BIOGRAPHICAL SKETCH AND PROFESSIONAL ACTIVITIES
RENSSELAER POLYTECHNIC INSTITUTE

I. Name: Gaetano T. Montelione (orcid: 0000-0002-9440-3059)
Department: Chemistry and Chemical Biology
Current Rank: Professor, Endowed Constellation Chair in Structural Bioinformatics
School: School of Science

Current Appointment:

Professor of Chemistry and Chemical Biology, Rensselaer Polytechnic Institute	2019 – present
Endowed Constellation Chair of Structural Bioinformatics, RPI	2019 – present

Educational Preparation

Southampton College, Long Island University, Southampton NY Marine Biology	1974 – 1976
Cornell University, Ithaca NY B.S. Biochemistry, with Highest Honors	1977 – 1980
University of Oregon, Eugene OR Physical Chemistry	1980 – 1981
Cornell University, Ithaca, NY M.A., Physical Chemistry	1981 – 1983
Cornell University, Ithaca NY with studies at ETH, Zurich, Switzerland Ph.D., Physical Chemistry Advisor: Prof. Harold A. Scheraga, Co-Advisor: Prof. Kurt Wüthrich	1983 – 1987

II. Professional Experience

Postdoctoral Fellowships

Postdoctoral Appointment, Molecular Biophysics University of Michigan, Ann Arbor, MI Advisor: Prof. Gerhard Wagner	1987 – 1988

Academic Appointments

Research Assistant Professor, University of Michigan	1988 – 1989
Resident Faculty, Center for Advanced Biotechnology and Medicine	1989 – 2019
Assistant Professor, Rutgers University	1989
Associate Professor, Rutgers University	1995
Visiting Professor, Department of Physical Chemistry, University of Valencia, Spain	1997
Professor, Rutgers University	1998 – 2005
Member, Rutgers Cancer Institute of New Jersey	2000 – present
Director, Northeast Structural Genomics Consortium, NIH Protein Structure Initiative	2000 – 2016
Adjunct Professor, Department of Biochemistry, Robert Wood Johnson Medical School	2001 – present
Distinguished Professor, Rutgers University	2005 – 2019

Foreign Expert Advisor, Jiangnan University, Wuxi, Peoples Republic of China	2007 – 2017
Jerome and Lorraine Aresty Chair, Rutgers University	2010 – 2019
Professor of Chemistry and Chemical Biology, Rensselaer Polytechnic Institute	2019 – present
Constellation Chair of Structural Bioinformatics, Rensselaer Polytechnic Institute	2019 – present
Visiting Professor, University of Florence, Florence ITALY	2019

Industry Consulting

Consultant, Pharmacia, A.B., Stockholm, Sweden	1990 – 1997
Consultant, Chiron Corp., Emeryville, CA	1990 – 1999
Visiting Scientist, Pharmacia, A.B., Stockholm, Sweden	1993
Consultant, Wyeth-Ayerst Research Laboratories, Princeton, NJ	1993 – 1999
Consultant, Novartis Pharmaceutical Corp., East Hanover, NJ	1995 – 2003
Consultant, Eli Lilly and Co., Indianapolis, IN	1996 – 1999
Scientific Advisory Board and Consultant, GeneFormatics, San Diego, CA	2000 – 2002
Scientific Advisory Board and Consultant, Influmedics, Philadelphia, PA	2006 – 2008
Scientific Advisory Board and Founder, Nexomics Biosciences, NJ	2007 – present

III. Teaching

Courses

Undergraduate Courses

MBB 407	Molecular Biology and Biochemistry (20 contact hrs.)	1995 – 2003
MBB 412	Proteomics and Functional Genomics (25 contact hrs.)	2004 – 2019
Byrne Seminar	Astrobiology, Can Life Evolve on Other Planets (15 contact hrs.)	2012 – 2019
CHEM 4962*	Proteomics and Structural Bioinformatics (50 contact hrs.)	2021 – 2022
CHEM 4965*	Protein Structure and Deep Learning (25 contact hrs.)	2023

Graduate Courses

	Rutgers University Bootcamp in Molecular Biophysics (6 contact hrs.)	2014, 2015
CHEM 695:539	Experimental Methods in Molecular Biosciences (4 contact hrs.)	2015
CHEM 6962*	Proteomics and Structural Bioinformatics (50 contact hrs.)	2021 – 2022
CHEM 6965*	Protein Structure and Deep Learning (25 contact hrs.)	2023

*courses offered at RPI

On Line International Symposia (organized at RPI)

2020 – 2021	Coordinator, **Structural Biology of Corona Viruses Journal Club**. Monthly international special interest group by zoom on the structural biology of corona virus, attended by about 50 people per month.
2023 – present	Coordinator, **CASP Special Interest Group on Modeling Multiple Conformational States of Proteins**. Monthly international special interest group by zoom on experimental and computational methods for modeling multiple conformational states of proteins, attended by 50 - 100 people per month.

A. Student Thesis Supervision

A.1. Undergraduate Research Theses as Primary Advisor

1. Mark Olszyk (Computational Biology, Rutgers University) Henry Rutgers Honors Thesis: "New Computational Methods for Homology Modeling of Proteins." 1991
2. Rajiv Prasad (Computational Biology, Rutgers University) "Development of New Computer Graphics Tools for Molecular Modeling." 1992
3. Yasir Ahmad (Computational Biology, Rutgers University) "Computer Analysis of Protein Structures." 1992
4. Haicheng (Heather) Li (Biomolecular NMR, Rutgers University) Henry Rutgers Honors Thesis: "Homology Modeling of DNA-Binding Proteins." 1995
5. Valerie Schannen Cavett (Computational Biology, Rutgers University) "Structural Analysis of IgG – Protein A Complexes Using Computer Graphics." 1994
6. Lorraine Snyder Dougherty (Molecular Biology, Rutgers University) "Development of High-Level Recombinant Expression System for the Alzheimer's Precursor Protein Protease Domain." 1995
7. Staci Lieberman Bodner (Biomolecular NMR, Rutgers University) Henry Rutgers Honors Thesis: "NMR Solution Structure Determination of the Murine Homeodomain Protein MSX-1." 1996
8. Shabbar Danish (Biomolecular NMR, Rutgers University) Henry Rutgers Honors Thesis: "Biophysical Studies of CspA, the Major Cold-Shock Protein of *Escherichia coli"* 1997
9. Lisa Seufert (Molecular Biology, Rutgers University) Henry Rutgers Honors Thesis: "Expression and Purification of ^{15}N-enriched Alzheimer's Amyloid β-Protein Precursor Kunitz Inhibitor Domain (APP-KI)." 1997
10. Mousumi Roy (Molecular Biology, Rutgers University) "Molecular Modeling of Protein Structures." 1997
11. Michael Mehnert (Computational Biology, Rutgers University) "Bioinformatic Analysis of Protein Domain Structures" 1998
12. Alexandra Gardino (Computational Biology, Rutgers University) Henry Rutgers Honors Thesis: "Clusters of Orthologous Groups: Applications in Bioinformatics, Structural Biology, and Structure-Based Functional Genomics." 1999
13. Ram Mani (Molecular Biology, Rutgers University) Henry Rutgers Honors Thesis: "Structural Genomics of Conserved Gene Families." 2000
14. Reza Y. Akhtar (Molecular Biology, Rutgers University) Henry Rutgers Honors Thesis: "High Throughput Homology Modeling for Structural Genomics." 2000
15. Manju Goyal (Computational Biology, Rutgers University) 2001
16. Bonnie Cooper (Molecular Biology, Rutgers University) 2002
17. Rebecca Liu (Molecular Biology, Rutgers University) 2002
18. Gurmukh Sahota (Computational Biology, Rutgers University) Henry Rutgers Honors Thesis: "Solution NMR Structure of the BRCT Domain of *Thermus thermophilus* DNA Ligase." 2002
19. Jennifer Chen (Molecular Biology, Rutgers University) 2002
20. Taylor Graham (Molecular Biology, Rutgers University) 2003
21. Helen Chow (Molecular Biology, Rutgers University) 2003
22. Nadia Khan (Molecular Biology, Rutgers University) 2003
23. Marvin Bayro (Computational Biology, Rutgers University) Henry Rutgers Honors Thesis: "AutoProc: Automated Processing of Protein NMR Data Through a Generalized Experimental Model in a Relational Database Approach." 2003

