.
- Li, B., Alonso, D.O.V., and **Daggett, V.**, Stabilization of Globular Proteins via Introduction of Temperature-Activated Elastin-Based Switches, *Structure*, **10**, 989-998, 2002.
- Day, R., Bennion, B.J., Ham, S., & V. Daggett, Increasing Temperature Accelerates Protein Unfolding without Changing the Pathway of Unfolding. J. Mol. Biol., 322, 189-203, 2002.
- Bennion, B.J. and Daggett, V. Protein Conformation and Diagnostic Tests: The Prion Protein, *Clinical Chemistry*, 48, 2105-2114, 2002.
- Li, B., and **Daggett, V.**, Molecular Basis for Temperature- and pH-Induced Conformational Transitions in Elastin-Based Peptides, *Biopolymers*, **68**, 121-129, 2003.
- Beck, D.A., Alonso, D.O.V., Daggett, V., A Microscopic View of the Solvation of Peptides and Proteins, *Biophysical Chemistry*, 100, 221-237, 2003.
- Li, B. and V. Daggett, The Molecular Basis for the Extensibility of Elastin, *J. Muscle Res. Cell Motility*, 23, 561-573, 2003.
- **Daggett, V.** and A.R. Fersht, Is There a Unifying Mechanism for Protein Folding? *Trends in Biochem. Sci.*, **28**, 18-25, 2003.
- Day, R. and V. Daggett, All-Atom Simulations of Protein Folding and Unfolding, *Adv. Prot. Chem.*, 66, 373-403, 2003.
- Walsh, S.T.R., Cheng, R.P., Alonso, D.O.V., Daggett, V., Vanderkooi, J., and DeGrado, W.F. The Hydration of Amides in Helices: A Comprehensive Picture from Molecular Dynamics, IR and NMR, *Protein Science*, 12, 520-531, 2003.
- Mayor, U., Johnson, C.M., Grossmann, J.G., Sato, S., Jas, G.S., Freund, S.M.V., Guydosh, N.R., Alonso, D.O.V., Daggett, V. and A.R. Fersht, The Complete Folding Pathway of a Protein from Nanoseconds to Microseconds, *Nature*, 421, 863-867, 2003.
- Bennion, B. and **Daggett, V**., The Molecular Basis for the Chemical Denaturation of Proteins by Urea, *Proc. Natl. Acad. Sci. USA*, **100**, 5142-5147, 2003.
- Armen, R., Alonso, D.O.V., and **V. Daggett**, The Role of α , β_{10} , and π -helix in Helix Coil Transitions, *Prot. Sci.*, **12**, 1145-1157, 2003.
- Daggett, V. and Fersht, A.R. The present view of the mechanism of protein folding, *Nat. Rev. Mol. Cell. Biol.*, 4, 497-502, 2003.
- Day, R., Beck, D., Armen, R. and **V. Daggett,** A Consensus View of Fold Space: Combining SCOP, CATH, and the Dali Domain Dictionary, *Protein Science*, **12**, 2150-2160, 2003.
- Gianni, S., Guydosh, N.R., Khan, F., Caldas, T.D., Mayor, U., White, G.W.N., DeMarco, M.L., Daggett, V. and A.R. Fersht, Unifying features in protein-folding mechanisms. *Proc. Natl. Acad. Sci. USA*, 100, 13286-13291, 2003.
- Zhu, Y, Alonso, D.O.V., Maki, K., Huang, C.-Y., Lahr, S.J., Daggett, V., Roder, H., DeGrado, W.F., and F. Gai, Ultrafast Folding of α₃D, A *De Novo* Designed Three-Helix Bundle Protein, *Proc. Natl. Acad. Sci. USA*, 100: 15486-15491, 2003.
- DeMarco, M.L. and V. Daggett, From Conversion to Aggregation: Protofibril Formation of the Prion Protein, *Proc. Natl. Acad. Sci. USA*, 101, 2293-2298, 2004.
- Bennion, B.J. and V. Daggett, Counteraction of urea-induced protein denaturation by TMAO: A chemical chaperone at atomic resolution, *Proc. Natl. Acad. Sci. USA*, **101**, 6433-6438, 2004.

