

# Curriculum vitae—Lila M. Gierasch

Distinguished Professor  
Departments of Biochemistry & Molecular Biology and Chemistry  
University of Massachusetts Amherst  
Amherst, MA 01003  
(413)545-6094; Fax (413)545-1289; email: gierasch@biochem.umass.edu

## EDUCATION

---

Mount Holyoke College, So. Hadley, MA	A.B. 1970	Chemistry
Harvard University, Cambridge, MA	Ph.D. 1975	Biophysics (E.R. Blout, advisor)

## PROFESSIONAL EXPERIENCE

---

1974-1979	Assistant Professor of Chemistry, Amherst College
1977-1978	Visiting Scientist, Université Louis Pasteur de Strasbourg (with J.M. Lehn)
1979-1981	Assistant Professor of Chemistry, University of Delaware
1981-1985	Associate Professor of Chemistry, University of Delaware
1983-1984	Visiting Scientist, Smith Kline & French
1985-1988	Professor of Chemistry, University of Delaware
1988-1994	Professor of Pharmacology and Robert A. Welch Professor of Biochemistry, The University of Texas Southwestern Medical Center at Dallas
1991-1994	Director, Molecular Biophysics Graduate Program, UT Southwestern
1994-1999	Head, Dept. of Chemistry, Univ. of Massachusetts Amherst
1999-2005	Head, Dept. of Biochem. & Mol. Biology, Univ. of Massachusetts, Amherst
1994-	Professor of Chemistry, Univ. of Massachusetts Amherst
1999-	Professor of Biochemistry & Molecular Biology, Univ. of Massachusetts Amherst
2006-	Distinguished Professor, University of Massachusetts, Amherst

## HONORS AND AWARDS

---

1970	A. B. conferred summa cum laude and with great distinction
1970-1973	NSF Predoctoral Fellowship
1977-1978	French Ministry of Foreign Affairs Fellowship
1984-1986	A.P. Sloan Fellowship
1984	Vincent du Vigneaud Award for Young Investigators in Peptide Research
1985	Mary Lyon Award, Mount Holyoke College
1986	Guggenheim Fellowship
1987	Distinguished Faculty Lecturer, College of Arts & Science, Univ. of Delaware
1989	Fellow, American Association for the Advancement of Science
1999	Distinguished Faculty Lecturer/Chancellor's Medal, Univ. of Massachusetts
2002	D. Sc. Honoris Causa, Mount Holyoke College
2002	Samuel F. Conti Faculty Fellowship, University of Massachusetts, Amherst
2002	Outstanding Service Award, College of Nat. Sci. & Math., UMass, Amherst
2006	Named Distinguished Professor, University of Massachusetts, Amherst
2006	Francis P. Garvan-John M. Olin Medal of the American Chemical Society
2006	Award for Outstanding Accomplishments in Research & Creative Activity, UMass
2006	NIH Director's Pioneer Award
2008	Fellow, Massachusetts Academy of Science
2008	Goodman Lecturer, Univ. of California, San Diego
2009	Welch Lecturer, Texas
2010	Dorothy Crowfoot Hodgkin Award, The Protein Society
2014	Fellow, Biophysical Society
2014	Mildred Cohn Award, ASBMB

2016 Francis D. Carlson Lecturer, Johns Hopkins University  
2016 Elected Fellow, American Academy of Arts and Sciences  
2016 Outstanding Investigator Grant (Maximizing Investigators' Research Award (MIRA)),  
National Institute of General Medical Sciences, NIH  
2016 Editor-in-Chief, *The Journal of Biological Chemistry*  
2018 American Chemical Society Ralph F. Hirschmann Award in Peptide Chemistry

## SERVICE TO PROFESSION

---

1981-1983 Consultant, NICHD Contracts Program on Peptides as Gonadotropin Inhibitors  
1983-1987 Member, BCB Study Section, NIH  
1985-1986 Consultant, Merck Sharp & Dohme Research Laboratories  
1986-1994 Member, Scientific Advisory Board, Biosym Technologies, Inc.  
1991-1994 Founder and Director, Molecular Biophysics Graduate Program, UT Southwestern  
1994-1998 Member, Scientific Advisory Board, Damon Runyon/Walter Winchell Foundation  
1995-2001 Member, Selection and Scheduling Committee, Gordon Res. Conferences  
1996 Member, Visiting Committee, Dept. of Chemistry, Duke University  
1997 Member, Chemical Sciences Roundtable, National Research Council  
1998-2001 Member, National Advisory General Medical Sciences Council, NIH  
1998-2001 Member, Advisory Committee, Directorate for Math and Physical Sciences, NSF  
1983-1991 Member, American Peptide Symposium Planning Committee  
1993-1999 Member, Council of the American Peptide Society  
1990-1993 Member, U.S. National Committee for IUPAC  
1991-1997 Member, U.S. National Committee for IUPAB (Chair, 1997)  
1991-1994 Chair, Biophysical Society Publications Committee  
1995-1996 President, Biophysical Society  
1996-1998 Member, FASEB Board  
1997-2000 Member, Finance Committee, Biophysical Society  
1994-1996 Executive Committee, Div. of Biol. Chem., Amer. Chem. Soc.  
1998-2001 Member, Nominating Committee, ASBMB  
1988 Chair, "Proteins" Gordon Research Conference  
1988 Co-Organizer, AAAS Symposium "Protein Folding"  
1991 Program Chair, Biophysical Society Annual Meeting  
1993,1995 Vice-Chair, Chair "Membrane-Molecular Biology" Gordon Research Conference  
2002,2004 Vice-Chair, Chair "Protein Folding Cell" FASEB Summer Conference  
2002 Outside Review Panel, Dept. of Biochemistry, Purdue University  
2003-2006 Member, Council, ASBMB  
2004-2010 Member, Finance Committee, Biophysical Society  
2003-2006 Member, Discussions Committee, Biophysical Society  
2004 Member, Physical Biochemistry Study Section, NIH  
2005-2008 Member, MSFB Study Section, NIH  
2005 Co-Organizer, Johns Hopkins Folding Meeting  
2006-2009 Executive Committee, Biological Division of the American Chemical Society  
2006-2007 Member, External Advisory Committee, University of Kansas COBRE Grant  
2006-2009 Member, Executive Council, The Protein Society  
2006- Member, Protein Structure Initiative Advisory Committee to NIGMS Council  
2008-2011 Member, Advisory Committee, FASEB Summer Conferences  
2009- Member, Scientific Advisory Board, Mass. Life Sciences Initiative  
2009 External Review Committee, Dept. of Chemistry, Univ. of Virginia  
2009- Consultant, Vertex Pharmaceuticals  
2009 Co-Organizer, Keystone Meeting on Protein Dynamics and Allostery  
2009-2012 Elected member, American Peptide Society Nominating Committee  
2011 External review committee, Boston University Med. School Graduate Program in  
Molecular Biophysics

2011	External review committee, UCSF Graduate Program in Biophysics
2012	Co-organizer, 6 <sup>th</sup> Peptide Engineering Meeting, Emory Univ., October 2012
2012-2013	Member, PSI:Biology Evaluation Team, NIGMS, NIH
2013-2014	Chair, Biopolymers In Vivo Subgroup, Biophysical Society
2013-2016	Elected member, ASBMB Nominating Committee
2013-2014	National Institutes of General Medical Sciences "Future of Structural Biology Committee"
2014-2015	Elected member, Biophysical Society Nominating Committee
2014	Dissertation Opponent, Linkoping University, Sweden
2014	External review committee, Wesleyan University Biophysics Program
2014	External review committee, University of Texas, Austin, Molecular Biosciences Department
2014-2017	Member, NIH Office of the Director Council of Councils
2016	External review committee, The Johns Hopkins University Jenkins Department of Biophysics
2017	External review committee, The University of Toronto Dept. of Biochemistry
2018	External review committee, The University of Texas Southwestern Medical Center Graduate Program in Molecular Biophysics
2018-2023	Member, Scientific Advisory Board, Max Planck Institute of Biochemistry

### **SOCIETY MEMBERSHIPS**

---

AAAS, ACS, ASBMB, Biophysical Soc., Amer. Soc. Cell Biol., Amer. Peptide Soc., The Protein Society

### **EDITORIAL ADVISORY BOARDS**

---

1988-1995	<i>Journal of Molecular Recognition</i>
1989-1996	<i>International Journal of Peptide and Protein Research</i>
1992-1999	<i>Biochemistry</i>
1996-1999	<i>Folding and Design</i>
1998-1993	<i>Peptide Research</i>
1997-2005	<i>Journal of Peptide Research</i>
2000-2003	<i>Journal of Biological Chemistry</i>
2006-2013	<i>Chemical Biology and Drug Design</i>
1987-2012	<i>Biopolymers</i>
1988-	<i>Proteins: Structure, Function and Genetics</i>
1993-2015	<i>Chemistry &amp; Biology</i>
1999-	<i>Structure with Folding &amp; Design</i>
2004-2008	Editor-in-Chief, <i>Peptide Science</i>
2009-2016	Associate Editor, <i>Peptide Science</i>
2006-	<i>Protein Science</i>
2007-	<i>Chemistry Central Journal</i>
2014-	<i>Accounts of Chemical Research</i>
2014-	<i>ACS Central Science</i>
2016-2020	Editor-in-Chief, <i>The Journal of Biological Chemistry</i>

### **KEYNOTE, PLENARY, AND MAJOR INVITED LECTURES (2010 TO PRESENT)**

---

Keynote Speaker, Peptides Gordon Conference, Ventura, California, February 2010.

Keynote Speaker, Dept. of Molecular, Microbial and Structural Biology Retreat, U. Conn. Health Center, May 2010.

Plenary Speaker, WorldWide Magnetic Resonance Conference, Florence, Italy, July 2010.

Plenary Speaker, Symposium in Honor of Johan Deisenhofer, Dallas, TX, July 2010.

Invited Speaker, FASEB Conference Protein Folding in the Cell. July 2010.

Award Lecture, Protein Society Annual Meeting, San Diego, CA, August 2010.

Plenary Speaker, Nobel Symposium on Protein Biophysics in the Cell, Stockholm, Sweden. August 2010.

Merck Lecturer, SUNY New Paltz. September 2010.

Plenary Lecture, Upstate NY NMR Conference. November 2010.

Plenary Lecture, 10<sup>th</sup> German Peptide Symposium. Halle, Germany, March 2011.

Plenary Lecture, City College of NY Frontiers of NMR Spectroscopy Symposium. March 2011.

Plenary Lecture, Barcelona BioMed Conference on Macromolecular Dynamics. Barcelona, Spain, October 2011.

Plenary Lecture, Cold Spring Harbor Asia Conference on Protein Homeostasis in Health & Disease, Suzhou, China, September 2011.

Invited Lecture, Protein Folding and Dynamic Gordon Conference, Ventura, California, January 2012.

Invited Lecture, Lorne Conference on Protein Structure and Function, Australia, February 2012.

Invited Lecture, Bijvoet Tutorial Symposium, Utrecht, Netherlands, April 2012.

Invited Lecture, Israel Science Foundation Workshop on Protein Folding and Misfolding: Moving Beyond Simple Model Systems, Israel, May 2012.

Keynote Lecture, Biopolymers Gordon Conference, June 2012.

Invited Lecture, FASEB Meeting on Protein Folding in the Cell, August 2012.

Srere Lecturer, Dept. of Biochemistry and Dept. of Biophysics, UT Southwestern, November 2012.

Keynote Lecture, IDP Subgroup, Biophysical Society, March 2013.

New & Notable Lecture, Biophysical Society, March 2013.

Invited Lecture, EMBO Conference "The Biology of Molecular Chaperones", Sardinia, Italy, May 2013.

Plenary Lecture, Swedish Structural Biology Network Annual Conference, Tällberg, Sweden, June 2013.

Lampton Lecturer, University of Washington, October 2013.

University Lecturer, UT Southwestern, January 2014.

Mildred Cohn Award Lecture, ASBMB, April 2014.

Invited Lecture, Linköping University, Sweden, May 2014.

Keynote Lecture, FASEB Meeting on Protein Folding in the Cell, July 2014.

Plenary Lecture, Belgian Society of Biophysics Annual Meeting, Brussels, Belgium, October 2014.

Invited Lecture, Takeda Pharmaceuticals, Cambridge, MA, May 2015.

Beckman Scholars Lecture, Univ. of Michigan, April 2015.

Frederic Richards Lecturer, Yale University, March 2015.

Invited Lecture, FASEB Meeting on Biophysical and Physiological Aspects of Amyloid, June 2015.

Invited Lecture, Cold Spring Harbor Meeting on Protein Homeostasis in Health and Disease, May 2016.