24. Zeba Wunderlich (Computational Biology, Rutgers University) Henry Rutgers Honors Thesis: "HOMA, Homology Modeling Automatically, and ZebaView: Two Bioinformatics Applications for Structural Genomics." 2003
25. Nadeem Riaz (Computational Biology, Rutgers University) Henry Rutgers Honors Thesis: "Automated Analysis of Peak Patterns in Multidimensional Nuclear Magnetic Resonance Spectroscopy." 2003
26. Raymond Mirasol (Protein Purification, Rutgers University) 2003
27. Kate Drahos Moreau (Molecular Biology, Rutgers University) Henry Rutgers Honors Thesis: "Protein Expression and Folding Optimization for High Throughput Proteomics." 2004
28. Lingyue Lee (Molecular Biology, Rutgers University) 2004
29. Tatiana Borissova (Biomolecular NMR, Rutgers University) Henry Rutgers Honors Thesis: "Protein Stability Measurements Using Hydrogen/Deuterium Exchange, Mass Spectrometry, and NMR Spectroscopy." 2004
30. Kellie Cunningham (Molecular Biology, Rutgers University) 2004
31. Melissa Ciano Byler (Molecular Biology, Rutgers University) 2004
32. Timothy Byler (Molecular Biology, Rutgers University) 2004
33. Pavithra Shivakumar. (Computational Biology, Rutgers University) Henry Rutgers Honors Thesis: "AutoQF Software for Validation of Protein NMR Structures." 2005
34. Chioma Nwosu (Protein Production, Rutgers University) 2006
35. Danielle Belsky Krause (Biomedical Engineering, Rutgers University) Aresty Research Center Summer Science Research Fellow, 2006
36. Pooja Dharia (Molecular Biology, Rutgers College of Pharmacy) 2006
37. Michael Fakhry (Computational Biology, Rutgers University) 2006
38. Brian Radvansky (Molecular Biology, Rutgers University) 2006
39. Dong Yup (Dan) Lee (Molecular Biology, Rutgers University) 2007
40. Colleen Ciccosanti (Molecular Biology, Rutgers University) 2007
41. Kate Stokes (Protein Production, Rutgers University) 2007
42. Keith Hamiliton (Molecular Biology, Rutgers University) 2007
43. Rushabh Vakharia (Molecular Biology, Rutgers University) 2008
44. Taral Patel (Protein Purification, Rutgers University) 2007
45. Norain Siddiqui (Molecular Biology, Rutgers University) 2008
46. Alisa Reznikov (Protein Purification, Rutgers University) Project Title: "Protein Aggregation Screening and Analysis." 2008
47. Justin Nistico (Molecular Biology, Rutgers University) Project Title: "Developing Purification Technologies and Optimization Buffer Solutions for the Full Length NS1A Protein Constructs and Complexes with Both the F2F3 Domain of CPSF-30 and dsRNA." 2008
48. Danielle DiStefano (Molecular Biology, Rutgers University) 2008
49. Irina Fridman (Protein Purification, Rutgers University) 2009
50. Will Buchwald (Molecular Biology, Rutgers University) 2009
51. Dayaben Patel (Protein Purification, Rutgers University) 2009
52. Joseph Wong (Protein Purification, Rutgers University) 2009
53. Paul Harvilla (Molecular Biology and NMR, Rutgers University) Henry Rutgers Honors Thesis: "Structural and Biophysical Studies of NonStructural Protein 1 of Influenza A and B Viruses." 2009
54. Gautam Singh (Bioinformatics, Rutgers University) 2010

55. Curtis Schauder (Molecular Biology, Rutgers University) Henry Rutgers Honors Thesis: "Biophysical Characterization of Influenza NS1A Protein's Ability to Self-Associate and Bind to the p85beta Subunit of PI3K." 2010
56. John Cafaro (Protein Production, Rutgers University) 2010
57. Eitan Kohan (Molecular Biology, Rutgers University) 2010
58. Rachael Belote (Molecular Biology, Rutgers University) 2010
59. Brendan R. Amer (Molecular Biology, Rutgers University) Honors Thesis: "The Characterization of the Influenza Viruses Non-structural Protein 1 and Its Interactions Leading to the Minimization of the Host Cell's Immune Response." 2011
60. Teddy John Wohlbold (Protein Purification, Rutgers University) Honors Thesis title: "The Biochemical Characterization of Influenza A Nonstructural Protein 1 (NS1A) and Its Interactions with Host Cell Proteins Involved in the Innate Immune Response." 2011
61. Hoi Wun Au (Molecular Biology, Rutgers University) 2011
62. Rokhsareh Eyvazkhany (Molecular Biology, Rutgers University) 2011
63. Wylie Lopez (Molecular Biology, Rutgers University) 2011
64. Ari Sapin (Molecular Biology, Rutgers University) 2011
65. Dhaval Ghandi (Protein Purification, Rutgers University) Honors Thesis: "Characterization of Complex Formation Between nSH2, iSH2 and cSH2 Domains of p85 Subunit of Pi3K with Different Non-Structural Protein 1 (NS1) Strains of Influenza Virus." 2011
66. Tina Bijlani (Protein Purification, Rutgers University) Honors Thesis: "High-throughput Screening for Refolding Human Proteins from Inclusion Bodies." 2011
67. Hy Le (Protein Purification, Rutgers University) Honors Thesis: "Purification, Characterization and Expression of Novel Oxidoreductase from *Zygosaccharomyces rouxii*." 2013
68. Seema Sahdev (Molecular Biology, Rutgers University) 2013
69. Ahmed Gad (Molecular Biology, Rutgers University) 2013
70. Chelsea Stahl Sapin (Molecular Biology, Rutgers University) 2012
71. Alex Bendik (Protein Purification, Rutgers University) 2012
72. Katherine Carrino-Bednarski (Molecular Biology, Rutgers University) 2012
73. Nicole Brunck (Molecular Biology, Rutgers University) 2012
74. Janna Sloand (Protein Purification, Rutgers University) 2013
75. Ya-Min Chin (Protein Purification, Rutgers University) 2013
76. Ashley Aya (Protein Production, Rutgers University) 2013
77. Sultan Khawam (Molecular Biology, Rutgers University) 2013
78. Patrick O'Connell (Molecular Biology, Rutgers University) 2013
79. Amy Suhotliv (Molecular Biology, Rutgers University) 2013
80. Samyukta Bengeri (Protein Purification, Rutgers University) 2013
81. Meenhaz Foysol (Molecular Biology, Rutgers University) 2013
82. Emily Grasso (Molecular Biology, Rutgers University) Honors Thesis: "Characterization of the Small-molecule and Protein-Protein Interactions of the Influenza A Virus NS1 Protein." 2014
83. Aparna Tatineni (Molecular Biology, Rutgers University) Honors Thesis: "High Throughput Methods for the Isolation and Identification of Stable Protein Complexes." 2014
84. Hersh Doshi (Molecular Biology, Rutgers University) 2014
85. Srushti Raja (Molecular Biology, Rutgers University) 2015
86. Ira Bhatnagar (Protein Purification, Rutgers University) 2015