- Sato, S., Religa, T., **Daggett, V**. and A.R. Fersht, Testing protein folding simulations by experiment, *Proc. Natl. Acad. Sci. USA*, **101**, 6952-6956, 2004.
- Jemth, P., Gianni, S., Day, R., Li, B., Johnson, C.M., Daggett, V. and A.R. Fersht, Demonstration of a low energy on-pathway intermediate in a fast folding protein, *Proc. Natl. Acad. Sci. USA*, 101, 6450-6455, 2004.
- Armen, R.S., DeMarco, M.L., Alonso, D.O.V. and V. Daggett, Pauling and Corey's α-pleated sheet structure may define the prefibrillar amyloidogenic intermediate in amyloid disease *Proc. Natl. Acad. Sci. USA*, 101, 11622-11627, 2004.
- DeMarco, M.L., Alonso, D.O.V. and V. Daggett, Diffusing and colliding: The atomic level folding/unfolding pathway of a small helical protein, J. Mol. Biol., 341, 1109-1124, 2004.
- Beck, D.A.C. and **V. Daggett**, Methods for Molecular Dynamics Simulations of Protein Folding / Unfolding in Solution, *Methods*, **34**, 112-120, 2004.
- Armen, R.S., Alonso, D.O.V. and **V. Daggett**, Anatomy of an amyloidogenic intermediate: Conversion of β-sheet to α-pleated sheet structure in transthyretin at acidic pH, *Structure*, **12**, 1847-1863, 2004.
- Bennion, B.J., DeMarco, M. and V. Daggett, Preventing misfolding of the prion protein by Trimethylamine N-oxide, *Biochemistry*, 43, 12955-12963, 2004.
- Rizzuti, B., Daggett, V., Guzzi, R., and L. Sportelli, The early steps in the unfolding of azurin, *Biochemistry*, 43, 15604-15609, 2004.
- Beck, D.A.C., Armen, R.S. and V. Daggett, Cutoff size need not strongly influence molecular dynamics results on solvated polypeptides. *Biochemistry*, 44, 609-616, 2005. (#12 most cited paper in 2005 in Biochemistry.)
- Esposito, L. and V. Daggett. Insight into ribonuclease A domain swapping by molecular dynamics unfolding simulations, *Biochemistry*, 44, 3358-3368, 2005.
- Ferguson, N., Day, R., Johnson, C.M., Allen, M.D., Daggett, V. and A.R. Fersht, Simulation and experiment at high temperatures: Ultrafast folding of a thermophilic protein by nucleationcondensation, J. Mol. Biol., 347, 855-870, 2005. (One of the Top 5 JMB downloads of 2005)
- Day, R. and V. Daggett, Sensitivity of the folding/unfolding transition state ensemble of chymotrypsin inhibitor 2 to changes in temperature and solvent, *Prot. Sci.*, 14, 1242-1252, 2005.
- White, G.W.N., Gianni, S., Grossman, J.G., Jemth, P., Fersht, A.R. and V. Daggett, Simulation and Experiment Conspire to reveal Cryptic Intermediates and the Slide from the Nucleation-Condensation to Framework Mechanism of Folding. J. Mol. Biol., 350, 757-775, 2005.
- DeMarco, M.L. and V. Daggett, Local Environmental Effects on the Structure of the Prion Protein, *Comptes Rendus Biologies* 328, 847-862, 2005.
- Jemth, P., Day, R., Gianni, S., Khan, F., Allen, M., Daggett, V., and A.R. Fersht, The structure of the major transition state for folding of an FF domain from experiment and simulation, *J. Mol. Biol.*, 350, 363-378, 2005. (One of the Top 5 *JMB* downloads of 2005)
- Day, R. and V. Daggett, Ensemble versus single-molecule protein unfolding. *Proc. Natl. Acad. Sci. USA*, 102, 13445-13450, 2005.
- Armen, R.S., Bernard, B., Day, R., Alonso, D.O.V. and V. Daggett, Characterization of a possible amyloidogenic precursor in glutamine-repeat neurodegenerative diseases, *Proc. Natl. Acad. Sci.* USA, 102, 13433-13438, 2005.
- Armen, R.S. and V. Daggett, β_2 -microglobulin may form amyloid through an α -pleated sheet intermediate, *Biochem.*, 44, 16098-16107, 2005.
- Rutherford, K., Bennion, B.J., Parson, W.W. and **V. Daggett**, The 108M polymorph of human catechol *O*-methyltransferase is prone to deformation at physiological temperatures, *Biochem.*, **45**, 2178-2188, 2006.

Daggett, V., Protein Folding Simulation, Chemical Reviews, 106, 1898-1916, 2006.