Francis D. Carlson Lecturer in Biophysics, Johns Hopkins University, May 2016.

Invited Lecture, Gordon Conference on Intrinsically Disordered Proteins, June 2016.

Invited Lecture, FASEB Meeting on Protein Folding in the Cell, July 2016.

Invited Lecture, Workshop on Chaperones in the maintenance of cellular proteostasis, Baeza, Spain, October 2016.

Invited Lecture, Third Protein Folding Symposium, Bangalore, India, November 2016.

Mary Jane Osborne Lecturer, The Univ. of Connecticut Health Science Center, June 2017.

Invited Speaker, Nobel Symposium on Protein Folding, Stockholm, Sweden, June 2017.

Invited Speaker, Proteins Gordon Research Conference, June 2017.

Keynote Lecture, Univ. of Liege Graduate Student Symposium, Liège, Belgium, November 2017.

Invited Speaker, Cold Spring Harbor meeting "Protein Homeostasis in Health and Disease", April 2018.

Keynote Lecture, Protein Folding Diseases Initiative Symposium, Univ. of Michigan, October 2018.

---

## TEACHING AND ACADEMIC LEADERSHIP

*At Amherst College (1974-79):*

My first academic position included teaching responsibilities in Introductory Chemistry, Organic Chemistry, Biochemistry, and Spectroscopy classes, all with laboratories. I created several laboratory

experiments for the Spectroscopy course. I mentored 2 to 3 undergraduates each year in research. Amherst College became a coeducational institution while I was there, and there were few women faculty members. I was the only one in the sciences or mathematics. As a result, I played many roles, from informal academic and career mentoring to coaching women's teams (track, cross-country, and horseback riding) and serving on advisory committees to the administration on the transition to coeducation.

*At the University of Delaware (1979 to 1987):*

My principal undergraduate teaching responsibility was a one-semester Biochemistry class taken by chemistry majors and graduate students from a variety of programs. This was a very well rated course. In addition, I taught graduate courses in Biophysical Methods and Protein Structure. I mentored 4 or so undergraduates in my lab each year. I did not have any formal academic leadership positions.

*At the University of Texas Southwestern Medical Center (1988 to 1994):*

While at UT Southwestern, I held the Robert A. Welch Chair in Biochemistry, with a primary appointment in Pharmacology and a joint appointment in Biochemistry. I was an active participant in the reorganization of the graduate programs at UT Southwestern in 1988. I spearheaded the creation of a training program in Molecular Biophysics, which successfully obtained an NIH training grant. This paved the way for this training program to become an official graduate program during the reorganization. I served as PI of the Training Grant and Director of the Graduate Program until my departure in 1994. This graduate program has since thrived, and recently, a Department of Molecular Biophysics was created from the strong community that dates back to the early organization of the graduate training program in Molecular Biophysics. As part of the reorganization of the Graduate School, I was one of a small group who created a highly successful core course for all incoming students in Biomedical Sciences, and I was one of the principal instructors in this course during my years at UT Southwestern. I also spearheaded the creation of several modular Biophysics courses and taught several of these.

*At the University of Massachusetts-Amherst (1994 to present):*

I was recruited to UMass to be Head of the Chemistry Department, and after 5 years moved to become Head of the Biochemistry & Molecular Biology Department. I have retained joint membership in the two departments. Under my leadership, a novel first year core course was established in the Chemistry graduate program, and laboratory rotations were initiated for first year students. During my two Headships, ten faculty were hired in the Chemistry Department and four in Biochemistry & Molecular Biology. In addition, I served for many years on the Steering Committee for both the NIH Chemistry-Biology Interface (CBI) Training Program and as a co-PI of the NSF IGERT on Cellular Engineering. While at UMass., my group has typically comprised 4 to 7 postdoctoral fellows, 4 to 6 graduate students, and 3 to 4 students. I also have had a number of high school students work in the lab. In 1999, I created and taught a course in Drug Design that has become a centerpiece of our NIH-funded CBI training program (it is the only course all CBI students must take). This class is now offered every year to advanced undergraduates and graduate students. In addition to my teaching roles, I have spearheaded the successful building of two major new interdisciplinary research and teaching buildings at UMass Amherst, which helped to dislodge a logjam in new science building. I was instrumental in the establishment of an Institute for Applied Life Sciences in 2015 and organized and led the Models to Medicine Center of IALS until last year. IALS garnered a \$95M grant from the Life Sciences Institute of the Commonwealth of Massachusetts, and I helped to organize a number of new core facilities with this support.

## MENTORSHIP

---

On the following pages are listed names and current positions for all graduate students and postdoctoral associates who have worked under my direction. Many undergraduates have worked in the lab as well, and I keep in touch with most; they are a highly successful and scientifically passionate group.

I care deeply about those who work with me and take very seriously my responsibility for their growth as scientists and their successful navigation of a career path. I have always given high priority to the quality of the training a student or postdoctoral fellow receives, even when this might conflict with the expediency of attaining research results or publications. Happily, the latter flourish when the former is nourished.

In addition to the mentoring of my own research group, I have both formally and informally invested considerable energy in mentoring students and junior colleagues. Examples include my efforts to foster the careers of junior faculty when I was Head of either the Chemistry or Biochemistry & Molecular Biology Departments, my continuing commitment and efforts to work with faculty at earlier stages in their careers, my serving on multiple occasions on panels giving advice and perspective on tenure and other career stages, both on campus and at professional society annual meetings, and my having served on panels at several institutions as a role model or mentor to students at several levels. Whenever a visit a campus or attend a meeting, I make a point of meeting students, seeing and discussing posters, and, in any way I can, sharing whatever wisdom that I have gained during my career.

## GRADUATE STUDENTS AND POST-DOCTORAL FELLOWS TRAINED IN THE GIERASCH LAB

---

### Masters students

<u>Name</u>	<u>Year</u>	<u>Current Position</u>
Karyn O'Neil	1985	CSO and Founder at Aro Biotherapeutics
Terry Triplett	1995	Senior Java consultant, Ericsson
Guenter Wittrock	1999	Senior IT Applications Analyst, Seattle Children's Hospital
Rebecca Eden	2000	Graduate Student in Linguistics, University of Oklahoma
Jason Griffin	2001	High school science teacher
Bing Gong	2004	Senior Director, Compass Therapeutics LLC
Mangai Periasamy	2010	DST-INSPIRE faculty, CSIR-Indian Institute of Chemical Technology
Joseph Tilitsky	2017	Research Associate, Kanyos Bio

### Doctoral Students

<u>Name</u>	<u>Year</u>	<u>Current Position</u>
Jeffrey Lacy	1986	Professor, Shippensburg State College
Martha S. Briggs	1986	High school chemistry teacher, Atlanta, GA
Edmund Baniak	1987	Senior Standards Associate, American Petroleum Inst.
Alvin C. Bach	1988	Associate Professor, University of Rhode Island
Adam N. Stroup	1989	Research Scientist, US Army
C. James McKnight	1990	Professor, Boston University Medical School
David Hoyt	1990	Senior Research Scientist, Pacific Northwest Research Labs
Laura Lark	1990	Project Leader, Emergency Medical Associates, Dallas, TX
Anu Bansal	1991	Senior Principal Scientist, Genentech
Zhi-Ping Liu	1993	Associate Professor, University of Texas Southwestern
Ning Zheng	1997	Professor, HHMI, University of Washington

Patricia Clark	1997	Professor, Notre Dame University
Richard Kibbey	2000	Associate Professor, Yale Univ. School of Medicine
Robert Cleverley	2002	Research Associate, Newcastle University, England
Kenneth Rotondi	2002	Laboratory Instructor in Chemistry, Amherst College
Renuka Sivendran	2003	Director Analytical Development at Five Prime Therapeutics, Inc.
Catherine Goodman	2003	Scientific Editor, JBC
Yi-Te Chou	2004	Research Scientist, Amgen
Gizem Dinler	2006	Professor, Istanbul Technical University, Turkey
Anne Marie Marcelino	2008	Research Scientist, Regeneron
Jenny Lynn Maki	2009	Scientific Recruiter and Consultant at Recruitomics Consulting
TJ Brunette (co-mentored)	2010	Postdoctoral Fellow, University of Washington
Rob Smock	2011	Postdoctoral Fellow, EMBL Hamburg, Germany
Mylene Castell Ferrolino	2013	Postdoctoral Fellow, St. Jude Children's Research Hospital
Kristine Faye Pobre	2016	Postdoctoral Fellow, St. Jude Children's Research Hospital
Karan Hingorani	2016	Medical student, Boston University Medical School
Robert G. Smock	2011	Postdoctoral Fellow, EMBL Hamburg, Germany
Mylene Castell Ferrolino	2013	Postdoctoral Fellow, St. Jude Children's Research Hospital
Kristine Faye Pobre	2016	Postdoctoral Fellow, St. Jude Children's Research Hospital
Karan S. Hingorani	2016	Medical student, Boston University Medical School

### **Postdoctoral Fellows and Research Associates**

<b><u>Name</u></b>	<b><u>Years in lab</u></b>	<b><u>Current Position</u></b>
Maria Rafalski	85-88	Senior Research Scientist, Incyte Corp.
Madan Dhingra	88-89	Retired
Jose Rizo Rey	89-91	Professor, University of Texas Southwestern
Rachelle Bienstock	89-91	Guest Researcher NIH
Jeffrey Jones	89-93	Police officer, Dallas, TX
Samuel Landry	89-93	Associate Professor, Tulane Univ. Med. School
Francisco Blanco	90-90	Principal Investigator, CIC bioGUNE, Derio, Spain
Carolyn Lee	90-92	Postdoctoral Fellow, Sci & Tech Policy Institute
Zhulun Wang	91-94	Science Director, Amgen
Muppalla Sukumar	93-98	Research Advisor, Eli Lilly
Michael Goger	94-98	Director NMR Facility, NY Structural Biology Consortium
Hwa-Ping Feng	94-99	Research Scientist, Merck
Stephen Eyles	95-00	Director Mass Spec. Facility, University of Massachusetts
Diana Montgomery	96-99	Principal Scientist, Merck
Joanna Swain	97-07	Director, Protein Engineering, Cogen Therapeutics
Kannan Gunasekaran	99-01	Senior Director, Biotherapeutics at Denali Therapeutics
Muthu Dhanasekaran	00-01	Research Scientist, University of Arizona
Zoya Ignatova	00-04	Professor, University of Hamburg, Germany
Elaine Allen McVey	01-02	Business Owner, Municipal Market at TransLoc
Elena Falkovskaia	01-04	EQA Editor, McGraw-Hill Education
Marc Vogt	02-05	Engineer/Technologist, General Electric
Aneta Szymanska	03-04	Assistant Professor, University of Gdansk, Poland
Jiang Hong	06-10	Assistant Professor, Shanghai University, China
Qinghua Wang	06-10	Bioinformatics Scientist, University of Delaware
Harekrushna Sahoo	07-10	Assistant Professor, Natl. Inst. of Technology, Rourkela, India
Beena Krishnan	04-11	Senior Scientist, IMTECH, Chandigarh, India
Santosh Kumar	10-11	Newton International Fellow, Univ. of Birmingham, England
Ivan Budyak	07-13	Research Scientist, Eli Lilly

---

Anastasia Zhuravleva	07-13	Lecturer, Univ. of Leeds, UK
Mandy Blackburn	09-14	Assistant Professor, Univ. of Central Missouri
Weiwei Kuo	12-16	Staff Fellow, US FDA
Abhay Thakur	11-16	Senior Scientist, Lake Pharma
Charles English	15-18	Data Incubator Fellow, NY

## RESEARCH OVERVIEW

---

Our work has the overarching goal of understanding the relationship between amino acid sequence and the preferred conformations of peptides and proteins. Our early work helped establish the now-common approach of using peptide fragments to examine functionally important interactions of proteins. Initially, I designed peptide models of reverse turns. This work has shed light on turn propensities in proteins and offered a basis for design of analogues of bioactive peptides. With collaborators, we developed potent, conformationally-constrained antagonists of gonadotrophin-releasing hormone. We elucidated conformational propensities and physical properties of signal sequences, which helped to explain how diverse sequences target polypeptide chains to the secretory pathway. We were among the first to describe how molecular chaperones recognize 'unfoldedness' in their protein substrates: We showed that the chaperonin GroEL exploits hydrophobic surfaces to recognize substrates, while Hsp70s bind polypeptides as extended chains. Our laboratory discovered the GroEL-interactive 'mobile loop' on GroES. More recent work is focused on understanding of the mode of action of these molecular machines, in particular the Hsp70 family. We have investigated the folding mechanism of  $\beta$ -rich proteins. Recently, we have developed strategies to explore protein folding landscapes in the cell. Genetic incorporation of a specific binding site for a cell-permeable fluorescent dye has provided a measure of protein stability in vivo and allowed off-pathway aggregation events to be observed. We are combining our interrogation of protein folding networks in the cell with computational modeling of all reactions involving protein folding and quality control in *E. coli*. Taken together, our approach enables fundamental study of conformational defects that are implicated in human misfolding diseases such as Alzheimer's, Huntington's, and others.