87. Gopal Govindraj (Molecular Biology, Rutgers University) 2015
88. Marium Javed (Protein Production, Rutgers University) 2015
89. Kaustubh Kulkarni (Molecular Biology and NMR/Bioinformatics, Rutgers University) 2015
90. Jason Lin (Bioinformatics, Rutgers University) 2015
91. Jennifer Wong (Molecular Biology, Rutgers University) 2015
92. Tyler Zukofsky (Molecular Biology, Rutgers University) 2015
93. Adam Schwing (Protein Purification, Rutgers University) Honors Thesis: "Solution NMR Studies of the Complex Formed Between the Human Retinoblastoma-associated Protein and the Human Adenovirus E1A Protein." 2016.
94. Natalia Patel (Molecular Biology, Rutgers University) Honors Thesis "The Key Interactions between Influenza A Viral Protein NS1 and Human Host Proteins are Mediated by RNA" 2017
95. Rachel John (Molecular Biology, Rutgers University) 2019. NMR studies of influenza Non-Structural Protein 1.
96. Carlie Hanlon (Molecular Biology, Rutgers University) 2019
97. Christopher Kim (Molecular Biology, Rutgers University) 2019
98. Jingzhou Hao* (NMR studies of the MLV IN – BRD3 ET complex, Rutgers University) "Conformational dynamics of murine leukemia virus integrase in its complex with chromosomal bromodomain-containing protein 3" 2020
99. Chris Damone* (Computer Programming, RPI) 2021
100. Monali Ardeshna* (Structural Biology, RPI) 2021
101. John Liu* (Computational Biology, RPI) 2022
102. Reena Caplan* (Biology, RPI) 2023 – present
103. Suren Zakian* (Biology, RPI) 2023 – present
104. Emma Gormley* (Biophysics, RPI) 2023 – present

*trained at RPI

A.2. Student Thesis Supervision as Primary Advisor, Masters Degree

1. David Yorio (M.S.) 1997 – 1998
2. Subir Kumedan (M.S.) 1997 – 1999
3. Ying Xiong (M.S.) 1997 – 2000
4. Elisabet Wahlberg (M.S.) 1999 – 2001
5. Yisha Yao (M.S.) 2014 – 2017
6. Sofia Ranieri (M.S., Univ of Bologna) 2023 – present

A.3. Student Thesis Supervision at Primary Advisor, Ph.D Degree

1. Yuchin Li (Ph.D.) 1989 – 1994
2. Clelia Biamonte (Ph.D.) 1990 – 1996
3. Franklin Moy (Ph.D.) 1990 – 1993 Co-advisor w/ H.A. Scheraga, Cornell University
4. Sakurako Shimotakahara (Ph.D.) 1994–1996 Co-advisor w/ H. A. Scheraga, Cornell University
5. Wenqing (Wendy) Feng (Ph.D.) 1993 – 1997
6. Chen-ya Chen (Ph.D.) 1994 – 1999
7. Yuanpeng (Janet) Huang (Ph.D.) 1997 - 2001
8. Deyou Zheng (Ph.D.), 1999 – 2003
9. Michael Baran (Ph.D.) 2000 – 2005

10. Gregory Kornhaber (Ph.D.) 2000 – 2005
11. Cuifeng Yin (Ph.D.) 2000 – 2005
12. Aneerban Bhattacharya (Ph.D.), 2000 – 2006
13. David Snyder (Ph.D.) 2000 – 2006
14. John Everett (Ph.D.) 2000 – 2006
15. Asli Ertekin (Ph.D.) 2005 – 2011
16. Binchen Mao (Ph.D.) 2006 – 2013
17. Patrick Nosker (Ph.D.) 2012 – 2016 Co-advisor w/ V. Nanda, Rutgers University
18. Ryan Woltz (Ph.D.) 2014 – 2019
19. Rebecca Greene-Cramer* (Ph.D.) 2021 – present
20. Laura Spaman* (Ph.D.) 2022 – present
21. Tiburon Benavides* (Ph.D.) 2023 – present

*trained at RPI

A.4. Graduate Student Advisory Committee Member

Montelione was member of PhD and Undergraduate Honors Research Committees for > 100 students over 30 year period at Rutgers University.

<u>At RPI (2019 – present)</u>

1. Benavides, Tiburon	Biophysics and Biochemistry	Primary advisor for Ph.D.
2. Edson Cody	Chemistry and Chemical Biology	
3. Christian Franquiz	Chemistry and Chemical Biology	
4. Lauren Gandy	Chemistry and Chemical Biology	
5. Rebecca Greene-Cramer	Chemistry and Chemical Biology	Primary advisor for Ph.D.
6. Noam Hantman	Biophysics and Biochemistry	
7. Patrick Landry	Chemistry and Chemical Biology	
8. Rebecca Miceli	Chemistry and Chemical Biology	
9. Caitlin Moustouka	Biophysics and Biochemistry	
10. Edgar Peters	Biophysics and Biochemistry	
11. Kavita Ramanth	Chemistry and Chemical Biology	
12. Isha Shah	Chemistry and Chemical Biology	
13. Laura Spaman	Chemistry and Chemical Biology	Primary advisor for Ph.D.
14. Lukas Sutton	Biophysics and Biochemistry	
15. Elinor Tai	Biology	
16. Jasmine Yang	Chemical Engineering	

At outside institutions:

17. Brandon Schweibenz	Biochemistry, Rutgers University	Ph.D. committee
18. Sofia Ranieri	Biotechnology, University of Bologna, ITALY	M.S. committee