- Scott, K.A., Alonso, D.O.V., Pan, Y. and V. Daggett, The importance of context in protein folding: Secondary structural propensities versus tertiary contact-assisted secondary structure formation, *Biochem.*, 45, 4153-4163, 2006.
- Scott, K.A., Randles, L.G., Moran, S.J., Daggett, V. and J. Clarke. The folding pathway of spectrin R17 from experiment and simulation: Using experimentally validated MD simulations to characterize states hinted at by experiment. J. Mol. Biol., 359, 159-173, 2006.
- Day, R. and V. Daggett, Protein unfolding at atomic resolution, In *Modelling Molecular Structure and Reactivity in Biological Systems*, Royal Society of Chemistry Publishing, 2006.
- Daggett, V. α-sheet: The toxic conformer in amyloid diseases? Acc. Chem. Res., 39, 594-602, 2006.
- Petrovich, M., Jonsson, A.L., Ferguson, N., Daggett, V., and A.R. Fersht. Φ-analysis at the experimental limits: Mechanism of β-hairpin formation. J. Mol. Biol., 360, 865-881, 2006.
- DeMarco, M.L., Silveira, J., Caughey, B., and V. Daggett, Structural Properties of Prion Protein Protofibrils and Fibrils: An Experimental Assessment of Atomic Models, *Biochem.*, 45, 15573-15582, 2006.
- Beck, D.A.C., White, G.W.N. and V. Daggett, Exploring the Energy Landscape of Protein Folding using Replica-Exchange and Conventional Molecular Dynamics Simulations, J. Struct. Biol., 157, 514-523, 2007.
- Day, R. and V. Daggett, Direct observation of microscopic reversibility in protein folding, *J. Mol. Biol.*, **366**, 677-686, 2007.
- Scott, K.A. and V. Daggett, The folding mechanisms of proteins with high sequence identity but different folds, *Biochem.*, **46**, 1545-1556, 2007. (*The #8 most-accessed article in Biochemistry Jan-Mar* 2007.)
- Scott, K.A., Alonso, D.O.V., Sato, S., Fersht, A.R. and V. Daggett, Conformational Entropy of Alanine versus Glycine in Protein Denatured States, *Proc. Natl. Acad. Sci. USA*, 104, 2661-2666, 2007.
- DeMarco, M.L. and V. Daggett, Molecular Mechanism for Low pH-Triggered Misfolding of the Human Prion Protein, *Biochem.*, 46, 3045-3054, 2007. (*Designated a 'Hot Article'*. *The #17 most*accessed article in 2007)
- Beck, D.A.C., Bennion, B.J., Alonso, D.O.V. and V. Daggett, Simulations of Macromolecules in Protective and Denaturing Osmolytes: Properties of Mixed Solvent Systems and their Effects on Water and Protein Structure and Dynamics, *Methods in Enzymology* volume titled "Osmosensing and Osmosignaling," edited by Dieter Häussinger and Helmut Sies, 428, 373-396, 2007.
- Beck, D.A.C. and V. Daggett, A one-dimensional reaction-coordinate for identification of transition states from explicit solvent P_{fold}-like calculations, *Biophys. J.*, 93, 3382-3391, 2007.
- Sharpe, T.D., Jonsson, A.L., Rutherford, T.J., **Daggett, V**. and A.R. Fersht. The role of the turn in β-hairpin formation during WW domain folding. *Prot. Sci.* **16**, 2233-2239, 2007.
- Fersht, A.R. and V. Daggett. Folding and binding: implementing the game plan, *Current Opinion in Structural Biology*, **17**, 1-2, 2007.
- Merkley, E.D., Bernard, B. and V. Daggett, Conformational changes below the T_m : molecular dynamics studies of the thermal pretransition of ribonuclease A, *Biochemistry*, 47, 880-892, 2008.
- Rutherford, K., Parson, W.W. and **V. Daggett**, The Histamine *N*-Methyltransferase T105I Polymorphism Affects Active Site Structure and Dynamics, *Biochemistry*, **47**, 893-901, 2008.
- Steward, R.E., Armen, R.S. and V. Daggett, Different disease-causing mutations in transthyretin accelerate the same conformational conversion, *Protein Engineering Design and Selection*, 21, 187-195, 2008.

- Schaeffer, R.D., Fersht, A. and V. Daggett, Combining Experiment and Simulation in Protein Folding: Closing the Gap for Small Model Systems, *Curr. Opin. Struct. Biol.* **18**, 4-9, 2008.
- Scouras, A.D. and **V. Daggett**, Species Variation in PrP^{sc} Protofibril Models, *J. Materials Sci.* Special volume on Nano- and micromechanical properties of hierarchical biological materials: Linking mechanics, chemistry and biology, edited by Markus Buehler, **43**, 3625-3637, 2008.
- Smolin, N. and V. Daggett, Formation of ice-like water structure on the surface of an antifreeze protein, *Journal of Physical Chemistry B*, **112**, 6193-6206, 2008.
- Beck, D.A.C., Jonsson, A.L., Schaeffer, D., Scott, K.A., Day, R., Toofanny, R.D., Alonso, D.O.V., and V. Daggett. Dynameomics: Mass annotation of protein dynamics and unfolding in water by high-throughput atomistic molecular dynamics simulations, *Protein Engineering Design and Selection*, 21, 353-368, 2008.
- Simms, A.M, Toofanny, R.D., Kehl, C., Benson, N.C. and V. Daggett. Dynameomics: Design of a computational lab workflow and scientific data repository for protein simulations, *Protein Engineering Design and Selection*, 21, 369-377, 2008.
- Kehl, C.E., Simms, A.M., Toofanny, R.D. and V. Daggett. Dynameomics: A multi-dimensional analysisoptimized database for dynamic protein data, *Protein Engineering Design and Selection*, 21, 379-386, 2008.
- Smolin, N., Li, B., Beck, D.A.C. and V. Daggett, Side-chain dynamics are critical for water permeation through aquaporin-1, *Biophysical Journal*, 95, 1089-1098, 2008.
- Rutherford, K. and V. Daggett. Four Human Thiopurine S-Methyltransferase Alleles Severely Affect Protein Structure and Dynamics, J. Mol. Biol., **379**, 803-814, 2008.
- Rutherford, K., Alphandéry, E., McMillan, A., Daggett, V. and W.W. Parson. Stability of Secondary and Tertiary Protein Structure in 108V and 108M Catechol O-methyltransferase, BBA, 1784, 1098-1105, 2008.
- McCully, M.E., Beck, D.A.C. and V. Daggett. Microscopic reversibility of protein folding in molecular dynamics simulations of the engrailed homeodomain, *Biochemistry*, 47, 4079-7089, 2008.
- Anderson, P.C. and **V. Daggett.** Molecular Basis for the Structural Instability of Human DJ-1 Induced by the L166P Mutation Associated with Parkinson's Disease, *Biochemistry*, **47**, 9380-9393, 2008.
- Beck, D.A.C., Alonso, D.O.V., Inoyama, D. and V. Daggett, The intrinsic conformational propensities of the twenty naturally occurring amino acids and reflection of these propensities in proteins, *Proc. Natl. Acad. Sci. USA*, 105, 12259-12264, 2008.
- Benson, N.C. and **V. Daggett**, Native Protein Flexibility as a Determinant of Dynamical Changes and Unfolding Events, *Protein Science*, **17**, 2038-2050, 2008.
- DeMarco, M.L. and **V. Daggett**, Characterization of cell-surface prion protein relative to its recombinant analogue: Insights from molecular dynamics simulations of diglycosylated, membrane-bound human prion protein, *J. Neuro. Chem.*, **109**: 60-73, 2009.
- Daggett V. and Fersht A.R. Protein folding and binding: moving into unchartered territory. *Current Opinion in Structural Biology* **19**:1-2, 2009.
- Rutherford K. and V. Daggett. A Hotspot of Inactivation: The A22S and V108M Polymorphisms Individually Destabilize the Active Site Structure of Catechol O-Methyltransferase. *Biochemistry*, 48: 6450-6460, 2009.
- Anderson P.C. and V. Daggett. The R46Q, R131Q and R154H Polymorphs of Human DNA Glycosylase/β-Lyase hOgg1 Severely Distort the Active Site and DNA Recognition Site but do not Cause Unfolding. *Journal of the American Chemical Society*, 131: 9506-9515, 2009.