## GRANT SUPPORT (last 15 years, reverse chronological order)

---

NIH R35 GM118161 Gierasch, PI

MIRA grant, Protein Folding in the Cell: Challenges and Coping Mechanisms  
6/1/2016 to 5/31/2021

Funding level \$515,702 (TDC, steady state, lower in years 1 and 2 to phase out other funding)

Alpha1 Foundation Hebert, Gershenson, & Gierasch, co-PIs

Optimizing Alpha1-antitrypsin Folding for Gene Therapy  
7/1/16 to 2/28/19

Funding level \$100,000 (Annual TDC)

NIH R01 GM101644 Multi-PI grant, with Gierasch, L and Powers, E., PIs.

Modeling a Cellular Protein Homeostasis Network  
9/3/2013 to 8/31/2017 (terminating because of grant consolidation in MIRA)



Funding level \$408,725 (TDC for the last year, UMass and Scripps)

NIH R01 GM027616 Gierasch, PI

Allosteric Mechanism of Hsp70 Molecular Chaperones. [Former title: Peptide and Protein Conformations.]

Continuous support for 37 years; ended 7/31/2016 when MIRA was funded.

Funding level \$318,000 (TDC for the last year).

NIH R01 GM094848 Gierasch, co-PI with Anne Gershenson and Dan Hebert.

Post-Reductionist Protein Folding [Eureka grant]

9/1/2010 to 8/31/2015

Funding level \$300,000 (TDC for the last year).

International Rett Syndrome Foundation Woodcock, C, PI, Gierasch, L, co-PI

Rett Syndrome - a Protein Folding Disease?

1/1/2007 to 12/31/2008

Funding level \$50,000 (TDC annually)

NIH DP1 OD000945 Gierasch, PI

NIH Director's Pioneer Award

9/28/2006 to 7/31/2013

Funding level \$785,000 (TDC annually).

NIH R01 GM076706 Gierasch, PI; co-PI Oliver Brock (originally PI with Gierasch co-PI)

Predicting Protein Structure with Guided Conformation Space Search

8/1/2006 to 7/31/2013

Funding level \$227,860 (TDC for the last year)

NIH R01 GM34962 Gierasch, PI

Signal Sequences – Conformations and Membrane Binding

1/1/1986 to 12/30/2007; ended when Pioneer grant was awarded

Funding level \$212,233 (TDC for the last year)

## PUBLICATIONS

---

1. L. G. (Gierasch) Pease, C. M. Deber, and E. R. Blout, Cyclic Peptides, V.  $^1\text{H}$  and  $^{13}\text{C}$  nuclear magnetic resonance determination of the preferred  $\beta$  conformation for proline-containing cyclic hexapeptides, *J. Am. Chem. Soc.*, 95, 258-260 (1973).
2. E. R. Blout, C. M. Deber, and L. G. Pease, Cyclic peptides, in *Polypeptides, Peptides, and Proteins*, E. R. Blout, F. A. Bovey, M. Goodman, and N. Lotan, Eds., Interscience, New York, pp. 266-281 (1974).
3. D. Baron, L. G. Pease, and E. R. Blout, Cyclic peptides, 19. Cation binding of a cyclic dodecapeptide cyclo-(L-Val-Gly-Gly-L-Pro)<sub>3</sub> in an aprotic medium, *J. Am. Chem. Soc.*, 99, 8299-8306 (1977).
4. L. G. Pease and C. Watson, Conformational and ion binding studies on a cyclic pentapeptide: evidence for  $\beta$  and  $\gamma$  turns in solution, in *Peptides: Proceedings of the Fifth American Peptide Symposium*, M. Goodman, and J. Meienhofer, Eds., John Wiley and Sons, New York, pp. 346-349 (1977).

5. C.-H. Niu, L. G. Pease and E. R. Blout, Cyclic peptides. XVIII.  $^{13}\text{C}$  spin-lattice relaxation times of  $(\text{X-L-Pro-Y})_2$  cyclic hexapeptides, *Biopolymers*, 17, 115-123 (1978).
6. L. G. Pease and C. Watson, Conformational and ion binding studies of a cyclic pentapeptide: evidence for  $\beta$  and  $\gamma$  turns in solution, *J. Am. Chem. Soc.*, 100, 1279-1286 (1978).
7. C.-H. Niu, V. Madison, L. G. Pease and E. R. Blout, Cyclic peptides, XXII. Cation binding by a cyclic hexapeptide, Cyclo-(D-Ala-L-Pro-Gly) $_2$ , *Biopolymers*, 17, 2747-2751 (1978).
8. B. Dietrich, T. Fyles, J. M. Lehn, L. G. Pease and D. L. Fyles, Anion receptor molecules. synthesis and some anion binding properties of macrocyclic guanidinium salts, *JCS Chem. Comm.*, pp. 934-936 (1978).
9. K. L. Williamson, L. G. Pease and J. D. Roberts, Conformational analysis by nuclear magnetic resonance spectroscopy:  $^{15}\text{N}$  NMR of a cyclic pentapeptide, *J. Am. Chem. Soc.*, 101, 714-716 (1979).
10. K. R. K. Easwaran, L. G. Pease and E. R. Blout, Cyclic Peptides, XXIII. Conformations of an ion-binding cyclic peptide analog of valinomycin, Cyclo-(L-Val-Gly-Gly-L-Pro) $_3$ , *Biochemistry*, 18, 61-67 (1979).
11. L. G. Pease, C.-H. Niu and G. Zimmermann, Solution conformation of cyclo(Gly-Pro-Ser-D-Ala-Pro). Hydrogen-bonded reverse turns in cyclic pentapeptides, *J. Am. Chem. Soc.*, 101, 184-191 (1979).
12. L. G. Pease, Preferred hydrogen-bonded conformations of cyclic pentapeptides, in *Peptides: Structure and Biological Function, Proceedings of the Sixth American Peptide Symposium*, E. Gross and J. Meienhofer, Eds., Pierce Chem. Co., Rockford, IL, pp. 197-200 (1979).
13. L. G. Pease, D. Baron, K. R. K. Easwaran and E. R. Blout, A valinomycin analogue containing only naturally-occurring amino acids, in *Frontiers of Bio-Organic Chemistry and Molecular Energy*, S. N. Ananchenko, Ed., Pergamon Press, Oxford, pp. 81-91 (1980).
14. J. A. Smith and L. G. Pease, Reverse turns in peptides and proteins, *CRC Crit.Rev. Biochemistry*, 8, 315-400 (1980).
15. L. G. Pease, M. H. Frey and S. J. Opella, Observation of conformationally distinct proline residues in two model peptides by solid-state nuclear magnetic resonance, *J. Am. Chem. Soc.*, 103, 467-468 (1981).
16. L. M. Gierasch, C. M. Deber, V. Madison, C.-H. Niu and E. R. Blout, Conformations of  $(\text{X-L-Pro-Y})_2$  cyclic hexapeptides. preferred  $\beta$ -turn conformers and implications for  $\beta$  turns in proteins, *Biochemistry*, 20, 4730-4738 (1981).
17. T. H. Walter, G. L. McIntire, E. E. Bancroft, E. R. Davis, L. M. Gierasch and H. N. Blount, Interfacial spin trapping in model membrane systems, *Biochem.Biophys. Res. Comm.*, 102, 1350-1357 (1981).
18. J. E. Lacy, K. F. Thompson, P. I. Watnick and L. M. Gierasch, Conformations of model peptides in membrane-mimetic environments, in *Peptides: Synthesis, Structure and Function*, D. H. Rich and E. Gross, Eds., Pierce Chem. Co., Rockford, IL, pp. 339-342 (1981).
19. A. C. Bach, II, A. A. Bothner-By and L. M. Gierasch, Estimation of proline ring nonplanarity in cyclic pentapeptides from proton spin-spin coupling constants, in *Peptides: Synthesis, Structure and Function*, D. H. Rich and E. Gross, Eds., Pierce Chem. Co., Rockford, IL, pp. 343-346 (1981).
20. L. M. Gierasch, S. J. Opella and M. H. Frey, Solid-state NMR of peptides, in *Peptides: Synthesis, Structure and Function*, D. H. Rich and E. Gross, Eds., Pierce Chem. Co., Rockford, IL, pp. 267-275 (1981).
21. L. M. Gierasch, J. E. Lacy, K. F. Thompson, A. L. Rockwell and P. I. Watnick, Conformations of model peptides in membrane-mimetic environments, *Biophys. J.*, 37, 275-284 (1982).

22. A. C. Bach, II, A. A. Bothner-By and L. M. Gierasch, Determination of proline ring nonplanarity from proton spin-spin coupling constants: applications to two cyclic pentapeptides, *J. Am. Chem. Soc.*, 104, 572-576 (1982).
23. L. M. Gierasch, M. H. Frey, J. G. Hexem and S. J. Opella, Solid state NMR of linear and cyclic peptides, in *NMR Spectroscopy: New Methods and Applications*, George C. Levy, Ed., ACS Symposium Ser. No. 191, Washington, D.C., 233-247 (1982).
24. T. H. Walter, E. E. Bancroft, G. L. McIntire, E. R. Davis, L. M. Gierasch, H. N. Blount, H. J. Stronks and E. G. Janzen, Spin trapping in heterogeneous electron transfer processes, *Canadian J. Chem.*, 60, 1621-1636 (1982).
25. A. F. Spatola, L. M. Gierasch and A. L. Rockwell, A conformational comparison of cyclic peptide and pseudopeptide structures with intramolecular hydrogen bonding, *Biopolymers*, 22, 147-151 (1983).
26. L. M. Gierasch, J. E. Lacy, G. Anderle, R. Lalancette and R. Mendelsohn, Spectroscopic studies of a hydrophobic peptide in membrane-like environments, *Biopolymers*, 22, 381-385 (1983).
27. G. D. Rose, W. B. Young and L. M. Gierasch, Interior Turns in Globular Proteins, *Nature*, 304, 654-657 (1983).
28. J. L. Flippen-Anderson, R. Gilardi, I. L. Karle, M. H. Frey, S. J. Opella, L. M. Gierasch, M. Goodman, V. Madison and N. G. Delaney, Crystal structures, molecular conformations, infrared spectra and <sup>13</sup>C NMR spectra of methylproline peptides in the solid state, *J. Am. Chem. Soc.*, 105, 6609-6614 (1983).
29. M. H. Frey, J. G. Hexem, G. D. Leo, P. Tsang, S. J. Opella, A. L. Rockwell and L. M. Gierasch, Solid state NMR of peptides in membrane bilayers, in *Proceedings of the Eighth American Peptide Symposium*, V. Hruby and D. H. Rich, Eds., Pierce Chem. Co., Rockford, IL, pp. 763-771 (1983).
30. K. Yenai, A. L. Rockwell, J. P. Cook, S. Dworetzky and L. M. Gierasch, Comparison of cation binding by three cyclic pentapeptides, in *Proceedings of the Eighth American Peptide Symposium*, V. Hruby and D. H. Rich, Eds., Pierce Chem. Co., Rockford, IL, pp. 499-502 (1983).
31. A. C. Bach, II, B. S. Dunn, L. M. Gierasch, Y. Shimohigashi and C. S. Stammer, Conformational consequences of incorporating ΔPhe in an enkephalin analogue and in related peptides, in *Proceedings of the Eighth American Symposium*, V. Hruby and D. H. Rich, Eds., Pierce Chem. Co., Rockford, IL, pp. 299-302 (1983).
32. J. E. Lacy, L. M. Gierasch, A. L. Rockwell, and G. D. Rose, Reverse turns in hydrophobic environments, in *Proceedings of the Eighth American Peptide Symposium*, V. Hruby and D. H. Rich, Eds., Pierce Chem. Co., Rockford, IL, pp. 781-784 (1983).
33. A. C. Bach, II, A. A. Baldwin, L. M. Gierasch and A. L. Rheingold, Characterization of a methoxylated 5-oxazolone derivative: an unexpected intermediate in a dehydropeptide synthesis, *JCS Chem. Comm.*, pp. 1398-1399 (1983).
34. L. M. Gierasch, K. F. Thompson, J. E. Lacy and A. L. Rockwell, Exploring peptide interactions with interfacial water using reversed micelles, in *Biological and Technological Relevance of Reverse Micelles and Other Amphiphilic Structures in Apolar Media*, P. L. Luisi, Ed., Plenum Press, New York, pp. 265-277 (1984).
35. K. F. Thompson and L. M. Gierasch, The conformation of a peptide solubilize in a reversed micelle water pool, *J. Am. Chem. Soc.*, 106, 3648-3652 (1984).
36. M. S. Briggs and L. M. Gierasch, Exploring the conformational roles of signal sequences: synthesis and conformational analysis of lambda receptor protein wild type and mutant signal peptides, *Biochemistry*, 23, 3111-3114 (1984).