B. **Primary Mentorship of Postdoctoral Fellows (and Staff Scientists)**

1. Dr. Barbara A. Lyons 1990 – 1993

2. Dr. Donald Emerson 1991 – 1993
3. Dr. Keith Newkirk 1992 – 1994
4. Dr. Mitsuru Tashiro 1992 – 1996
5. Dr. Carlos Rios 1993 – 1997
6. Dr. GVT Swapna* dates (Postdoc, Res. Assoc Professor, Sr. Res. Scientist)
7. Dr. Zhigang Shang 1993 – 1997
8. Dr. Diane Zimmerman 1994 – 1998
9. Dr. Sakurako Shimotakahara 1997
10. Dr. Michael Andrec 1997 – 1999
11. Dr. Kristin Gunsalus 1997 – 2000
12. Dr. Parag Sahasrabudhe 1997 – 2000
13. Dr. James Aramini dates (Postdoc, Res. Assoc Professor)
14. Dr. Bonnie Dixon 1998 – 2000
15. Dr. Daniel Monleon 1999 – 2002
16. Dr. Hunter Moseley 1998 – 2002 (Postdoc, Res. Asst Professor)
17. Dr. Yuanpeng Janet Huang* 2001 – present (Postdoc, Res. Assoc Professor, Sr. Res. Scientist)
18. Dr. Thomas Acton* 2001 - dates
19. Dr. Michael Baran 2005 - 2012 (Postdoc, Res. Asst. Professor)
20. Dr. Paolo Rossi 2005 - 2012 (Postdoc, Res. Asst. Professor)
21. Dr. Dehua Hang 2006 - 2007
22. Dr. Yuefeng Tang 2006 – 2014
23. Dr. John Everett 2006 – 2017 (Postdoc, Res. Asst. Professor)
24. Dr. Seema Sharma dates
25. Dr. Rajeswari Mani 2007 – 2010
26. Dr. Gregory Kornhaber dates (Res. Asst Professor)
27. Dr. Fei Xu 2013 - 2014
28. Dr. Fei Song 2013 – 2016
29. Dr. Khushboo Bafna* 2019 – 2022
30. Dr. Theresa Ramelot* 2020 – present (Sr. Res. Scientist)
31. Dr. Benjamin Shurina* 2021- present
32. Dr. Namita Dube* 2022 – present (Res. Scientist)
33. Dr. Anna De Falco* 2022 – present (Postdoc, Res. Scientist)
34. Dr. Keith Fraga* 2022 – present
35. Dr. Amit Guar* 2023 – present (Res. Scientist)

*Postdocs and Research Scientists employed at RPI

C. Research Training Other than Primary Mentorship

Visiting Students

1. David Pantoja, Visiting Ph.D. candidate from Madrid, SPAIN. 2000 – 2001
2. Sriram Aiyer, Co-advisor with M. Roth, Biochemistry, Rutgers Robert Wood Johnson Medical School, Rutgers Biomedical Health Sciences. 2010 – 2014

3. Anastasia Chernyatina, Visiting postdoctoral trainee from KU Leuven University, Brussels, BELGIUM. 2014
4. Sofia Ranieri, Visiting student from Depart of Biotechnology, University of Bologna, ITALY. 2023.
5. Ethan Li. High school student. 2022, 2023
6. Anjali Patel, High school student. 2022
7. Alex Li, High school student 2023

Students and postdocs trained in our lab have gone on to prestigious positions in academics and industry.

- Dr. James Aramini (postdoc trainee) Staff Scientist, Lewis Kay Lab, Univ of Toronto
- Prof. Rachael Belote (undergrad trainee) Associate Professor, Ohio State University
- Dr. Michael Baran (grad student and postdoc trainee) Vice President, Pfizer Ventures
- Prof. Marvin Bayro (undergrad trainee) Assistant Professor, Univ of Puerto Rico
- Prof. Kristin Gunsalus (postdoc trainee) Associate Professor, New York University
- Prof. Barbara Lyons (postdoc trainee) Associate Professor, Univ of New Mexico
- Prof. Ram Mani, M.D. (undergrad trainee) Assistant Professor, UT Southwest Medical Center
- Prof. Daniel Monleon (postdoc trainee) Associate Professor, Univ of Valencia, Spain
- Prof. Hunter Moseley (postdoc trainee) Associate Professor, University of Kentucky
- Prof. Sakurako Shimotakahara (graduate student) Associate Professor – Tokyo University of Pharmacy and Life Science
- Prof. Gurmukh Sahota. M.D. (undergrad trainee) Assistant Professor, University of Penn Medical School
- Prof. Mitsuru Tashiro (graduate student) Associate Professor, Tokyo Metropolitan University, Japan
- Prof. Zeba Wunderlich (undergrad trainee) Associate Professor, Boston University
- Prof. Fei Xu (postdoc trainee) Associate Professor, Jiangnan University, Wuxi, PRC.
- Prof. Deyou Zheng (graduate student) Associate Professor, Albert Einstein Medical School

D. Course and Curriculum Development

Introduced new course at RPI in 2020
Course Title: Proteomics and Structural Bioinformatics
Course Number: CHEM 4962 / CHEM 6962
Credit Hours: 3

Course Description
Proteomics and Structural Bioinformatics is a survey of modern techniques of protein biochemistry, bioinformatics, and proteomics, and their applications in the broad field of protein chemistry and functional genomics. It is targeted to upper-level undergraduate and graduate students in chemistry and/or biology (co-listed). It includes a discussion of basic concepts of protein structure and function, protein characterization and purification, enzyme kinetics, NMR, cryoEM, X-ray crystallography, mass spectrometry, molecular modeling, bioinformatics, and various techniques of functional and structural genomics, together with readings from current literature. Special emphasis is placed on protein structure prediction with new AI-based methods, including *AlphaFold* and *RosettaFold*.

Students participate in reading and presenting papers from the recent scientific literature in the areas of structural virology (including structural biology of corona viruses), cancer biology, de novo protein design,

structural bioinformatics, protein dynamics, ordered water, membrane proteins, protein interaction networks, drug design, structure prediction, deep learning, protein folding, and protein evolution. Students develop skills in bioinformatic database searching, molecular modeling with PyMol, and presentation of scientific data and results. Graduate students also complete exercises in writing a scientific paper or preparing a short research grant proposal.

Introduced new course at RPI in 2023
Course Title: Protein Structure and Deep Learning
Course Number: CHEM 4965 / CHEM 6965
Credit Hours: 1

Course Description
Protein Structure and Deep Learning is a seminar course of readings and student presentations from recent literature. It is targeted to upper-level undergraduate and graduate students in chemistry and/or biology (co-listed); computer science students are also welcome. Students will participate in reading and presenting papers from the recent scientific literature in the areas of protein and nucleic acid structure prediction, structural virology (including structural biology of corona viruses), cancer biology, de novo protein design, generative AI, structural bioinformatics, protein dynamics, protein interaction networks, drug design, deep learning, protein folding, and protein evolution. Special emphasis will be placed on protein structure prediction with new AI-based methods, including AlphaFold2, RosettaFold, ESMFold (Evolutionary Scale Modeling), and generative AI methods for de novo protein design.

IV. Publications

Montelione has published more than 387 scientific journal articles and book chapters. His Google citation H-index is 85 with > 26,500 citations as of **November 8, 2023**. Found on Google Scholar and Montelione Lab Publications Page

Protein Structures Deposited in the Protein Data Bank (PDB)
Montelione is co-author of more than 1,149 PDB depositions, including more than 488 structures determined by solution NMR spectroscopy methods.