- Schmidlin T., Kennedy B., and V. Daggett. Structural changes to monomeric CuZn Superoxide Dismutase caused by the familial Amyotrophic Lateral Sclerosis mutation A4V. *Biophysical Journal*, 97: 1709-1718, 2009.
- Van der Kamp, M.W. and V. Daggett. The consequences of pathogenic mutations to the human prion protein. *Protein Engineering, Design and Selection*, **22**: 461-468, 2009.
- **Daggett V**. Shedding light on amyloidosis with protein engineering. *Protein Engineering Design & Selection* **22**:445, 2009.
- Rutherford K. and V. Daggett The V119I Polymorphism in Protein *L*-Isoaspartate *O*-Methyltransferase Alters the Substrate-Binding Interface. *Protein Engineering Design & Selection*, 22: 713-721, 2009.
- Key, J., Scheuermann, T.H., Anderson, P.C., Daggett, V., and K.H. Gardner. Principles of ligand binding within a completely buried cavity in HIF2α PAS-B., *Journal of the American Chemical Society*, 131: 17647-17654, 2009.
- Jonsson, A.L., Scott, K.A. and V. Daggett. Dynameomics: A consensus view of the protein unfolding/folding transition state ensemble across a diverse set of protein folds. *Biophysical Journal*, 97: 2958-2966, 2009.
- Law, P.B. and V. Daggett. The relationship between water bridges and the left-handed polyproline II conformation: A large-scale joint analysis of molecular dynamics simulations and crystal structures. *Protein Engineering, Design and Selection*, 23: 27-33, 2010.
- Merkley, E.D., Parson, W.W. and V. Daggett. Temperature Dependence of the Flexibility of Thermophilic and Mesophilic Flavoenzymes of the Nitroreductase Fold, *Protein Engineering Design and Selection*, 23: 327-336, 2010.
- Toofanny, R.D., Jonsson, A.L. and **V. Daggett**. A Comprehensive One-Dimensional Reaction Coordinate for Protein Unfolding/Folding. *Biophysical Journal*, **98**: 2671-2681, 2010.
- Van der Kamp, M.W., Anderson, P.C., Beck, D.A.C., Benson, N.C., Jonsson, A.L., Merkley, E.D., Schaeffer, R.D., Scouras, A.D., Simms, A., Toofanny, R.D., and V. Daggett. Dynameomics: A comprehensive database of protein dynamics. *Structure*, 18, 423-435, 2010. (Journal cover)
- McCully, M., Fersht, A.R. and V. Daggett. Refolding of the Engrailed Homeodomain protein at atomic resolution: Structural basis for accumulation of a folding intermediate, *Biophysical Journal*, 99, 1628-1636, 2010.
- Rutherford, K. and V. Daggett. Polymorphisms and Disease: Hotspots of Inactivation in Methyltransferases, *Trends in Biochem. Sci.*, **35**, 531-538, 2010.
- van der Kamp, M.W. and V. Daggett, The influence of pH on the human prion protein: Insights into the early steps of misfolding. *Biophys. J.*, **99**, 2289-2298, 2010.
- van der Kamp, M.W. and **V. Daggett**. Pathogenic mutations in the hydrophobic core of the human prion protein can promote structural instability and misfolding. *J. Mol. Biol.*, **404**, 732-748, 2010.
- Chen, W., van der Kamp, M.W., and **V. Daggett**, Diverse Effects on the Native β-Sheet of the Human Prion Protein due to Disease-Associated Mutations, *Biochemistry*, **49**, 9874-9881, 2010.
- Jonsson, A., Schaeffer, R.D., van der Kamp, M. and V. Daggett. Dynameomics: Protein dynamics and unfolding across fold space. *BioMolecular Concepts*, 1, 335-344, 2010.
- Schaeffer, R.D., Jonsson, A.L., Simms, A.M. and V. Daggett. Generation of a Consensus Protein Domain Dictionary, *Bioinformatics*, 27, 46-54, 2011.
- Daggett, V. Introduction to a special issue 'Three Decades of Protein Engineering: Impact on Structural Biology and Therapy', Prot. Eng. Des. Sel., 24, 1, 2011.
- Schaeffer R.D. and Daggett V. Protein folds and protein folding. *Protein Engineering Design & Selection* 24,11-19, 2011