37. L. M. Gierasch, A. L. Rockwell, K. F. Thompson and M. S. Briggs, Conformation-function relationships in hydrophobic peptides: interior turns and signal sequences, *Biopolymers*, 24, 117-135 (1985).
38. M. D. Bruch, J. H. Noggle and L. M. Gierasch, Conformational analysis of a cyclic pentapeptide by one- and two-dimensional nuclear overhauser effect spectroscopy, *J. Am. Chem. Soc.*, 107, 1400-1407 (1985).
39. G. D. Rose, L. M. Gierasch and J. A. Smith, Turns in peptides and proteins, *Adv. Protein Chem.*, Vol. 37, C. B. Anfinsen, J. T. Edsall and F. M. Richards, Eds., Academic Press, New York, pp. 1-109 (1985).
40. M. H. Frey, S. J. Opella, A. L. Rockwell and L. M. Gierasch, Solid state NMR of cyclic pentapeptides, *J. Am. Chem. Soc.*, 107, 1946-1951 (1985).
41. M. S. Briggs, L. M. Gierasch, A. Zlotnick, J. Lear and W. F. DeGrado, In vivo function and membrane binding properties are correlated for E. coli LamB signal peptides, *Science*, 228, 1096-1099 (1985).
42. L. M. Gierasch, I. L. Karle, A. L. Rockwell and K. Yenai, Crystal and solution structures of Cyclo(Ala-Pro-Gly-D-Phe-Pro): A new type of cyclic pentapeptide which undergoes cis-trans isomerization of the ala-pro bond, *J. Am. Chem. Soc.*, 107, 3321-3327 (1985).
43. A. C. Bach, II and L. M. Gierasch, Dehydrophenylalanine as the i+2th residue of a  $\beta$ -turn: synthesis and conformation analysis of cyclo-(Gly-Pro- $\Delta^2$ -Phe-D-Ala-Pro) and cyclo(Gly-Pro-D-Phe-D-Ala-Pro), *J. Am. Chem. Soc.*, 107, 3349-3350 (1985).
44. M. K. Jain, J. Rogers, L. Simpson, and L. M. Gierasch, Effect of tryptophan derivatives on the phase properties of bilayers, *Biochim. Biophys. Acta*, 816, 153-162 (1985).
45. S. J. Opella and L. M. Gierasch, Solid state nuclear magnetic resonance of peptides, in *The Peptides*, Vol. 7, V. J. Hruby and J. Meienhofer, Eds., Academic Press, NY, pp. 405-436 (1985).
46. M. S. Briggs and L. M. Gierasch, Biophysical studies of genetically defined synthetic signal sequences, in *Proceedings of the Ninth American Peptide Symposium*, K. D. Kopple and C. M. Deber, Eds., Pierce Chem. Co., Rockford, IL, pp. 883-886 (1985).
47. A. C. Bach, II, L. M. Gierasch, and A. L. Rheingold, Synthesis and conformational analysis of three dehydrophenylalanine-containing cyclic pentapeptides, in *Proceedings of the Ninth American Peptide Symposium*, K. D. Kopple and C. M. Deber, Eds., Pierce Chem. Co., Rockford, IL, pp. 181-184 (1985).
48. L. M. Mueller, M. H. Frey, A. L. Rockwell, L. M. Gierasch and S. J. Opella, Dynamics of a hydrophobic peptide in membrane bilayers by solid state NMR, *Biochemistry*, 25, 557-561 (1986).
49. A. F. Spatola, M. K. Anwer, A. L. Rockwell and L. M. Gierasch, Compatibility of  $\beta$ - and  $\gamma$ -turn features with a peptide backbone modification: synthesis and conformational analysis of a model cyclic pseudopeptide, *J. Am. Chem. Soc.*, 108, 825-831 (1986).
50. L. M. Gierasch, M. S. Briggs, and D. G. Cornell, Physical properties of genetically-defined synthetic signal sequences suggest initial steps in protein export, in *Protein Engineering*, M. Inouye and R. Sarma, Eds., Academic Press, Orlando, FL, pp. 173-191 (1986).
51. M. S. Briggs and L. M. Gierasch, Molecular mechanisms of protein secretion: the role of the signal sequence, *Adv. Protein Chem.*, Vol. 38, C. B. Anfinsen, F. M. Richards and J. T. Edsall, Eds., Academic Press, 109-180 (1986).
52. A. C. Bach, II and L. M. Gierasch, Dehydrophenylalanine can occur in various reverse turn sites: conformational analysis of  $\Delta$ Phe-containing model peptides, *Biopolymers*, 25, S175-S191 (1986).
53. M. S. Briggs, D. G. Cornell, R. A. Dluhy and L. M. Gierasch, Conformations of signal peptides induced by lipids suggest initial steps in protein export, *Science*, 233, 206-208 (1986).

54. D. W. Hoyt, C. J. McKnight, M. S. Briggs, A. N. Stroup and L. M. Gierasch, Biophysical properties of synthetic presequences suggest conformations important for protein localization, in *Peptides 1986*, D. Theodoropoulos, Ed., Walter de Gruyter & Co., Berlin, pp. 373-376 (1986).
55. E. L. Baniak, II, J. E. Rivier, A. T. Hagler, and L. M. Gierasch, Nuclear magnetic resonance analysis and conformational characterization of a cyclic decapeptide antagonist of gonadotropin-releasing hormone, *Biochemistry*, 26, 2642-2656 (1987).
56. L. Chen, P. C. Tai, M. S. Briggs and L. M. Gierasch, Protein translocation into *E. coli* membrane vesicles is inhibited by functional synthetic signal sequences, *J. Biol. Chem.*, 262, 1427-1429 (1987).
57. K. G. Valentine, A. L. Rockwell, L. M. Gierasch and S. J. Opella,  $^{15}\text{N}$  chemical shift tensor of the imide nitrogen in the alanyl-prolyl peptide bond, *J. Mag. Res.*, 73, 519-523 (1987).
58. A. N. Stroup, A. L. Rockwell and L. M. Gierasch, Crystal structure of cyclo(Gly-L-Pro-D-Phe-Gly-Val): An example of a new type of three residue turn, *J. Am. Chem. Soc.*, 109, 7146-7150 (1987).
59. E. L. Baniak and L. M. Gierasch, NMR analysis and conformational characterization of cyclic antagonists of gonadotropin releasing hormone, in *Peptides: Chemistry and Biology*, G. Marshall, Ed., ESCOM Science Publishers, Leiden, The Netherlands, pp. 457-458 (1988).
60. L. R. Sanza, L. M. Gierasch, J. A. Berzofsky, G. K. Buckenmeyer, K. B. Cease and C. S. Ouyang, formation of amphipathic secondary structure is correlated to T-cell antigenicity in a series of synthetic peptides from sperm whale myoglobin, in *Peptides: Chemistry and Biology*, G. Marshall, Ed., ESCOM Science Publishers, Leiden, The Netherlands, pp. 549-550 (1988).
61. L. M. Gierasch, M. S. Briggs and C. J. McKnight, Role of the signal sequence in protein secretion, in *Peptides: Chemistry and Biology*, G. Marshall, Ed., ESCOM Science Publishers, Leiden, The Netherlands, pp. 313-317 (1988).
62. A. N. Stroup, A. L. Rockwell, A. L. Rheingold and L. M. Gierasch, Crystal structure of cyclo(Gly<sub>1</sub>-L-Pro<sub>2</sub>-D-Phe<sub>3</sub>-L-Ala<sub>4</sub>-L-Pro<sub>5</sub>): A cyclic pentapeptide with a Gly-L-Pro  $\delta$  turn, *J. Am. Chem. Soc.*, 110, 5157-5161 (1988).
63. R. A. Schiksnis, A. L. Rockwell, L. M. Gierasch, and S. J. Opella, Detection of a Structural interconversion in a peptide in solution with sensitivity-enhanced  $^{15}\text{N}$  chemical-exchange NMR spectroscopy, *J. Mag. Res.*, 79, 318-321 (1988).
64. L. M. Gierasch, Signal sequences, *Biochemistry*, 28, 923-930 (1989).
65. D. G. Cornell, R. A. Dluhy, M. S. Briggs, C. J. McKnight, and L. M. Gierasch, Conformations and orientations of a signal peptide interacting with phospholipid monolayers, *Biochemistry*, 28, 2789-2797 (1989).
66. E. L. Baniak II, Y.-C. Ma, L. M. Gierasch, and B. Munson, Ring-opening of cyclic pentapeptides by electron impact mass spectrometry: correlation with peptide bond nonplanarity, *J. Am. Chem. Soc.*, 111, 5487-5488 (1989).
67. C. J. McKnight, M. S. Briggs, and L. M. Gierasch, Functional and nonfunctional LamB signal sequences can be distinguished by their biophysical properties, *J. Biol. Chem.*, 264, 17293-17297 (1989).
68. M. D. Bruch, C. J. McKnight, and L. M. Gierasch, Helix formation and stability in a signal sequence, *Biochemistry*, 28, 8554-8561 (1989).
69. L. R. Lark, J. A. Berzofsky, and L. M. Gierasch, T-Cell Antigenic Peptides from Sperm Whale Myoglobin Fold as Amphipathic Helices: A Possible Determinant for Immunodominance?, *Peptide Research*, 2, 314-321 (1989).
70. M. D. Bruch and L. M. Gierasch, Comparison of helix stability in wildtype and mutant LamB signal sequences, *J. Biol. Chem.*, 265, 3851-3858 (1990).

71. S. J. Stradley, J. Rizo, M. D. Bruch, A. N. Stroup, and L. M. Gierasch, Cyclic pentapeptides as models for reverse turns: determination of the equilibrium distribution between Type I and Type II conformations of Pro-Asn and Pro-Ala  $\beta$ -turns, *Biopolymers*, 29, 263-287 (1990).
72. J. Rivier, C. Rivier, W. Vale, S. Koerber, A. Corrigan, J. Porter, L. Gierasch, and A. Hagler, Bicyclic gonadotropin releasing hormone (GnRH) antagonists, in *Peptides: Chemistry, Structure, and Biology*, J. Rivier and G. Marshall, Eds., ESCOM Science Publishers, Leiden, The Netherlands, pp. 33-37 (1990).
73. S. J. Stradley, J. Rizo, M. D. Bruch, Z.-P. Liu, and L. M. Gierasch, Influence of asparagine on turn formation in cyclic pentapeptides, in *Peptides: Chemistry, Structure, and Biology*, J. Rivier and G. Marshall, Eds., ESCOM Science Publishers, Leiden, The Netherlands, pp. 644-646 (1990).
74. T. Siahaan, L. R. Lark, M. Pierschbacher, E. Ruoslahti, and L. M. Gierasch, A conformationally constrained 'RGD' analogue specific for the vitronectin receptor: a model for receptor binding, in *Peptides: Chemistry, Structure, and Biology*, J. Rivier and G. Marshall, Eds., ESCOM Science Publishers, Leiden, The Netherlands, pp. 699-701 (1990).
75. M. D. Bruch, C. J. McKnight, and L. M. Gierasch, NMR analysis of structural stability and specific residue conformations in wild type and mutant LamB signal sequences, in *Peptides: Chemistry, Structure, and Biology*, J. Rivier and G. Marshall, Eds., ESCOM Science Publishers, Leiden, The Netherlands, pp. 548-551 (1990).
76. L. M. Gierasch, Conformation and interactions of signal peptides: approaches to elucidating the role of the signal sequence in protein secretion, in *Protein Folding: Deciphering the Second Half of the Genetic Code*, L. M. Gierasch and J. King, Eds., AAAS Publications, Washington, D.C., pp. 211-219 (1990).
77. *Protein Folding: Deciphering the Second Half of the Genetic Code*, L. M. Gierasch and J. King, Eds., AAAS Publications, Washington, D.C. (1990).
78. A. Bansal, S. J. Stradley, and L. M. Gierasch, Conformational studies of peptides corresponding to the LDL receptor cytoplasmic tail and transmembrane domain, in *Current Research in Protein Chemistry*, J. Villafranca, Ed., Academic Press, San Diego, CA, pp. 331-338 (1990).
79. J. D. Jones, C. J. McKnight, and L. M. Gierasch, Biophysical studies of signal peptides: implications for signal sequence functions and the involvement of lipid in protein export, *J. Bioenerg. Biomembr.*, 22, 213-232 (1990).
80. A. N. Stroup and L. M. Gierasch, Reduced tendency to form a  $\beta$  turn in peptides from the P22 tailspike protein correlates with a temperature-sensitive folding defect, *Biochemistry*, 29, 9765-9771 (1990).
81. R. S. Struthers, G. Tanaka, S. Koerber, T. Solmajer, E. L. Baniak, L. M. Gierasch, W. Vale, J. Rivier, and A. T. Hagler, Design of conformationally constrained GnRH antagonists, *Proteins: Structure, Function, and Genetics*, 8, 295-304 (1990).
82. A. N. Stroup, L. B. Cole, M. M. Dhingra, and L. M. Gierasch, Synthesis and crystal structures of Boc-L-Asn-L-Pro-OBzl CH<sub>3</sub>OH and dehydration side product, Boc- $\beta$ -Cyano-L-Alanine-L-Pro-OBzl, *Intl. J. Pept. Prot. Res.*, 36, 531-537 (1990).
83. Y. Reiss, S. J. Stradley, L. M. Gierasch, M. S. Brown, and J. L. Goldstein, Sequence requirement for peptide recognition by rat brain p21<sup>ras</sup> protein farnesyltransferase, *Proc. Natl. Acad. Sci. USA*, 88, 732-736 (1991).
84. S. J. Landry and L. M. Gierasch, Recognition of nascent polypeptides for targeting and folding, *Trends Biochem. Sci.*, 16, 159-163, (1991).
85. J. Rizo, M. M. Dhingra, and L. M. Gierasch, A Cyclic hexapeptide model for asparagine side-chain/backbone interactions in a protein  $\beta$  turn, in *Peptides: Proceedings of the Twenty-First*