A. Journal Articles

Refereed Original Articles in Scientific Journals

1. **Montelione, G.T.**, Callahan, S., and Podleski, T.R. Physical and chemical characterization of the major lactose-blockable lectin activity from fetal calf skeletal muscle. **Biochim. Biophys. Acta** 1981, 670: 110 - 123.
2. Stimson, E.R., **Montelione, G.T.**, Meinwald, Y.C., Rudolph, R.K., and Scheraga, H.A. Equilibrium ratios of cis- and trans-proline conformers in fragments of ribonuclease A from nuclear magnetic resonance spectra of adjacent tyrosine ring resonances. **Biochemistry**, 21: 5252-5262, 1982.
3. **Montelione, G.T.**, Arnold, E., Meinwald, Y.C., Stimson, E.R., Denton, J.B., Huang, S.G., Clardy, J., and Scheraga, H.A. Chain-folding initiation structures in ribonuclease-A: Conformational analysis of trans-Ac-Asn-Pro-Tyr-NHMe and trans-Ac-Tyr-Pro-Asn-NHMe in water and in the solid-state. **J. Am. Chem. Soc**., 106: 7946-7958, 1984.
4. Oka, M., **Montelione, G.T.,** and Scheraga, H.A. Chain-folding initiation structures in ribonuclease-A: Conformational free-energy calculations on Ac-Asn-Pro-Tyr-NHMe, Ac-Tyr-Pro-Asn-NHMe, and related

peptides **J. Am. Chem. Soc.**, 106: 7959-7969, 1984.

5. Swadesh, J.K., **Montelione, G.T.**, Thannhauser, T.W., and Scheraga, H.A. Local structure involving histidine-12 in reduced S-sulfonated ribonuclease A detected by proton NMR spectroscopy under folding conditions **Proc. Natl. Acad. Sci. U.S.A.**, 81: 4606-4610, 1984.

6. **Montelione, G.T.**, Hughes, P., Clardy, J., and Scheraga, H.A. Conformational properties of 2,4-methanoproline (2-carboxy-2,4-methanopyrrolidine) in peptides: Determination of preferred peptide-bond conformation in aqueous-solution by proton Overhauser measurements. **J. Am. Chem. Soc.**, 108: 6765-6773, 1986.

7. **Montelione, G.T.**, Wüthrich, K., Nice, E.C., Burgess, A.W., and Scheraga, H.A. Identification of two anti-parallel beta-sheet conformations in the solution structure of murine epidermal growth factor by proton magnetic resonance **Proc. Natl. Acad. Sci. U.S.A.**, 83: 8594-8598, 1986.

8. Stimson, E.R., Meinwald, Y.C., **Montelione, G.T.,** and Scheraga, H.A. Conformational properties of trans Ac-Asn-Pro-Tyr-NHMe and trans Ac-Tyr-Pro-Asn-NHMe in dimethylsulfoxide and in water determined by multinuclear NMR spectroscopy. **Int. J. Pept. Protein Res.**, 27: 569-582, 1986.

9. Haas, E., **Montelione, G.T.**, McWherter, C.A., and Scheraga, H.A. Local structure in a tryptic fragment of performic acid oxidized ribonuclease A corresponding to a proposed polypeptide chain-folding initiation site detected by tyrosine fluorescence lifetime and proton magnetic resonance measurements. **Biochemistry**, 26: 1672-1683, 1987.

10. **Montelione, G.T.**, Wüthrich, K., Nice, E.C., Burgess, A.W., and Scheraga, H.A. Solution structure of murine epidermal growth factor: determination of the polypeptide backbone chain-fold by nuclear magnetic resonance and distance geometry **Proc. Natl. Acad. Sci. U.S.A.**, 84: 5226-5230, 1987.

11. Talluri, S., **Montelione, G.T.**, Vanduyne, G., Piela, L., Clardy, J., and Scheraga, H.A. Conformational properties of 2,4-methanoproline (2-carboxy-2,4-methanopyrrolidine) in peptides: Evidence for 2,4-methanopyrrolidine asymmetry based on solid-state x-ray crystallography, H-1-NMR in aqueous-solution, and CNDO/2 conformational energy calculations. **J. Am. Chem. Soc.**, 109: 4473-4477, 1987.

12. **Montelione, G.T.**, Wüthrich, K., and Scheraga, H.A. Sequence-specific 1H-NMR assignments and identification of slowly exchanging amide protons in murine epidermal growth factor. **Biochemistry**, 27: 2235-2243, 1988.

13. Ray, P., Moy, F.J., **Montelione, G.T.**, Liu, J.F., Narang, S.A., Scheraga, H.A., and Wu, R. Structure-function studies of murine epidermal growth factor: Expression and site-directed mutagenesis of epidermal growth factor gene **Biochemistry**, 27: 7289-7295, 1988.

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PATENTS

Issued Patents

1. United States Patent 6,210,655 Date of Issue: April 3, 2001.
"Site-specific 13C-Enriched Reagents for Diagnostic Medicine by Magnetic Resonance Imaging"
Inventors: Stein S., **Montelione G.T**.

2. United Kingdom Patent Patent Issued 2006
"Linking Gene Sequence to Gene Function by 3D Structure Determination"
Inventors: **Montelione G.T.**, Anderson S., Huang Y.P.
European Patent Application No: 99935746.0-2402. Publication No: 1104488.

3. United States Patent 7,709,190. Date of Issue: May 4, 2010.
"Influenza A Virus Vaccines and Inhibitors"

Inventors: **Montelione G.T.**, Das K., Arnold E., Ma L.-C., Xiao R., Krug R.M., Twu K.Y., Kuo R.-L.

4. United States Patent 8,450,085. Date of Issue: May 28, 2013.
"Labeled Biomolecular Compositions and Methods for the Production and Uses Thereof".
Inventors: **Montelione G.T.**, Inouye M., Tang Y., Roth M., Schneider W.

5. United States Patent 8,455,621. Date of Issue: June 4, 2013.
"Influenza A Virus Vaccines and Inhibitors".
Inventors: **Montelione G.T**., Krug R.M., Twu K.Y., Kuo, R.-L, Arnold E., Das K, Ma, L.-C., Xiao R.

6. Peoples Republic of China Patent #: 2014051400411580
Date of Issue: 5/28/2014
Application Number: CN 102482649 B
Title: Stereospecific Carbonyl Reductases; 立体专一性羰基还原酶
Inventors: **Montelione G.T.**, Xiao R., Nie Y., Xu Y.
盖塔诺·蒙泰莱奥, 肖荣, 聂尧, 徐岩

7. United States Patent 8,796,008 Date of issue: Aug 5, 2014
"Influenza A Virus Vaccines and Inhibitors".
Inventors: **Montelione G.T.**, Krug R., Das K., Arnold E.; Ma L.-C., Xiao R., Kuo R.-L., Twu K.Y.

8. United States Patent 8,916,519 Date of issue: Dec 23, 2014
"Influenza A Virus Vaccines and Inhibitors".
Inventors: **Montelione G.T.**, Das K., Arnold E.; Ma L.-C.; Xiao R., Krug R.M., Twu, K.Y., Kuo, R.-L.

9. United States Patent 9,119,810 Date of Issue: Sept. 1, 2015
"Novel Compositions and Vaccines Against Influenza A and Influenza B Infection".
Inventors: **Montelione G.T.**, Krug R., Ma L.-C, Yin C.

10. United States Patent 9,228,368 Date of Issue: Jan. 5, 2016.
"Labeled Biomolecular Compositions and Methods for the Production and Uses Thereof".
Inventors: **Montelione G.T.**, Inouye M., Tang Y., Roth M., Schneider W.