- Scouras, A.D. and V. Daggett, The Dynameomics Rotamer Library: Amino Acid Side Chain Conformations and Dynamics from Comprehensive Molecular Dynamics Simulations in Water, *Protein Science*, 20, 341-352, 2011. (Also subject of Editorial Highlight in the same issue.)
- Dar, T.A., Schaeffer, R.D., Daggett, V. and B.E. Bowler. Manifestations of native topology in the denatured state ensemble of *Rhodopseudomonas palustris* cytochrome c', *Biochemistry*, 50, 1029-1041, 2011. (Also subject of Editorial Highlight in the same issue.)
- Morrone, A., McCully, M.E., Bryan, P.N., Brunori, M., Gianni, S., Daggett, V. and C. Travaglini-Allocatelli. The denatured state dictates the topology of two proteins with almost identical sequence but different native structure and function. J. Biol. Chem., 286, 3863-3872, 2011.
- Banachewicz W., Religa T.L., Schaeffer R.D., Daggett V., and Fersht A.R. Malleability of folding intermediates in the homeodomain superfamily. *Proc. Natl. Acad. Sci. USA*, 108, 5596-5601, 2011.
- Van der Kamp, M.W. and V. Daggett, Molecular dynamics as an approach to study prion protein misfolding and the effect of pathogenic mutations, *Topics in Current Chemistry*, Special Prion Issue, J. Tatzelt, Editor, 1-29, 2011.
- Calhoun S. and **Daggett V**. Structural effects of the L145Q, V157F, and R282W cancer-associated mutations in the p53 DNA-binding core domain. *Biochemistry*, **50**, 5345-5353, 2011.
- Jonsson, A.L. and V. Daggett, The Effect of Context on the Folding of β-Hairpins, J. Struct. Biol., 176, 143-150, 2011.
- Toofanny, R.D., Simms, A.M., Beck, D.A.C. and **V. Daggett**, Implementation of 3D spatial indexing and compression in a large-scale molecular dynamics simulation database for rapid atomic contact detection, *BMC Bioinformatics*, **12**, 334, 2011.
- Morrone, A., Giri, R., Toofanny, R.D., Travaglini-Allocatelli, C., Brunori, M., Daggett, V. and S. Gianni, GB1 is not a two-state folder: identification and characterization of an on-pathway intermediate, *Biophys. J.*, 101, 2053-2060, 2011.
- Merkley, E.D., **Daggett, V.** and W.W. Parson, A Temperature-Dependent Conformational Change of NADH Oxidase from *Thermus thermophiles* HB8, *Proteins*, **80**, 546-555, 2012.
- Toofanny, R.D. and **V. Daggett**, Understanding protein unfolding from molecular simulations, *WIREs Comput. Mol. Sci.*, **2**, 405-423, 2012.
- Scouras, A.D. and **V. Daggett**, Disruption of the X-Loop Turn of the Prion Protein Linked to Scrapie Resistance, *Prot. Eng. Design. Sel.*, **25**, 243-249, 2012. (Journal Cover)
- Benson, N.C. and V. Daggett, Wavelet Analysis of Protein Motion, J. Wavelets, Multiresol. Info. Processing, 10, 1250040, 2012.
- Towse, C.L. and **V. Daggett**, Molecular Dynamics Simulations, in *Encyclopedia of Biophysics*, Springer, in press, 2012.
- Simms, A.M. and V. Daggett, Protein simulation data in the relational model, *J. of Supercomp.*, 62, 150-173, 2012.
- Benson, N.C. and V. Daggett, A Chemical Group Graph Representation for Efficient High-Throughput Analysis of Atomistic Protein Simulations, J. of Bioinf. And Comp. Biol., 10, 1250008-1250024, 2012.
- Wang, D., Robertson, I.M., Si, M.X., McCully, M., Crane, M.L., Luo, Z., Daggett, V., Sykes, B.D., and M. Regnier. Structural and functional consequences of the cardiac troponin C L48Q Ca²⁺sensitizing mutation, *Biochemistry*, 51, 4473-4487, 2012.
- Benson, N. and V. Daggett. A comparison of multiscale methods for analysis of molecular dynamics simulations, *J. Phys. Chem.*, **116**, 8722-8731, 2012. (Journal Cover)