*European Peptide Symposium*, E. Giralt and D. Andreu, Eds., ESCOM Science Publishers, Leiden, The Netherlands, pp. 468-471 (1991).

86. M. D. Bruch, M. M. Dhingra, and L. M. Gierasch, Side chain-backbone hydrogen bonding contributes to helix stability in peptides derived from an  $\alpha$ -helical region of carboxypeptidase A, *Proteins: Structure, Function, and Genetics*, 10, 130-139 (1991).

87. C. J. McKnight, M. Rafalski, and L. M. Gierasch, Fluorescence analysis of tryptophan-containing variants of the LamB signal sequence upon insertion into a lipid bilayer, *Biochemistry*, 30, 6241-6246 (1991).

88. C. J. McKnight, S. J. Stradley, J. D. Jones, and L. M. Gierasch, Conformational and membrane-binding properties of a signal sequence are largely unaltered by its adjacent mature region, *Proc. Natl. Acad. Sci. USA*, 88, 5799-5803 (1991).

89. S. J. Landry and L. M. Gierasch, The chaperonin GroEL binds a polypeptide in an  $\alpha$ -helical conformation, *Biochemistry*, 30, 7359-7362 (1991).

90. D. W. Hoyt and L. M. Gierasch, A peptide corresponding to an export-defective mutant OmpA signal sequence with asparagine in the hydrophobic core is unable to insert into model membranes, *J. Biol. Chem.*, 266, 14406-14412 (1991).

91. J. L. Goldstein, M. S. Brown, S. J. Stradley, Y. Reiss, and L. M. Gierasch, Nonfarnesylated tetrapeptide inhibitors of protein farnesyltransferase, *J. Biol. Chem.*, 266, 15575-15578 (1991).

92. D. W. Hoyt, D. M. Cyr, L. M. Gierasch, and M. G. Douglas, Interaction of peptides corresponding to mitochondrial presequences with membranes, *J. Biol. Chem.*, 266, 21693-21699 (1991).

93. D. W. Hoyt and L. M. Gierasch, Hydrophobic content and lipid interactions of wild-type and mutant OmpA signal peptides correlate with their in vivo function, *Biochemistry*, 30, 10155-10163 (1991).

94. A. Bansal and L. M. Gierasch, The NPXY internalization signal of the LDL receptor adopts a reverse turn conformation, *Cell*, 67, 1195-1201 (1991).

95. J. Rizo, M. M. Dhingra, and L. M. Gierasch, Peptide models for reverse turns, The role of asparagine in the i position of a  $\beta$  turn, in *Molecular Conformation and Biological Interactions*, P. Balaram and S. Ramaseshan, Eds., Indian Academy of Sciences, Bangalore, India pp. 469-496 (1991).

96. L. M. Gierasch, Relation of amino acid sequence to structure and folding, in *Conformations and Forces in Protein Folding*, Barry T. Nall and Ken A. Dill, Eds., American Association for the Advancement of Science, Washington, D.C., pp. 67-68 (1991).

97. S. J. Landry, R. Jordan, R. McMacken, and L. M. Gierasch, Different conformations for the same polypeptide bound to chaperones DnaK and GroEL, *Nature*, 355, 455-457 (1992).

98. L. M. Gierasch, J. D. Jones, S. J. Landry, and S. J. Stradley, Biophysical studies of recognition sequences for targeting and folding, *Antonie van Leeuwenhoek, Journal of Microbiology*, 61, 93-99 (1992).

99. S. J. Stradley, Y. Reiss, M. S. Brown, J. L. Goldstein, and L. M. Gierasch, Tetrapeptides compete with p21<sup>ras</sup> for farnesylation catalyzed by protein farnesyltransferase, in *Peptides: Chemistry and Biology*, J. A. Smith, Ed., ESCOM Science Publishers, Leiden, The Netherlands, pp. 933-934 (1992).

100. J. Rizo, F. Blanco, B. Kobe, M. D. Bruch, D. W. Hoyt, and L. M. Gierasch, Conformations of wild-type and mutant OmpA signal sequences in membrane-mimetic environments, in *Peptides: Chemistry and Biology*, J. A. Smith, Ed., ESCOM Science Publishers, Leiden, The Netherlands, pp. 265-267 (1992).

101. R. J. Bienstock, S. C. Koerber, J. Rizo, J. Rivier, A. T. Hagler, and L. M. Gierasch, Conformation of a highly potent bicyclic GnRH antagonist by combined molecular dynamics and two-

- dimensional NMR analyses, in *Peptides: Chemistry and Biology*, J. A. Smith, Ed., ESCOM Science Publishers, Leiden, The Netherlands, pp. 262-264 (1992).
102. S. J. Landry and L. M. Gierasch, Recognition of peptides by the *E. coli* molecular chaperones, GroEL and DnaK, in *Peptides: Chemistry and Biology*, J. A. Smith, Ed., ESCOM Science Publishers, Leiden, The Netherlands, pp. 206-208 (1992).
103. J. Rizo and L. M. Gierasch, Constrained peptides: models of bioactive peptides and protein substructures, *Ann. Rev. Biochem.*, 61, 387-418 (1992).
104. B. Nagel, H. Dellweg and L. M. Gierasch, Glossary for chemists of terms used in biotechnology (IUPAC Recommendations 1992), *Pure & Appl. Chem.*, 64, 143-168 (1992).
105. J. Rizo, S. C. Koerber, R. J. Bienstock, J. Rivier, A. T. Hagler, and L. M. Gierasch, Conformational analysis of a highly potent, constrained gonadotropin-releasing hormone antagonist I. Nuclear magnetic resonance, *J. Am. Chem. Soc.*, 114, 2852-2859 (1992).
106. J. Rizo, S. C. Koerber, R. J. Bienstock, J. Rivier, L. M. Gierasch, and A. T. Hagler, Conformational analysis of a highly potent, constrained gonadotropin-releasing hormone antagonist II. Molecular dynamics simulations, *J. Am. Chem. Soc.*, 114, 2860-2871 (1992).
107. W. Zhi, S. J. Landry, L. M. Gierasch, and P. A. Srere, Renaturation of citrate synthase: influence of denaturant and folding assistants, *Protein Sci.*, 1, 522-529 (1992).
108. J. Zhang, Z.-P. Liu, T. A. Jones, L. M. Gierasch, and J. F. Sambrook, Mutating the charged residues in the binding pocket of cellular retinoic acid-binding protein simultaneously reduces its binding affinity to retinoic acid and increases its thermostability, *Proteins: Structure, Function, and Genetics*, 13, 87-99 (1992).
109. J. Rivier, S. Koerber, C. Rivier, A. Hagler, M. Perrin, L. Gierasch, A. Corrigan, J. Porter, and W. Vale, Design, physico-chemical characterization, and biological activity of gonadotropin releasing hormone (GnRH) antagonists as potential contraceptives, in *Proceedings of the International Symposium on Frontiers in Reproductive Research: the Role of Growth Factors Oncogenes, Receptors and Gonadal Polypeptides*, Li, Chen, Hahn and McGuire, Eds., Beijing Medical University, The National Institute of Child Health and Human Development, U. S. Department of Health and Human Services, pp. 15-37 (1992).
110. A. N. Stroup, A. L. Rockwell, and L. M. Gierasch, Solution conformation of two flexible cyclic pentapeptides: cyclo(Gly-Pro-D-Phe-Gly-Ala) and cyclo(Gly-Pro-D-Phe-Gly-Val), *Biopolymers*, 32, 1713-1725 (1992).
111. Z.-P. Liu and L. M. Gierasch, Combined use of molecular dynamics simulations and nmr to explore peptide bond isomerization and multiple intramolecular hydrogen bonding possibilities in a cyclic pentapeptide, cyclo(Gly-Pro-D-Phe-Gly-Val), *Biopolymers*, 32, 1727-1739 (1992).
112. M. D. Bruch, J. Rizo, and L. M. Gierasch, Impact of a Micellar Environment on the Conformations of Two Cyclic Pentapeptides, *Biopolymers*, 32, 1741-1754 (1992).
113. J. Rizo, F. J. Blanco, B. Kobe, M. D. Bruch and L. M. Gierasch, Conformational behavior of *E. coli* OmpA signal peptides in membrane mimetic environments, *Biochemistry*, 32, 4881-4894 (1993).
114. S. J. Landry, J. Zeilstra-Ryalls, O. Fayet, C. Georgopoulos, and L. M. Gierasch, Characterization of a functionally important mobile domain of GroES, *Nature*, 364, 255-258 (1993).
115. R. J. Bienstock, J. Rizo, S. C. Koerber, A. T. Hagler, J. Rivier, and L. M. Gierasch, Conformational analysis of a highly potent dicyclic gonadotropin-releasing hormone antagonist by nuclear magnetic resonance and molecular dynamics, *J. Med. Chem.*, 36, 3265-3273 (1993).
116. J. D. Miller, H. Wilhelm, L. M. Gierasch, R. Gilmore and P. Walter, GTP binding and hydrolysis by the signal recognition particle during initiation of protein translocation, *Nature*, 366, 351-354 (1993).