11. United States Patent 9,328,217 Date of Issue: May 3, 2016.
"Labeled Biomolecular Compositions and Methods for the Production and Uses Thereof".
Inventors: **Montelione G.T**., Inouye M., Tang Y., Roth M., Schneider W.

12. United States Patent 9,422,583 Date of Issue: Aug. 23, 2016.
"Stereospecific Carbonyl Reductases".
Inventors: **Montelione G.T**., Xiao R., Nei Y., Xu Y.

13. United States Patent 10,131,915 B2 Date of Issue: Nov. 20, 2018
"Independently Inducible System of Gene Expression"
Inventors: Roth M, Schneider W, **Montelione GT**, Inouye M, Tang, Y..

14. United States Patent 10,385,350B2 Date of Issue: Aug 20, 2019
"System for High-level Production of Proteins and Protein Domains"
Inventors: Acton TB, Anderson S, **Montelione, GT**, Huang YJ, Provisional Filed 11/10/11. PCT Filed 11/09/12. Serial No: 61/558,277. Rutgers Tech ID: 2012-056

Pending Patents

1. Hunt JF, Price WM, Acton TB, **Montelione GT**, "Methods for Altering Polypeptide Expression". Provisional US Patent filed 2/9/2010 Appl No 61/320.805. Provisional Filed 9/22/2011. Nationalized PCT – United States. Nationalized PCT – Europe. Filed 2/9/2010 PCT/US2011024251. Nationalized PCT – China. Rutgers Tech ID: 2010-133.
2. Klessig D, Park S-W., **Montelione GT**, Hamilton K, Gurla S, Bianchi ME. "Structure and Function of The Salicylic Acid Binding Sites on Human HMGB1 and Methods and Use Thereof for the Rational Design of Both Salicylic Acid Analogs and Other Agents that Alter Animal and Plant HMGBs Activities. Provisional US patent filed 6/2013. PCT filed 6/2014. Rutgers Tech ID: 2013-114.
3. **Montelione GT**, Bafna K, Krug RM, Garcia-Sastre A, White K. "Protein inhibitors for inhibition of SARS-CoV2 virus". Provisional US Patent filed 7/31/20. Attorney Docket: 104576-100. Updated 10/05/20 Attorney Docket: 104576-200. PTC Filed 2002. US Patent Filed 2023. Published 11/23/2023

V. Research Grants and Contracts

Prof. Montelione has brought more than $8 million in federal and foundation funding to Rensselaer Polytechnic Institute and subcontract institutes 2019-2023.

Prof. Montelione brought more than $120 million in federal funding to Rutgers University and subcontract institutes 1990 - 2019.

V.A. Proposals Approved and Funded – at RPI

As Principal Investigator

1R35 GM141818-01 (Montelione, PI/PD) 07/01/21 – 06/30/26
NIH NIGMS MIRA Program
Hybrid Methods for Dynamic Structure Analysis of Proteins from Pathogenic Microorganisms
Integral Membrane Proteins (IMPs) include many biomedically-important gate keepers, receptors, transporters, homeostasis regulators, and potential drug discovery targets. We are developing a robust and reproducible platform for accurate, reliable, validated, and reproducible structure determination of IMPs, and applying this platform for structure determination of IMPs selected from the genomes of NIH priority pathogens. We also propose to develop novel and robust methods for quantifying distributions of conformational states of proteins, and to apply these technologies in structure-dynamic-function studies of key proteins from pathogenic bacteria, g-retroviruses, influenza viruses, and coronaviruses.
Total Award Amount (including Indirect Costs): $3,290,000 total for 5 years

R01 GM120574 (G.T. Montelione, PD/PI) 07/01/17 – 06/30/22
NIH-NIGMS
Membrane Protein Structure Using Evolutionary Couplings and Sparse NMR Data

The major goal of this research program is to create new NMR and computational methods for studying structure and dynamics of integral membrane proteins, and to apply these methods in biophysical studies of biologically important membrane proteins.
Total Award Amount (including Indirect Costs): $2,040,375 total for 4 years (~ $1,000,000 at RPI)

National Research Council (NRC), National Academies of Science 12/01/22 – 11/30/23
Anton2 Supercomputer Access (G.T. Montelione, PI, N. Dube, co-PI)
Mechanisms of Antimicrobial Drug Transport by Integral Membrane Protein MltA Interacting Protein
454,950 MD simulation units (~ 300 microsec of MD simulations for membrane proteins embedded in lipid bilayers) on Anton-2 supercomputer.

National Research Council (NRC), National Academies of Science 12/01/23 – 11/30/24
Anton2 Supercomputer Access (G.T. Montelione, PI, N. Dube, co-PI, GVT Swapna, co-PI)
Structural Dynamics of Integral Membrane Proteins Mediating Drug Transport
400,000 MD simulation units (~ 275 microsec of MD simulations for membrane proteins embedded in lipid bilayers) on Anton-2 supercomputer.

CEPM CTSA Pilot Grant.
K. White, A. Garcia-Sastre, GT Montelione, C. Cioffi co-PIs) 02/01/23 – 06/30/23
***Mechanism(s) of Synergy Between Coronavirus Protease and Polymerase Inhibitors*.**
Total Award Amount (including Indirect Costs): $35,000

R01 GM120574-S1(G.T. Montelione, PD/PI) 07/01/17 – 06/30/21
NIH-NIGMS
Equipment Supplement to Membrane Protein Structure Using Evolutionary Couplings and Sparse NMR Data
The goal of this equipment supplement is to acquire a multi-angle static light scattering system to be used as part of an integrated analytical gel filtration with multi-angle static light scattering (AFG-MALS) system. This system is required for determining the oligomerization state of soluble and integral membrane proteins.
Total Award Amount (including Indirect Costs): $60,000 total for 1 yr

R01 GM120574-S2 (G.T. Montelione, PI/PD) 07/01/17 – 06/30/21
NIH-NIGMS
He Recovery Equipment Supplement to Membrane Protein Structure Using Evolutionary Couplings and Sparse NMR Data
This equipment supplement funds acquisition of a Liquid Helium Cryogen Recovery System.
This He Recovery Cryogen Recovery supports NMR data collection for the Montelione lab in the RPI CBIS NMR Core Facility
Total Award Amount (including Indirect Costs): $249,820 total for 1 yrs

S10 OD030482-01 (G.T. Montelione, PI/PD; S. McCallum, co-PI) 05/03/21 – 05/02/23
NIH High End Instrumentation Program
Regional 800 MHz NMR System Upgrade

The proposed 800 MHz NMR console, cryogenic NMR probe, and magnet pump control unit will replace equipment that is some 15 years old, to support research and teaching in some 21 laboratories at Rensselaer Polytechnic Institute and at several other research universities and colleges in the upstate New York and New Jersey region.
Total Award Amount (including Indirect Costs): $1,315,168.

As Co-Investigator

U19 - AI171443 S. Chanda (Scripps), A. Garcia-Sastre (MSSM) PI/PDs; Montelione, coI 05/22 – 04/25
NIH-NIAID AViDD Centers for Pathogens of Pandemic Concern
Center for Antiviral Medicines and Pandemic Preparedness (CAMPP)
Montelione and Cioffi Labs at RPI will be responsible for leading antiviral drug development program on SARS-CoV2 PL^{pro} protease, and for supporting antiviral drug development program on SARS-CoV2 3CLpro protease. The total amount shown are the subcontract costs assigned to RPI.
Total Award Amount (including Indirect Costs): $1,829,619 total for 3 yrs (shared by Montelione and Cioffi labs at RPI).