- McCully M.E. and Daggett V. Folding and Dynamics of Engineered Proteins. In **Protein Engineering Handbook**, vol. III. Eds. Lutz S and Bornscheuer UT. Wiley-VCH, Weinheim. Chapter 5, pgs. 89-114, 2012.
- Towse C.L., **Daggett V**. When a domain is not a domain, and why it is important to properly filter proteins in databases. **BioEssays**, 34:1060-1069, 2012. (Journal Cover)
- McCully M.E., Beck D.A.C., **Daggett V.** Multimolecule test-tube simulations of protein unfolding and aggregation. *Proc. Natl. Acad. Sci. USA*, **109**, 17851-17856 2012.
- Jonsson, A.L., Fersht, A.R., and V. Daggett. Combining simulation and experiment to map protein folding, In Comprehensive Biophysics, Elsevier, E. Egelman Editor-in-Chief, Volume 3: The folding of proteins and nucleic acids, V. Daggett, Editor. Chapter 3.1, 2012.
- McCully, M.E., Beck, D.A.C. and V. Daggett. Promiscuous contacts and heightened dynamics increase thermostability in engineered proteins, *Prot. Eng. Des. Selec.*, 26, 34-45, 2013.
- Rizzuti, B., **Daggett V**. Using simulations to provide the framework for experimental protein folding studies. *Arch. Biochem. Biophys.*, **531**, 128-135, 2013.
- Wang, D., McCully, M.E., Luo, Z., McMichael, J., Tu, A., Daggett, V., Regnier, M. Structural and function consequences of cardiac tropinin C L57Q and I61Q Ca2+-desensitizing variants. Arch. Biochem. Biophys., 535, 68-75, 2013.
- Schmidlin, T., Ploeger, K., Jonsson, A.L. Daggett, V. Early steps in thermal unfolding of superoxide dismutase 1 are similar to the conformational changes associated with the ALS-associated A4V mutation. *Protein Engineering, Design and Selection*, 26: 503-513, 2013.
- Bromley, D., Anderson, P.C., Daggett, V. Structural consequences of mutations to the alpha-tocopherol transfer protein associated with the neurodegenerative diseae ataxia with vitamin E deficiency. *Biochemistry*, 52: 4264-4273, 2013.
- Hopping, G., Kellock, J., Caughey, B., **Daggett**, V. The designed trpzip-3 beta-hairpin inhibits amyloid formation in two different amyloid systems. *ACS Medicinal Chemistry Letters*, **4**: 824-828, 2013.
- Cheng, C.J., **Daggett, V.** Molecular dynamics simulations capture the misfolding of the bovine prion protein at acidic pH. *Biomolecules* **4**: 181-201, 2014.
- Bromley, D., Rysavy, S.J., Su, R., Toofanny, R.D., Daggett, V. DIVE: A data intensive visualization engine. *Bioinformatics* 30: 593-595, 2014.
- Chen, W., van der Kamp, M.W., **Daggett, V**. Structural and dynamic properties of the human prion protein. *Biophysical Journal* **106**: 1152-1163, 2014.
- Rysavy, S.J., Bromley, D., **Daggett, V**. DIVE: A graph-based visual analytics framework for big data. *IEEE Computer Graphics and Application's: Visual Analytics for Biological Data*. **March/April**: 26-37, 2014.
- Cheng, C.J., **Daggett, V.** Different misfolding mechanisms converge on common conformational changes: Human prion protein pathogenic mutants Y218N and E196K. *Prion* 8: 1-11, 2014.
- Merkley, E.D., Rysavy, S., Kahraman, A., Hafen, R.P., Daggett, V., Adkins, J.N. Distance restraints from cross-linking mass spectrometry: Mining a molecular dynamics simulation database to evaluate lysine-lysine distances. *Protein Science*, 23: 747-759, 2014.
- Hopping, G., Kellock, J., Barnwal, R.P., Law, P., Bryers, J.D., Varani, G., Caughey, B., Daggett, V. Designed α-Sheet Peptides Inhibit Amyloid Formation by Targeting Toxic Oligomers. *eLIFE* 3: e01681, 2014.
- Towse, C.-L., Hopping, G., Vulovic, I., **Daggett, V**. Nature versus design: The conformational propensities of D-amino acids and the importance of side chain chirality. *Protein Engineering*, *Design, and Selection*, **27**: 447-455, 2014.