117. S. J. Stradley, J. Rizo, and L. M. Gierasch, The conformation of a heptapeptide substrate bound to protein farnesyltransferase, *Biochemistry*, 32, 12586-12590 (1993).
118. Z. Wang, J. D. Jones, J. Rizo, and L. M. Gierasch, Membrane-bound conformation of a signal peptide: A transferred nuclear overhauser effect analysis, *Biochemistry*, 32, 13991-13999 (1993).
119. L. M. Gierasch, Signal sequences: roles and interactions by biophysical methods, in *Biological Membranes: Structure, Biogenesis and Dynamics*, J.A. F. Op den Kamp, Ed., Springer-Verlag, New York, pp. 191-198 (1993).
120. Z. P. Liu, J. Rizo, and L. M. Gierasch, Equilibrium folding studies of cellular retinoic acid binding protein, a predominantly  $\beta$ -sheet protein, *Biochemistry*, 33, 134-142 (1994).
121. L. M. Gierasch, Panning for chaperone-binding peptides, *Current Biology*, 4, 173-174 (1994).
122. S. J. Landry and L. M. Gierasch, Polypeptide interactions with molecular chaperones and the relationship to *in vivo* protein folding, *Ann. Rev. Biophys. Biomol. Struct.*, 23, 645-669 (1994).
123. M. B. Sankaram, D. Marsh, L. M. Gierasch and T. E. Thompson, Reorganization of lipid domain structure in membranes by a transmembrane peptide, *Biophys. Journal*, 66, 1959-1968 (1994).
124. J. Rizo, R. B. Sutton, J. Breslau, S. C. Koerber, J. Porter, J. E. Rivier, A. T. Hagler and L. M. Gierasch, Defining the active conformation of gonadotropin releasing hormone (GnRH) through design and conformational analysis of constrained GnRH analogs, in *Proceedings of the Thirteenth American Peptide Symposium*, R. S. Hodges and J. A. Smith, Eds., ESCOM Science Publishers, Lieden, The Netherlands, pp. 766-768 (1994).
125. J. D. Jones and L. M. Gierasch, Effect of charged residue substitutions on the membrane-interactive properties of signal sequences of the Escherichia coli LamB protein, *Biophys. Journal*, 67, 1534-1545 (1994).
126. J. D. Jones and L. M. Gierasch, Effect of Charged Residue Substitutions on the Thermodynamics of signal peptide-lipid interactions of the Escherichia coli LamB signal sequence, *Biophys. Journal*, 67, 1546-1561 (1994).
127. J. Rizo, Z.-P. Liu and L. M. Gierasch,  $^1\text{H}$  and  $^{15}\text{N}$  resonance assignments and secondary structure of cellular retinoic acid binding protein with and without bound ligand, *J. Biomol. NMR*, 4, 741-760 (1994).
128. C. H. Wu, A. Ramamoorthy, L. M. Gierasch, and S. J. Opella, Simultaneous characterization of the amide  $^1\text{H}$ - $^{15}\text{N}$  dipolar, and  $^{15}\text{N}$  chemical shift interaction tensors in a peptide bond by three-dimensional solid-state NMR spectroscopy, *J. Am. Chem. Soc.*, 117, 6148-6149 (1995).
129. L. M. Gierasch, Z. Wang, J. Hunt, S. J. Landry, A. Weaver, and J. Deisenhofer, Chaperone-substrate interactions, *Protein Eng.*, 8, Suppl., 14-18 (1995).
130. M. Sukumar, J. Rizo, M. Wall, L. A. Dreyfus, Y. M. Kuperstoch, and L. M. Gierasch, The structure of Escherichia coli heat-stable enterotoxin B by nuclear magnetic resonance and circular dichroism, *Protein Sci.*, 4, 1718-1729 (1995).
131. A. Ramamoorthy, L. M. Gierasch, and S. J. Opella, Four-dimensional solid-state NMR experiment that correlates the chemical shift and dipolar coupling frequencies of two heteronuclei with the exchange of dilute spin magnetization, *J. Magn. Res., Ser. B*, 109, 112-116 (1995).
132. J. F. Hunt, A. Weaver, S. J. Landry, L. M. Gierasch, and J. Deisenhofer, The crystal structure of the GroES co-chaperonin at 2.8 Å resolution, *Nature*, 379, 37-45 (1996).
133. J. Rizo and L. M. Gierasch, Peptide and Protein Secondary Structure Elements:  $\beta$ -turns,  $\alpha$ -helices and  $\beta$ -sheets, in *Encyclopedia of NMR*, Eds. D. M. Grant and R. K. Harris, John Wiley & Sons, pp. 3517-3526 (1996).

134. A. Ramamoorthy, L. M. Gierasch, and S. J. Opella, Resolved two-dimensional anisotropic chemical shift/heteronuclear dipolar coupling powder pattern spectra by three-dimensional solid-state NMR spectroscopy, *J. Magn. Res., Ser. B*, 110, 102-106 (1996).
135. J. Rizo, R. B. Sutton, J. Breslau, S. C. Koerber, J. Porter, A. T. Hagler, J. E. Rivier, and L. M. Gierasch, A novel conformation in a highly potent, constrained gonadotropin releasing hormone antagonist, *J. Am. Chem. Soc.*, 118, 970-976 (1996).
136. P. L. Clark, Z. P. Liu, J. H. Zhang, and L. M. Gierasch, Intrinsic tryptophans of CRABPI as probes of structure and folding, *Protein Sci.*, 5, 1108-1117 (1996).
137. N. Zheng and L. M. Gierasch, Signal Sequences: The same yet different, *Cell*, 86, 849-852 (1996).
138. B. Bechinger, L. M. Gierasch, M. Montal, M. Zasloff, and S. J. Opella, Orientations of helical peptides in membrane bilayers by solid-state NMR spectroscopy, *J. Solid State Nuclear Magnetic Resonance*, 7, 185-191 (1996).
139. A. Ramamoorthy, L. M. Gierasch, and S. J. Opella, Three-dimensional solid-state NMR correlation experiment with  $^1\text{H}$  homonuclear spin-exchange, *J. Magn. Reson. B*, 111, 81-84 (1996).
140. J. Rivier, G. C. Jiang, S. L. Lahrachi, J. Porter, S. C. Koerber, J. Rizo, A. Corrigan, L. Gierasch, A. Hagler, W. Vale, and C. Rivier. Dose relationship between GnRH antagonists and pituitary suppression. *Hum. Reprod. (Suppl.)* 3, 133-147 (1996).
141. M. Sukumar and L. M. Gierasch, Local interactions in a schellman motif dictate interhelical arrangement in a protein fragment, *Folding & Design*, 2, 211-222 (1997).
142. P. L. Clark, Z.-P. Liu, J. Rizo, and L. M. Gierasch, Cavity formation before stable hydrogen bonding in the folding of a  $\beta$ -clam protein, *Nature Struct. Biol.*, 4, 883-886 (1997).
143. N. Zheng and L. M. Gierasch, Domain Interactions in E. coli SRP: Stabilization of M domain by RNA is required for effective signal sequence modulation of NG domain, *Mol. Cell*, 1, 79-87 (1997).
144. N. Zheng, J. L. Feltham, and L. M. Gierasch, In vitro studies of the interactions between signal peptides and signal recognition factors, in *Molecular Mechanisms of Lipid and Protein Traffic*, J. A. F. Op den Kamp, Ed., Springer-Verlag, pp. 125-139 (1998).
145. Z. P. Liu, J. Rizo, and L. M. Gierasch, Protein folding, in *Bioorganic Chemistry*, S. M. Hecht, Ed., Oxford Press, pp. 224-257 (1998).
146. H. P. Feng and L. M. Gierasch, Molecular Chaperones: Clamps for the clips, *Current Biology*, 8, R464-R467 (1998).
147. R. G. Kibbey, J. Rizo, L. M. Gierasch, R. G. W. Anderson, The LDL receptor clustering motif interacts with the clathrin terminal domain in a reverse turn conformation, *J. Cell Biol.*, 142, 59-67 (1998).
148. P. L. Clark, B. F. Weston, and L. M. Gierasch, Probing the folding pathway of a  $\beta$ -clam protein with single-tryptophan constructs, *Folding & Design*, 3, 401-412 (1998).
149. S. J. Eyles, I. Kaltashov, and L. M. Gierasch, Probing the folding and unfolding dynamics of cellular retinoic acid-binding protein using H/D exchange and electrospray ionization mass spectrometry, *Proc. Amer. Soc. Mass Spectrom.*, 46, 380 (1998).
150. D. L. Montgomery, R. I. Morimoto, and L. M. Gierasch, Mutations in the substrate binding domain of the *Escherichia coli* 70 kDa molecular chaperone, DnaK, which alter substrate affinity or interdomain coupling, *J. Mol. Biol.*, 286, 915-932 (1999).
151. K. S. Rotondi and L. M. Gierasch, Using peptides to study the folding of a predominantly  $\beta$ -sheet protein, in *Peptide Science—Present and Future*, Y. Shimonishi, Ed., Kluwer Acad. Publ., pp. 228-231 (1999).

152. P. L. Clark, Z.-P. Liu, J. Rizo, M. Sukumar, K. S. Rotondi, and L. M. Gierasch, Folding of a predominantly  $\beta$  sheet protein with a central cavity, in *Peptides: Frontiers of Peptide Science*, J.P. Tam and P. T. P. Kaumaya, Eds., Kluwer/ESCOM, pp. 349-351 (1999).
153. Z. Wang, H. P. Feng, S. J. Landry, J. Maxwell, and L. M. Gierasch, Basis of substrate binding by the chaperonin GroEL, *Biochemistry*, 38, 12537-12546 (1999).
154. S. J. Eyles, T. Dresch, L. M. Gierasch, and I. A. Kaltashov, Unfolding dynamics of a  $\beta$ -sheet protein studied by mass spectrometry, *J. Mass Spectrometry*, 34, 1289-1295 (1999).
155. S. J. Eyles, J. P. Speir, G. H. Kruppa, L. M. Gierasch, and I. A. Kaltashov, Protein conformational stability probed by fourier transform ion cyclotron resonance mass spectrometry, *J. Am. Chem. Soc.*, 122, 495-500 (2000).
156. J. L. Feltham and L. M. Gierasch, GroEL-substrate interactions: Molding the fold, or folding the mold? *Cell*, 100, 193-196 (2000).
157. M. Pellecchia, D. L. Montgomery, S. Y. Stevens, C. W. Vander Kooi, H. P. Feng, L. M. Gierasch, and E. R. P. Zuiderweg, Structural insights into substrate binding by the molecular chaperone DnaK, *Nat. Struct. Biol.*, 7, 298-303 (2000).
158. Stephen J. Eyles and Lila M. Gierasch, Multiple roles of prolyl residues in structure and folding. *J. Mol. Biol.*, 301, 737-747 (2000).
159. V. Krishnan, M. Sukumar, L. M. Gierasch, and M. Cosman, Dynamics of cellular retinoic acid binding protein i on multiple time scales with implications for ligand binding, *Biochemistry*, 39, 9119-9129 (2000).
160. K. S. Rotondi, K. Gunasekaran, and L. M. Gierasch, Investigating the roles of turns in the folding of a predominantly  $\beta$ -sheet protein, in *Peptides for the New Millennium*, G. B. Fields, J.P. Tam and G. Barany, Eds., Kluwer/ESCOM, 32-33 (2000).
161. S. J. Eyles, J. A. Habink, K. Gunasekaran, and L. M. Gierasch, Roles of proline residues in the structure and folding of a  $\beta$ -clam protein, in *Peptides for the New Millennium*, G. B. Fields, J.P. Tam and G. Barany, Eds., Kluwer/ESCOM, pp. 313-315 (2000).
162. K. Gunasekaran, S. J. Eyles, A. T. Hagler, and L. M. Gierasch, Keeping it in the family: folding studies of related proteins, *Curr. Opin. Struc. Biol.*, 11, 83-93 (2001).
163. J. Feltham Swain, and L.M. Gierasch, Signal peptides bind and aggregate RNA: an alternative explanation for GTPase inhibition in the signal recognition particle, *J. Biol. Chem.*, 276, 12222-12227 (2001).
164. R. M. Cleverley, N. Zheng, and L. M. Gierasch, The cost of exposing a hydrophobic 'finger' loop and implications for the functional role of 4.5S RNA in the *E. coli* SRP, *J. Biol. Chem.*, 276, 19327-19331 (2001).
165. T. L. Triplett, A. R. Sgrignoli, F. B. Gao, Y. B. Yang, P. C. Tai, and L. M. Gierasch, functional signal peptides bind a soluble N-terminal fragment of SecA and inhibit its ATPase activity, *J. Biol. Chem.*, 276, 19648-19655 (2001).
166. J. L. Swain, R. Sivendran, and L. M. Gierasch, Defining the structure of the substrate-free state of the DnaK molecular chaperone, in *Biochemical Society Symposia No. 68: From Protein Folding to New Enzymes*, A. Berry and S. E. Radford, Eds. Portland Press Ltd., London, 69-82 (2001).
167. C. M. McIntosh, K. S. Rotondi, M. Dhanasekaran, K. Gunasekaran, A. Kazantzis, A. Kapurniotu, and L. M. Gierasch, Conformational analysis of human calcitonin in aqueous solution and comparison with a highly potent lactam-bridged analogue, in *Proceedings of the Seventeenth American Peptide Symposium*, 338-339 (2001).