Open Philanthropy Project (D. Baker, PI) 09/01/19 - 06/30/23
G.T. Montelione, Funded Collaborator
NMR Studies of Computationally Designed Proteins
The Montelione lab at RPI is collaborating with University of Washington Institute for Protein Design to design protein sequences based on computational methods, express and purify these proteins, and to conduct NMR studies of their structure and dynamics.
Total Award Amount (including Indirect Costs): $407,000

R35 GM122518 (M. Roth, PD/PI) 09/30/17 – 08/31/22
NIH/NIGMS G.T. Montelione, Funded Collaborator
Targeting Retroviral and Virus-like Particles for Gene and Protein Delivery
This is a MIRA award to M. Roth that addresses the fundamental mechanisms of directing murine leukemia viruses (MLV) to preferentially integrate at active promoters and transcriptional start sites. Montelione's role includes structure determination by NMR and X-ray crystallography of domains of MLV integrase, of corresponding human host proteins, and of complexes formed between viral and human host proteins.
Total Award Amount (including Indirect Costs): XXXXX

V.B. Completed Grant Funding History – at Rutgers University

As Principal Investigator

1. Rutgers Cancer Institute of New Jersey and National Institute of Cancer Research Precision Medicine Award. "Targeted Proteomics of Clinically Relevant Mutations Driving Human Cancers" J. Drake and G.T. Montelione, coPIs. 10/01/17 – 9/30/19. $60,000 total award.
2. NIH NIAID "A Novel RNA Recognition Site on the Influenza B Virus NS1 Protein" (R21 AI117510) 01/01/15 – 12/31/17. G.T. Montelione, PI. $534,312 total costs.
3. Rutgers Biomedical Health Sciences Program. "Targeting Protein Complexes Mediating DNA Repair with Computationally Designed Peptides". 06/01/14 – 12/31/17. $40,000 total award (shared with 5 co-investigators).

4. Rutgers University Office of Global Advancement and International Affairs. "International Collaborative Research Project in Protein Dynamics and Industrial Enzyme Engineering". G.T. Montelione, PI. 03/1/16 – 12/31/16. $8,000 total award.
5. Rutgers University China Office. "CABM Summer Training Program with Jiangnan University, Wuxi, China. 4/1/15 – 3/31/16. G.T. Montelione, PI. $6,000 total award.
6. NIH NIGMS Center for High-Throughput Structure Determination "PSI:Biology - Structural Genomics of Eukaryotic Domain Families" (U54 GM094597) 09/01/10 – 06/30/16 G.T. Montelione, PI. ~38,000,000 total costs (shared with 8 Consortium institutions)
7. NIH ORIP "600 MHz NMR RF Console with ^{19}F NMR Probe" (S10 OD018207) 04/01/2014 - 03/31/2015. $439,792 G.T. Montelione, PI; M. Roth, Co-PI; V. Nanda, Co-PI
8. National Science Foundation BRAIN EAGER "The Molecular Interactome of Synaptogenesis" (MCB 1450895) 09/01/14 – 08/31/16. G.T. Montelione and D. Comeletti, coPIs. $43,387 annual direct (Montelione portion)
9. NIH-NIGMS "Structural Genomics of Eukaryotic Model Organisms (U54-GM074958) 07/01/05 –06/30/10. G.T. Montelione, PI. $51,000,000 total cost (shared with 9 Consortium institutions).
10. NIH-NIGMS "Instrumentation for Protein Production and Structural Genomics." Supplement to P50 GM62413. 9/02 – 1/03. G.T. Montelione, PI. Direct costs: $1,500,000 over 1 year.
11. CINJ "CINJ Protein Production and Structural Genomics Project" 02/01/04 – 01/31/06. G.T. Montelione, PI. $70,000 annual direct cost
12. NIH-NIGMS "Structural Genomics of Eukaryotic Model Organisms"(P50-GM62413) 09/30/00 – 8/31/05 $31,800,000 total cost (shared with 8 Consortium institutions)
13. Merck Research Foundation. "Structure-based Functional Genomics of Strongly-Conserved Microbial Gene Families. 9/98 - 9/00. Direct costs: $306,000 over two years.
14. NIH Center for Research Resources "Acquisition of 800 MHz NMR System with Cryogenic Probe" (S10 RR019928) 07/01/04 – 06/30/06 $760,000 direct cost.
15. NIH "Structures of RNA-binding Proteins from Influenza Virus". (R01-GM-47014). 4/ 97 - 4/02. Direct costs: ~ $712,440 over 5 years.
16. Geneformatics Inc. "Improved Methods for Automated Analysis of Protein Structure from NMR Data." 01/01 – 12/02. Direct costs: $400,000 total direct cost.
17. Camille and Henry Dreyfus Teacher Scholar Award. 5/95 - 5/00. Direct costs: $55,000 over five years.
18. Hoffmann-LaRoche, Inc., Nutley, NJ. "Development of NMR as a Tool for Structural Bioinformatics". 1/97 - 12/97. Direct costs: $30,000 over 1 year.
19. AGENE Research Institute Co., Ltd., Kanagawa, JAPAN. "Solution Structures of Genes Identified by Positional Cloning Methods". 1/97 - 12/99. Direct costs: $100,000 over three years.
20. NIH "Biophysics of Serine Protease-Kunitz Inhibitor Complexes". (R01-GM-50733). 2/97 - 2/02. Direct costs: ~ $982,167 over 5 years. (G.T. Montelione, S. Anderson).
21. NIH NIRR "Purchase of 600 MHz NMR and Upgrade of Existing NMR Facilities". 09/95 Direct costs: $400,000. (G. Montelione and J. Baum).
22. NIH Postdoctoral Grant. "Analysis of Protein NMR Spectra Using Artificial Intelligence." 9/94 - 8/97. Direct costs: $90,000 over 3 years. (NIH Postdoctoral Grant with Dr. D. Zimmerman).
23. Wyeth Ayerst Pharmaceutical Company. "Improved Software for NMR Analysis". 7/97 - 7/99. Direct costs: $75,000 over two years.
24. NSF Young Investigator Award. (MCB-9357526). 8/93 - 7/98. Direct costs: $500,000 over 5 years (including industrial matching funds from Chiron Corp., Proctor & Gamble Co., Schering-Plough, Inc. and Novartis Pharmaceutical Corp.).
25. NSF "Improved Technologies for Protein Structure Determination by NMR." (DIR-9019313 / MCB-9407569). 7/91-7/98. Direct costs: $463,000 over 6 years.
26. NIH ""Improved Technologies for Protein Structure Determination by NMR." (R01-GM-47014). 1992-1997.