- Rysavy, S.J., Beck, D.A.C., **Daggett, V.** Dynameomics: Data-driven methods and models for utilizing large-scale protein structure repositories for improving fragment-based loop prediction. *Protein Science*, **23**: 1584-1595, 2014.
- Towse, C.-L., Rysavy, S.J., Vulovic, I.M., **Daggett, V**. New Dynamic Rotamer Libraries: Data-Driven Analysis of Side Chain Conformational Propensities. *Structure* **24**: 187-199, 2016.
- Towse, C.-L., Vymetal, J., Vondrasek, J., **Daggett, V**. Insights into unfolded proteins from the intrinsic ϕ/ψ propensities of the AAXAA host-guest series. *Biophysical Journal* **110** : 348-361, 2016.
- Kellock, J., Hopping, G., Caughey, B., Daggett, V. Peptides composed of alternating L- and D-amino acids inhibit amyloidogenesis in three distinct amyloid systems independent of sequence. J. Mol. Biol., 428: 2317-2328, 2016.
- Bromley, D., Bauer, M., Fersht, A.R., Daggett, V. An in silico algorithm for identifying stabilizing pockets in proteins: Test case the Y220C mutant of the p53 tumor suppressor protein. *Protein Engineering Design and Selection*, 29: 377-390, 2016.
- Childers, M.C., Towse, C.-L., **Daggett**, **V**. The effect of chirality and steric hindrance on intrinsic backbone conformational propensities: Tools for protein design. *Protein Engineering Design and Selection*, **29**: 271-280, 2016.
- Bleem, A., Daggett, V. Structural and functional diversity among amyloid proteins: Agents of disease, building blocks of biology, and implications for molecular engineering. *Biotechnology and Bioengineering*, 114: 7-20, 2017.
- Childers, M.C., **Daggett, V.** Insights from molecular dynamics simulations for computational protein design. *Molecular Systems Design & Engineering* **2**: 9-33, 2017.
- Nowakowski, S.G., Regnier, M., **Daggett**, V. Molecular mechanisms underlying deoxy-ADP.Pi activation of pre-powerstroke myosin. *Protein Science* **26**: 749-462, 2017.
- Towse, C.-L., Akke, M., **Daggett, V.** The Dynameomics Entropy Dictionary: A large-scale assessment of conformational entropy across protein fold space, *Journal of Physical Chemistry B*, **121**: 3933-3945, 2017.
- Cheng, C.C., Koldsø, H., Van der Kamp, M.W., Schiøtt, B., Daggett, V., Simulations of Membranebound Diglycosylated Human Prion Protein Reveal Potential Protective Mechanisms against Misfolding, *Journal of Neurochemistry*, 142: 171-182, 2017.
- Bleem, A., Francisco, R., Bryers, J.D., **Daggett, V.** Designed α-sheet peptides suppress amyloid formation in *Staphylococcus aureus* biofilms, *Nature Biofilms and Microbiomes*, **3**:16, 2017.
- Maris, N.L., Shea, D., Bleem, A., Bryers, J.D., Daggett, V. Chemical and physical variability in structural isomers of an L/D α-sheet peptide designed to inhibit amyloidogenesis. *Biochemistry*, 57: 507-510, 2018.
- Gianni, S., McCully, M.E., Malagrino, F., Bonetti, D., De Simone, A., Brunori, M., **Daggett, V**. An hydroxyl to amine substitution tunes fold switching in a protein domain, *Angewandte Chemie*, in press, 2018.
- Childers, M.C., **Daggett, V.** Validating molecular dynamics simulations against experimental observables in light of underlying conformational ensembles. *J. Phys. Chem. B.*, in press, available online, 2018.
- Toofanny, R.D., Calhoun, S., Jonsson, A.L., **Daggett, V.** Shared unfolding pathways of unrelated immunoglobulin-like β-sandwich proteins. *Prot. Eng. Des. Sel.*, accepted, 2018.
- Bi, T., **Daggett**, V. The role of α-sheet in amyloid oligomer aggregation and toxicity, *Yale Journal of Biology and Medicine*, in press, 2018.
- Childers, M.C., Towse, C.-L., **Daggett, V.** Molecular dynamics-derived rotamer libraries for D-amino acids, *Protein Engineering, Design &* Selections, in press, 2018.

- Paranjapye, N., **Daggett, V.**α-sheet peptides inhibit functional amyloid formation of *Streptococcus mutans* biofilms. *J. Mol. Biol.*, in press, 2018.
- Hsu, C.-C., Templin, A., Shea, D., Kahn, S., **Daggett, V.** Novel α-sheet compounds inhibit aggregation and toxicity of islet amyloid polypeptide, to be submitted shortly, 2018.
- Bi, T.M., Hsu, C.-C., Shea, D., **Daggett, V**. Inhibition of a *de novo* synthetic amyloidogenic peptide's aggregation by naturally occurring amyloids, to be submitted shortly, 2018.
- Shea, D., Hsu, C.-C., Bi, T., Paranjapye, N., Childers, M., Cochran, J., Tomberlin, C.P., Wang, L., Paris, D., Zonderman, J., Mullan, M., Varani, G., Link, C., Daggett, V., α-sheet as driver of amyloid β-peptide aggregation and toxicity in Alzheimer's Disease, to be submitted shortly, 2018.
- Ferina, J., Childers, M.C., **Daggett, V**. Visualizing protein un/folding, *J. Mol. Biol.*, to be submitted shortly, 2018.

Lay publications about, or including, our research:

Our alpha-sheet design work was covered in an article in the November 2014 issue of the Alaska Airlines Magazine.

eLife paper by Hopping et al. has been featured in a press release from UW and many online news and other web sources including NIH NIGMS BioBeat, NIH NIGMS website, Kurzweil Ai, hcplive, SciCasts, Science Daily, Medical Xpress, the Alois Alzheimer Foundation and other patient support and Alzheimer's Disease websites. July and August, 2014.

Dynameomics figure and description (author, Jeff O'Brian) for a Centennial book celebrating IBM's 100 years entitled Making the World Work Better: The Ideas that Shaped a Century and a Company, 2011.

Supplied material for a Microsoft Report report to Craig Mundie to justify Microsoft support of external projects, 2011.