168. L. M. Gierasch, K. S. Rotondi, K. Gunasekaran, J. A. Habink, and A. T. Hagler, Local and long-range sequence contributions to the folding of a predominantly  $\beta$ -sheet protein, in *Proceedings of the Seventeenth American Peptide Symposium*, 391-393 (2001).
169. L. M. Gierasch, Caught in the act: How ATP binding triggers cooperative conformational changes in a molecular machine, *Mol. Cell*, 9, 3-5 (2002).
170. J. F. Swain and L. M. Gierasch, A new twist for an Hsp70 chaperone, *Nat. Struct. Biol.*, 9, 406-408 (2002).
171. R. M. Cleverley, and L. M. Gierasch, Mapping the signal sequence-binding site on SRP reveals a significant role for the NG-domain, *J. Biol. Chem.*, 277, 46763-46768 (2002).
172. Y. T. Chou, J. F. Swain, and L. M. Gierasch, Functionally significant mobile regions of *Escherichia coli* SecA ATPase identified by NMR, *J. Biol. Chem.*, 277, 50985-50990 (2002).
173. J. Benach, Y. T. Chou, J. J. Fak, A. Itkin, D. D. Nicolae, P. C. Smith, G. Wittrock, D. L. Floyd, C. M. Golsaz, L. M. Gierasch, and J. F. Hunt, Phospholipid-induced monomerization and signal peptide-induced oligomerization of SecA, *J. Biol. Chem.*, 278, 3628-3638 (2003).
174. K. S. Rotondi, L. F. Rotondi, and L. M. Gierasch, Native Structural Propensity in Cellular Retinoic Acid Binding Protein I 64-88: The role of locally encoded structure in the folding of a  $\beta$ -barrel protein, *Biophys. Chem.*, 100, 421-436 (2003).
175. M. Kabani, S. H. Stewart, M. W. Morrow, D. L. Montgomery, R. Sivendran, M. D. Rose, L. M. Gierasch, and J. L. Brodsky, Dependence of endoplasmic reticulum associated degradation on the peptide binding domain and concentration of BiP, *Mol. Biol. Cell*, 14, 3437-3448 (2003).
176. K. S. Rotondi and L. M. Gierasch, The role of local sequence in the folding of cellular retinoic acid-binding protein 1: structural propensities of reverse turns, *Biochemistry*, 42, 7976-7985 (2003).
177. K. S. Rotondi and L. M. Gierasch, Local sequence information in cellular retinoic acid-binding protein 1: specific residue roles in  $\beta$ -turns, *Peptide Science*, 71, 638-651 (2003).
178. K. Gunasekaran, A. T. Hagler, and L. M. Gierasch, Sequence and structural analysis of cellular retinoic acid binding proteins reveals a network of conserved hydrophobic interactions, *Proteins: Structure Function and Bioinformatics*, 54, 179-194 (2004).
179. Z. Ignatova and L. M. Gierasch, Monitoring protein stability and aggregation in vivo by real-time fluorescent labeling, *Proc. Natl. Acad. Sci. USA*, 101, 523-528 (2004).
180. J. J. Fak, A. Itkin, D. D. Ciobanu, E. C. Lin, X.-J. Song, Y.-T. Chou, L. M. Gierasch, and J. F. Hunt, Nucleotide exchange from the high-affinity ATP-binding site in SecA is the rate-limiting step in the ATPase cycle of the soluble enzyme and occurs through a specialized conformational state, *Biochemistry*, 43, 7307-27 (2004).
181. K. S. Rotondi and L. M. Gierasch, Solution structure of daptomycin, in *Peptide Revolution: Genomics, Proteomics & Therapeutics*, (M. Chorev and T. Sawyer, eds.), pp. 447-449 (2004).
182. K. S. Rotondi and L. M. Gierasch, A well-defined amphipathic conformation for the calcium-free cyclic lipopeptide antibiotic, daptomycin, in aqueous solution, *Peptide Science*, 80, 374-385 (2005).
183. N. Sinha, C. V. Grant, K. S. Rotondi, L. Feduik-Rotondi, L. M. Gierasch, and S. J. Opella, Peptides and the development of double- and triple- resonance solid-state NMR of aligned samples, *J. Pept. Res.*, 65, 605-620 (2005).
184. Z. Ignatova and L. M. Gierasch, Aggregation of a slow-folding mutant of a  $\beta$ -clam protein proceeds through a monomeric nucleus, *Biochemistry*, 44, 7266-7274 (2005).
185. Y.-T. Chou and L. M. Gierasch, The conformation of a signal peptide bound by *Escherichia coli* preprotein translocase SecA, *J. Biol. Chem.*, 280, 32753-32760 (2005).

186. J. F. Swain and L. M. Gierasch, First glimpses of a chaperonin-bound folding intermediate, *Proc. Natl. Acad. Sci. USA*, 102, 13715-13716 (2005).
187. R. G. Smock and L. M. Gierasch, Finding the fittest fold: using the evolutionary record to design new proteins, *Cell*, 122, 832-834 (2005).
188. K. S. Rotondi and L. M. Gierasch, Natural polypeptide scaffolds:  $\beta$ -sheets,  $\beta$ -turns, and  $\beta$ -hairpins, *Peptide Science*, 84, 13-22 (2006).
189. J. F. Swain, E. G. Schulz, and L. M. Gierasch, Direct comparison of a stable isolated Hsp70 substrate-binding domain in the empty and substrate-bound states, *J. Biol. Chem.*, 281, 1605-11 (2006).
190. J. F. Swain and L. M. Gierasch, The changing landscape of protein allostery. *Curr. Opin. Struct. Biol.* 16, 102-108 (2006).
191. A. C. Marcelino, R. G. Smock, and L. M. Gierasch, Evolutionary coupling of structural and functional sequence information in the intracellular lipid-binding protein family, *Proteins: Structure Function Bioinformatics*, 63, 373-384 (2006).
192. Z. Ignatova and L. M. Gierasch, Extended PolyQ tracts cause aggregation and structural perturbation of a neighboring  $\beta$ -barrel protein, *J. Biol. Chem.*, 281, 12959-67 (2006).
193. L. F. Cavanaugh, A. G. Palmer III, L. M. Gierasch, and J. F. Hunt, disorder breathes life into a DEAD motor, *Nature Struct. Mol. Biology*, 13, 566-569 (2006).
194. Z. Ignatova and L. M. Gierasch, The natural osmolyte proline prevents protein aggregation in vitro and in vivo, *Proc. Natl. Acad. Sci. USA*, 103, 13357-61 (2006).
195. I. L. Mainprize, D. R. Beniac, R. M. Cleverley, L. M. Cleverley, L. M. Gierasch, F. P. Ottensmeyer, and D. W. Andrews, The structure of *E. coli* SRP revealed by scanning transmission electron microscopy suggests interdomain movement is involved in signal sequence recognition, *Mol. Cell Biol.*, 17, 5063-5074 (2006).
196. B.-R. Lin, L. M. Gierasch, C. Jiang, and P. C. Tai, Electrophysiological studies in *Xenopus* oocytes for the opening of *Escherichia coli* SecA-dependent protein-conducting channels, *J. Membr. Biol.*, 214, 103-13 (2006).
197. B. Krishnan, A. Szymanska, and L. M. Gierasch, Site-specific fluorescent labeling of poly-histidine sequences using metal-chelating cysteine, *Chem. Biol. & Drug Design*, 69, 31-40 (2007).
198. Z. Ignatova, B. Krishnan, J. P. Bombardier, A. M. C. Marcelino, J. Hong, and L. M. Gierasch, From the test tube to the cell: exploring the folding and aggregation of a  $\beta$ -clam protein, *Biopolymers-Peptide Science*, 88, 157-163 (2007).
199. Z. Ignatova and L. M. Gierasch, Effects of osmolytes on protein folding and aggregation in cells, *Methods Enzymol.*, 428, 355-372 (2007).
200. J. F. Swain, G. Dinler, R. Sivendran, D. L. Montgomery, M. Stotz, and L. M. Gierasch, Hsp70 chaperone ligands control domain association via an allosteric mechanism mediated by the interdomain linker, *Molecular Cell*, 26, 27-39 (2007).
201. Z. Ignatova, A. K. Thakur, R. B. Wetzel, and L. M. Gierasch, In-cell aggregation of a polyglutamine-containing chimera is a multistep process initiated by the flanking sequence, *J. Biol. Chem.* 282, 36736-43 (2007).
202. E. M. Clérico, J. L. Maki, and L. M. Gierasch. Use of synthetic signal sequences to explore the protein export machinery. *Biopolymers-Peptide Science*, 90, 307-319 (2008).
203. A. M. C. Marcelino and L. M. Gierasch, Roles of  $\beta$ -turns in protein folding: from peptide models to protein engineering. *Biopolymers*, 89, 380-391 (2008).

204. J. Hinz, L. M. Gierasch, and Z. Ignatova, Orthogonal cross-seeding – an approach to explore protein aggregates in living cells. *Biochemistry*, 47, 4196-4200 (2008).
205. R. P. Ghosh, R. A. Horowitz-Scherer, T. Nikitina, L. M. Gierasch, and C. L. Woodcock. Rett syndrome-causing mutations in human MECP2 result in diverse structural changes that impact folding and DNA interactions. *J. Biol. Chem.* 283, 20523-34 (2008).
206. B. Krishnan and L. M. Gierasch, Cross-strand split tetra-Cys FIAsh-binding motifs as structure sensors in a  $\beta$ -sheet protein. *Chemistry & Biology* 15, 1104-1115 (2008). [Cover article]
207. Z. Ignatova and L. M. Gierasch, A fluorescent window into protein folding and aggregation in cells. *Methods Cell Biol.*, 89, 59-70 (2008).
208. Z. Ignatova and L. M. Gierasch, A method for direct measurement of protein stability in vivo. *Methods Mol. Biol.*, 490, 165-178 (2009).
209. R. G. Smock and L. M. Gierasch, Sending signals dynamically: how protein motions mediate cellular communication pathways, *Science*, 324, 198-203 (2009). [Cover article]
210. E. M. Clérico, A. Szymanska, and L. M. Gierasch. Exploring the interactions between signal sequences and *E. coli* SRP by two distinct and complementary cross-linking methods. *Biopolymers-Peptide Science*, 92, 201-211 (2009).
211. D. N. Hebert and L. M. Gierasch. The molecular dating game: an antibody heavy chain hangs loose with its chaperone while waiting for a life partner. *Mol. Cell*, 34, 635-636 (2009).
212. L. M. Gierasch and A. Gershenson. Post-reductionist protein science, or how to put Humpty Dumpty back together again. *Nat. Chem. Biol.*, 5, 774-777 (2009).
213. S. J. Eyles and L. M. Gierasch. Nature's molecular sponges: small heat shock proteins grow into their chaperone roles. *Proc. Natl. Acad. Sci. U.S.A.*, 107, 2727-2728 (2010).
214. R. P. Ghosh, T. Nikitina, R. A. Horowitz-Scherer, L. M. Gierasch, V. N. Uversky, K. Hite, J. C. Hansen, and C. L. Woodcock. Unique properties and interactions of the domains of the methylated DNA binding protein 2 (MeCP2). *Biochemistry*, 49, 4395-4410 (2010).
215. E. M. Clérico, A. Zhuravleva, R. G. Smock, and L. M. Gierasch. Segmental isotopic labeling of the Hsp70 molecular chaperone DnaK using expressed protein ligation. *Biopolymers-Peptide Science*, e-pub May 24 PMID: 20564022 (2010).
216. J. Hong and L. M. Gierasch. Macromolecular crowding remodels the energy landscape of a protein by favoring a more compact unfolded state. *J. Amer. Chem. Soc.*, 132, 10445-52 (2010).
217. R. G. Smock, O. Rivoire, W. P. Russ, J. F. Swain, S. Liebler, R. Ranganathan, and L. M. Gierasch. An interdomain sector mediating allostery in Hsp70 molecular chaperones. *Mol. Syst. Biol.*, 6:414 (2010).
218. Y. Liu, L. M. Gierasch, and I. Bahar. Interplay between structural dynamics and sequence co-evolution in nucleotide exchange factor/HSP70 interactions. *PLOS Comp. Biol.*, e1000931 (2010).
219. B. Krishnan and L. M. Gierasch. Dynamic local unfolding in the serpin alpha-1 antitrypsin provides a mechanism for loop insertion. *Nat. Struct. Mol. Biology*, 18, 222-226 (2011).
220. A. Gershenson and L. M. Gierasch, Protein folding in the cell: challenges and progress. *Curr. Opin. Struct. Biol.*, 21, 32-41 (2011).
221. L. M. Gierasch, The power of physical chemistry unleashed on proteins. *J. Phys. Chem. Lett.*, 2, 327-328 (2011).
222. L. M. Gierasch, How one bad protein spoils the barrel: structural details of  $\beta$ 2 microglobulin amyloidogenicity. *Mol. Cell*, 41, 129-131 (2011).

223. L. M. Gierasch, A career pathway in protein folding: From model peptides to post-reductionist protein science. *Protein Science*, 20, 783-790 (2011).
224. A. Zhuravleva and L. M. Gierasch, Allosteric signal transmission in the nucleotide-binding domain of Hsp70 molecular chaperones. *Proc. Natl. Acad. Sci. U.S.A.*, 108, 6987-92 (2011).
225. R. G. Smock, M. Blackburn, and L. M. Gierasch, The conserved, disordered C-terminus of DnaK enhances cellular survival after stress and DnaK in vitro chaperone function. *J. Biol. Chem.*, 286, 31821-31829 (2011).
226. I. Budyak, B. Krishnan, M. Ferrolino, E. M. Clerico, A. Clouser, K. F. Pobre, A. Zhuravleva, and L. M. Gierasch, The Inherently risky folding landscape of a  $\beta$ -barrel protein, CRABP1 in the test tube and in the cell. *Peptides. Building Bridges: The Proceedings of the 22<sup>nd</sup> Amer. Pept. Symp.*, M. Lebl, ed., Prompt Sci. Publishing, San Diego, pp. 128-129 (2011).
227. Q. Wang, A. Zhuravleva, and L. M. Gierasch, Exploring weak, transient protein-protein interactions in crowded *in vivo* environments by in-cell NMR spectroscopy, *Biochemistry*, 50, 9225-9236 (2011).
228. J. L. Maki, B. Krishnan, and L. M. Gierasch, Using a low denaturant model to explore the conformational features of translocation-active SecA. *Biochemistry*, 51, 1369-79 (2012).
229. E. T. Powers, D. L. Powers, and L. M. Gierasch, FoldEco: A model for proteostasis in *E. coli*, *Cell Reports*, 1, 265-276 (2012).
230. A. L. Horwich, J. Buchner, R. G. Smock, L. M. Gierasch, and H. R. Saibil. Chaperones and Protein Folding. *Comprehensive Biophysics*, Vol. 3, V. Daggett, Editor, Elsevier, pp. 212-237 (2012).
231. D. N. Hebert, K. D. Chandrasekhar, and L. M. Gierasch. You got to know when to hold (or unfold) 'em... *Mol. Cell*, 48, 3-4 (2012).
232. A. Zhuravleva, E. M. Clerico, and L. M. Gierasch. An interdomain energetic tug-of-war creates the allosterically active state in Hsp70 molecular chaperones. *Cell*, 151, 1296-307 (2012).
233. I. Budyak, B. Krishnan, A. Marcelino-Cruz, M. Ferrolino, A. Zhuravleva, and L. M. Gierasch. Early folding events protect aggregation-prone regions of a  $\beta$ -rich protein. *Structure*, 21, 476-485 (2013).
234. K. Hingorani and L. M. Gierasch, How bacteria survive an acid trip. *Proc. Natl. Acad. Sci. U. S. A.*, 110, 5279-5280 (2013).
235. I. L. Budyak, A. Zhuravleva, and L. M. Gierasch. The role of aromatic-aromatic interactions in strand-strand stabilization of  $\beta$ -sheets, *J. Mol. Biol.*, 425, 3522-35 (2013).
236. M. C. Ferrolino, A. Zhuravleva, I. L. Budyak, B. Krishnan, and L. M. Gierasch. Delicate balance between functionally required flexibility and aggregation risk in a  $\beta$ -rich protein. *Biochemistry*, 52, 8843-54 (2013).
237. E. M. Clerico and L. M. Gierasch. Structure and function of Hsp70 molecular chaperones. In "Inhibitors of Molecular Chaperones as Therapeutic Agents", T. D. Machajewski and Z. Gao, Editors, Royal Society of Chemistry Publishers, Ch. 3, pp. 65-125 (2014).
238. K. S. Hingorani and L. M. Gierasch. Comparing protein folding in vitro and in vivo: foldability meets the fitness challenge. *Curr. Opin. Struct. Biol.*, 24, 81-90 (2014).
239. F.-X. Theillet, A. Binolfi, T. Frembgen-Kesner, K. Hingorani, M. Sarkar, C. Kyne, C. Li, P. Crowley, L. Gierasch, G. Pielak, A. Elcock, A. Gershenson, P. Selenko. Physicochemical and biological properties of cells and their effects on IDPs. *Chem. Reviews*, 113, 6661-714 (2014).
240. I. General, Y. Liu, M. Blackburn, L. M. Gierasch, and I. Bahar. ATPase subdomain IA is a mediator of interdomain allostery in Hsp70 molecular chaperones. *PLoS Comput Biol* 10: e1003624 (2014).

241. A. Gershenson, L. M. Gierasch, A. Pastore, and S. E. Radford. Energy Landscapes of Functional Proteins Are Inherently Risky. *Nat. Chem. Biol.*, 10, 884-91 (2014).
242. P. Chien and L. M. Gierasch. Challenges and dreams: physics of weak interactions essential to life. *Mol. Biol. Cell*, 25, 3474-3477 (2014).
243. E. M. Clerico, W. Meng, J. M. Tilitsky, and L. M. Gierasch. How Hsp70 molecular machines interact with their substrates to mediate diverse physiological functions. *J. Mol. Biol.*, 427, 1575-1588 (2015).
244. Y. H. Cho, X. Zhang, K. F. R. Pobre, Y. Liu, J. C. Genereux, L. M. Gierasch, E. T. Powers, and J. W. Kelly. Individual and collective contributions of chaperoning and degradation to protein homeostasis in *E. coli*. *Cell Reports*, 11, 321-333 (2015).
245. A. Zhuravleva and L. M. Gierasch. Substrate-binding domain conformational dynamics mediate Hsp70 allostery. *Proc. Natl. Acad. Sci. USA*, 112, E2865-2873 (2015).
246. J. Hong, L. M. Gierasch, and Z. Liu, Its preferential interactions with biopolymers account for diverse observed effects of trehalose. *Biophys. J.* 109, 144-153 (2015).
247. K. Chandrasekhar, H. Ke, N. Wang, T. Goodwin, L. M. Gierasch, A. Gershenson, and D. N. Hebert, Cellular folding pathway of a metastable serpin. *Proc. Natl. Acad. Sci. USA*, 1113, 6484-6489 (2016).
248. D. N. Hebert, E. M. Clerico and L. M. Gierasch, Division of labor: ER-resident BiP co-chaperones match substrates to fates based on specific binding sequences. *Mol. Cell* 63, 721-723 (2016).
249. L. M. Gierasch, Hsp70 molecular chaperones: Versatile modular nanomachines that mediate multiple biological functions, in *Structure and Action of Molecular Chaperones*, ed. by L. M. Gierasch, A. L. Horwich, C. Slingsby, S. Wickner, and D. Agard, Series in Structural Biology – Vol. 6, World Scientific Publishers, Ch. 1, pp. 1-48 (2016).
250. L. M. Gierasch, A. L. Horwich, C. Slingsby, S. Wickner, and D. Agard, *Structure and Action of Molecular Chaperones Series in Structural Biology – Vol. 6*, World Scientific Publishers (2016).
251. K. S. Hingorani, M. Metcalf, S. C. Garman, E. T. Powers, and L. M. Gierasch, Ligand-promoted protein folding by biased kinetic partitioning. *Nat. Chem. Biol.*, 13, 369-371 (2017).
252. B. Krishnan, L. Hedstrom, D. Hebert, L. Gierasch, and A. Gershenson. Expression and purification of active recombinant human  $\alpha_1$ -antitrypsin. *Methods Mol. Biol.*, 1639, 195-209 (2017).
253. A. L. Lai, E. M. Clerico, M. E. Blackburn, N. A. Patel, C. V. Robinson, P. P. Borbat, J. H. Freed and L. M. Gierasch, The allosteric energy landscape of an Hsp70 molecular chaperone from ion mobility native mass spectrometry and double electron-electron resonance. *J. Biol. Chem.*, 292, 8773-8785 (2017).
254. C. A. English, W. Sherman, and L. M. Gierasch, The interdomain linker of Hsp70 chaperones enables allosteric communication by dynamically switching its conformations and interactions. *J. Biol. Chem.*, 292, 14765-14774 (2017).
255. A. Thakur, W. Meng, and L. M. Gierasch, Local and non-local topological information in the denatured state ensemble of a  $\beta$ -barrel protein in press. *Protein Science*, 12, 2062-2072 (2018).
256. W. Meng, E. Clerico, N. McArthur, and L. M. Gierasch, The allosteric landscapes of eukaryotic cytoplasmic Hsp70s are shaped by evolutionary tuning of key interfaces. *Proc. Natl. Acad. Sci. U.S.A.*, 115, 11970-11975 (2018).
257. M. P. Mayer and L. M. Gierasch, Hsp70 Molecular Chaperones: Emerging Concepts. *J. Biol. Chem.*, REV118.002810 (2018).



Editorials

- L. M. Gierasch and C.M. Deber, Editorial: In memory of Arno F. Spatola. *Biopolymers-Peptide Science* 71, 601 (2003).
- L. M. Gierasch, Inaugural editorial. *Biopolymers-Peptide Science* 76, 1-2 (2004)
- L. M. Gierasch, Editorial. *Biopolymers-Peptide Science* 76, 205 (2004).
- L. M. Gierasch, Editorial. *Biopolymers-Peptide Science* 76, 281 (2004).
- L. M. Gierasch, Editorial: The Murray Goodman memorial issue. *Biopolymers-Peptide Science* 80, 59-62 (2005).
- L. M. Gierasch, Passing of a gentle giant of peptide science: in memoriam, R. Bruce Merrifield. *Biopolymers-Peptide Science* 84, 433-444 (2006).
- L. M. Gierasch, Editorial: Peptides as templates. *Biopolymers-Peptide Science* 84, 1 (2006).
- L. M. Gierasch, In memoriam: A true statesman of science, Elkan R. Blout. *Biopolymers-Peptide Science* 88, 95 (2007); and *Biopolymers* 85, vi (2007).
- L. M. Gierasch, New and upcoming. *Biopolymers-Peptide Science* 88, iv (2007).
- L. M. Gierasch, A message from the editor-in-chief of *Biopolymers-Peptide Science*. *Biopolymers-Peptide Science* 89, vi (2008).
- L. M. Gierasch, C.M. Deber, and B. Brodsky. Celebrating the scientific legacy of Elkan R. Blout. *Biopolymers* 89, 323 (2008).
- L. M. Gierasch, A tribute to the career of a gentle giant of peptide science. *Biopolymers-Peptide Science* 90, 153 (2008).
- L. M. Gierasch, Our field is in good hands. *Biopolymers-Peptide Science* 90, 479 (2008).
- L. M. Gierasch, Highlighting an exciting topic as discussed in a stimulating venue. *Biopolymers-Peptide Science* 90, 587 (2008).
- L. M. Gierasch, Transitions: From the Editor-in-Chief of *Biopolymers-Peptide Science*. *Biopolymers-Peptide Science* 90, iv (2008).
- L. M. Gierasch, D. G. Lynn, J. Schneider. The Sixth Peptide Engineering Meeting PEM6, Emory University Conference Center, Atlanta, Georgia, October 2 to 5, 2012. *Biopolymers-Peptide Science* 98, iii (2012).
- L. M. Gierasch, The Journal of Biological Chemistry: 2016 Onward. *J. Biol. Chem.* 291, 15406-7 (2016).
- L. M. Gierasch, What's in a Name? *J. Biol. Chem.* 291, 19208-9 (2016)
- L. M. Gierasch, A Loyal Friend of ASBMB and JBC: Howard Schachman, 1918-2016. *J. Biol. Chem.* 291, 19724 (2016).
- F. P. Guengerich and L. M. Gierasch. What Happens When You Submit a Paper to JBC? *J. Biol. Chem.* 292, 1535-1537 (2017).
- L. M. Gierasch, JBC is on a mission to facilitate scientific discovery. *J. Biol. Chem.* 292, 6853-6854 (2017).
- L. M. Gierasch. ASBMB and JBC: A truly synergistic relationship. *J. Biol. Chem.* 292, 9857 (2017).

L. M. Gierasch, On the costs of scientific publishing. *J. Biol. Chem.* 292, 16395-16396 (2017).

L. M. Gierasch and G. DeMartino. The Herbert Tabor Best Paper Awards: Celebrating young authors who contribute top content to JBC. *J. Biol. Chem.* 292, 17576 (2017).

L. M. Gierasch. JBC's New Year's resolutions: Check them off! *J. Biol. Chem.* 292, 21705-21706 (2018).

L. M. Gierasch and G. DeMartino. The Herbert Tabor Young Investigator Awards: Meet the awardees! *J. Biol. Chem.* 293, 3468-3469 (2018).

L. M. Gierasch. A new journal from ASBMB. *J. Biol. Chem.* 293, 6212-6213 (2018).

L. M. Gierasch. Looking back at the last two years: Coming home to JBC. *J. Biol. Chem.* 293, 11254 (2018).

L. M. Gierasch. Happy centennial birthday to Herb Tabor, pillar of JBC. *J. Biol. Chem.* 293, 18803 (2018).

### Patent

US 6,991,927 B2 "Applying Far Infrared Radiation to Biological Matter", Inventors: M. R. Mross, T. H. Lowell, R. Durant, N. Dyer, L. M. Gierasch, and G. H. Pollack. Issued January 31, 2006.