Highlighted in a DOE report to be presented to congress to secure funding for DOE and NERSC, 2011.

"A Database of Dynamics" by Allison Doerr, *Nature Methods*, **7**, 426 (2010). This article profiles our Dynameomics Project and was written in response to our van der Kamp et al. paper in *Structure* (and on the cover of the journal).

"Proteins Unraveled" by Philip Ball. Chemistry World, Royal Society of Chemistry, 58-62, 2009.

The Microsoft External Research booklet on Socially Relevant Computing featured an article on the Dynameomics Project and how it pertains to understanding and developing treatments for diseases such as Alzheimers, Parkinson's, and cancer, 2009.

Our work with Microsoft External Research to create a GrayWulf cluster optimized to analyze our Dynameomics data was featured in a Microsoft Report, 2009. Read more about the project in this report from Microsoft and on the msdn eScience blog.

Various Microsoft books and brochures in 2009, including their publications on "Socially Relevant Computing" and an overview of Microsoft External Research, as well as a brochure put out jointly by Microsoft and IBM on personalized medicine. In addition, they featured our work in

a video: http://www.microsoft.com/showcase/en/us/details/fd3395a1-726b-4e6f-a9d6-75328429c6d0.

The <u>Dynameomics Project</u>, which has been running on the supercomputers at NERSC since 2005 with the goal of simulating the unfolding pathways of all known protein folds, was recently listed as <u>a major accomplishment in Advanced Scientific Computing Research</u> by the Office of Science, US Department of Energy.

Microsoft released a press release about our work at http://www.microsoft.com/presspass/press/2008/nov08/11-06AlzHeavensPR.mspx which was picked up by The New York Times, Forbes, CNBC and others.

A Case Study was done by Microsoft in August of 2008 investigating the data management scheme the group has developed for the Dynameomics Database. Microsoft SQL Server 2005 and OLAP are used to mine over 20 terabytes of simulation data which reside on three servers. (http://www.microsoft.com/casestudies/casestudy.aspx?casestudyid=4000002488).

The Washington Research Foundation highlighted the Group's in-house molecular dynamics software, *in lucem* molecular mechanics, in their 2007 Annual Report (http://www.wrfseattle.org/2007_Annual_Report.pdf).

Bioinform, one of GenomeWeb's Application-Focus Newsletters: "The integrated informatics news source", featured the Daggett Group's research in an article entitled UW Team Creates High-Performance Workflow To Explore Molecular Dynamics of Proteins by Vivien Marx, July 7, 2008 (http://depts.washington.edu/daglab/downloads/Bioinform_2008.pdf).

Microsoft featured the Group's integration of Windows software in a Case Study in June of 2008 (http://www.microsoft.com/casestudies/casestudy.aspx?casestudyid=4000002104). High-performance computing clusters running Windows Compute Cluster Server are used to run the lab's molecular dynamics software with better performance than the optimized Linux version, and Microsoft SQL Server powers the 14-terabyte Dynameomics Database.

The group's application of Microsoft's software was also featured in a Press Release (http://www.microsoft.com/presspass/press/2008/jun08/06-11HPCResearchPR.mspx).

Bleeding Edge Biotech, a blog hosted by Carnegie Mellon computational biologist Adam Kraut, highlighted the Dynameomics Project in April of 2008 (http://www.bleedingedgebiotech.com/blog/bioengineering/dynameomics-mass-annotation-of-protein-dynamics/).

Chemistry and Engineering News, Proteins from Birth to Death, August 27, 2007. Re. our prion research.

Big Picture on Epidemics, Wellcome Trust, Issue 6, September 2007. Re. our prion research.

Biomedical Computation Review, "Biocomputational Startups: Where Does Value Lie?" by Katharine Miller, Spring 2007, 6-15.

Department of Energy, *National Energy Research Scientific Computing Center Annual Report* 2005, "Proteins in Motion" by John Hules, Summer 2006. (http://www.nersc.gov/news/annual_reports/annrep05/research-news/11-proteins.html)

Our prion work is profiled in the 2006 UW Research Calendar, July.

The Scientist, "Unraveling Protein Folding" by Melissa Lee Phillips, 19, 42, 2005.

ProteoMonitor, The Global Newsweekly of Proteomics Technology, "Washington Group Awarded 2 Million Hours of Supercomputing Time to Study Protein Folding", by TSL, January 7, 2005.

Department of Energy press release December 22, 2004, "DOE Allocates Massive Supercomputer Resources to Drive Advances in Combustion, Astrophysics and Protein Structure Research", (http://www.energy.gov/news/1563.htm)

This press release was followed by approximately 200 secondary articles and announcements in magazines, websites, newspapers, etc. (not listed here)

Nature, "New Role for Pauling's Ribbons" by Christopher Surridge, **430**, 739, 2004.

Science, "A Neatly Pleated Alpha Sheet" by Orla Smith, 305, 1534, 2004.

IRIS Universe Magazine. "Romancing the Molten Globule" by Grant Ellis, **23**: 58-61, SGI Inc., 1993.

Computer Graphics World Magazine. "The Stuff of Life" by Diana P. Mahoney **16**(6): 54-60, Penwell Publications, 1993.