As Co-Investigator

1. NIH-NIGMS. “Interactions of MuLV IN with Host Proteins and DNA”. 05/01/16 – 04/30/19. M. Roth. PI. (Montelione Lab share of total support: $183,125).
2. NSF BRAIN EAGER “The Molecular Interactome of Synaptogenesis” (MCB 1450895) 09/01/14 – 08/31/16 $43,387 (Montelione portion) (Montelione & Comoletti, coPIs)
3. NIH/NIGMS “Structural Basis of Protein Homeostasis” (U01 GM098254-03) 09/30/12 – 07/31/15 $100,000 annual direct (Montelione portion).
4. NIH/NIDCD “Human Transcription Factor Immunologens: Generation of a Complete Set” 09/23/10 – 08/31/15 ~$350,000 total costs (G. Montelione share) (Anderson, PI; Montelione co-PI).
5. NIH Training Program: New Interdisciplinary Workforce “Training for Integrative Proteomics Technologies” (RFA-RM-04-015) 09/30/04 – 09/29/05 $2,967,942 total cost for 5 years (Levy, Montelione, Berman, Rutgers/RWJMS)
6. NJCST R&D Excellence Program "An Initiative in Structural Bioinformatics -- Connecting Gene Sequence to Function by 3D Structure Determination: A New Paradigm for Drug Discovery".10/97 – 9/02 Direct costs: $3,00,000 over one year. (G. Montelione, S. Anderson, E. Arnold, C. Kulikowski, P. Lobel, S. Stein, A. Stock).
7. New Jersey State Higher Education Leasing Fund - Jointly funded by Rutgers University and UMDNJ. "Purchase of 600 MHz NMR and Upgrade of Existing NMR Facilities". 1993 Direct costs: $985,000. (G. Montelione and J. Baum).
8. NSF "Acquisition of a 600 MHz NMR Spectrometer and Upgrade of Existing NMR Facilities at Rutgers University and at the University of Medicine and Dentistry of New Jersey". 09/94 Direct costs: $571,000. (J. Baum, G. Montelione, S. Anderson, and R. Jones).
9. WM Keck Foundation "Establishment of the W.M. Keck Laboratory for Computational Chemistry and Molecular Graphics." 07/94 Direct costs: $500,000. (E. Arnold, G. Montelione, and A. Stock).

V.C. Proposals Submitted and Not Funded with Current Status (at RPI)

National Science Foundation Graduate Training Grant.
NRT-GCR-HDR: Predoctoral Training Program for Sustainable Biomanufacturing at the Interface of Chemistry, Biology, Engineering and Data Science.
R. Gross, PI, GT Montelione (and others) coPI.
Total Request: $5,000,000??
Submitted: Sept 10, 2023
In review.

National Science Foundation Engineering Research Center Award
F Engineering Center for Transformation of American Rubber through Domestic Innovation for Supply Security: TARDIS.
Puskas JE, PI (Ohio State University), M Koffas, PI at RPI, GT Montelione, coPI at RPI.
Total Request: $25,000,000 ($1,007,765 total costs to RPI)
Submitted: May 5, 2023
In review.

National Science Foundation BII Center
The Institute for Molecular Evolution and Extreme Environments - IME3.
Royer, Makhatadze, Boyd (PI/PDs). GT Montelione, co-I
Total Request: $12,500,000
Submitted: Jan 5, 2022

Declined

National Institutes of Health / NIAID
HWI Center for Structural Genomics of Infectious Disease
Snell (HWI, PI). GT Montelione, co-PI
Total Request: $13,425,000
Submitted Sept 15, 2021
Declined

VI. Briefly Describe Your Current Research Interests

Gaetano Montelione is an internationally recognized expert and innovator in the fields of structural biology and protein NMR.

The unique strengths of our laboratory involve development of NMR methods and software for analysis of protein structures and dynamics, and in applying these methods in structure-function studies. As Director of the NIGMS-funded Northeast Structural Genomics Consortium (NESG) for 16 years (2000 – 2016), I lead a team that determined more than 1,200 3D structures by X-ray crystallography and NMR methods. Over the course of this project I developed expertise in protein expression and crystallization, and in reconstitution and structure determination of soluble proteins and membrane-associated lipoproteins. I also developed extensive experience in software development. In addition to coordinating the efforts of the whole team, I personally directed research programs in structural bioinformatics, protein expression, X-ray crystallography, small-angle X-ray scattering (SAXS), and protein NMR. I have published > 384 peer-reviewed papers, with an impact H-index of 85, and > 25,000 citations.

Our laboratory research program revolves around the themes of new technology development for protein structure production and computational analysis. Based on our experience as a central node for protein sample production and structure determination by NMR in the NIGMS PSI program, rigorous structure and dynamic analysis of small (< 15 kDa) proteins in our laboratory is largely automated and routine. However, most of our current research program focus on larger (> 20 kDa), more challenging systems, including integral membrane proteins and protein complexes. These projects require hybrid approaches, combining NMR data with X-ray crystallography, SAXS, paramagnetic NMR and EPR, and other biophysical methods, along with advanced computational modeling and structural bioinformatics. In order to ensure rigor in applying this broad range of methods, we collaborate intensively with internationally-recognized experts in these domains. For example, we work with experts to explore the impact of Evolutionary Coupling (C. Sander, D. Marks), Rosetta (D. Baker), and CHARMM (W. Im) modeling methods for determining 3D structures of larger proteins for which only sparse, incomplete experimental data is available, including integral membrane proteins. We also rely on our collaborators in paramagnetic NMR (C. Luchinat and G Parigi), SAXS (J. Tainer), fluorescence spectroscopy (C. Royer), EPR (M. Kennedy), and cryoEM (J. Hunt, K. Das) to provide expertise in these critical experimental methods. We also lead the structural biology components of several biomedical collaborations, including projects on viral-host protein/RNA interactions of influenza (with S. Patel, Rutgers) and murine leukemia (with M. Roth, Rutgers) viruses, SARS-CoV2 inhibitor development (with A. Garcia-Sastre, Mt. Sinai), DNA damage repair (with S. Bunting, Rutgers), and de novo protein design (with D. Baker, U Wash.). We also collaborate with the Critical Assessment of Protein Structure Prediction (CASP) program to organize efforts in sparse-NMR-guided structure prediction across the CASP community and AI-based methods for modeling multiple conformations of proteins, and with the wwPDB to develop robust and rigorous methods of protein and nucleic acid structure quality assessment. All of these collaborations are aimed at ensuring the highest rigor and quality control, and in addressing important biomedical questions.

Our laboratory has trained more than 45 graduate students and postdocs, and more than 100 undergraduate students. Many of these have gone on to leading positions in industry and academics. Several are professors at research universities. Others have scientist or management positions at pharmaceutical and biotechnology companies. A list of laboratory alumni, and their current positions, is available on our lab home page.

In order to organize the efforts of more than 12 research groups and more than 150 scientists who participated in the NIGMS NESG program over 16 years, and to support collaborative interactions across this multi-institutional team, I also lead the development of the NESG Protein Structure Production Platform and the SPiNE LIMS database. I have organized many national and international workshops and conferences, including The International Structural Genomics Conference, Keystone Symposia, NIGMS PSI workshops, NJ ACS NMR symposia, and many workshops. I am also a member of several international advisory groups in structural biology, CASP organizer, and the co-chair of the wwPDB Task Force on NMR Structure Validation.

1. Development of computational methods for analysis of protein NMR assignments and structures. The Montelione laboratory has developed widely used computational NMR methods and software for analysis of protein structures and dynamics. Early work developing triple-resonance NMR led us to the hypothesis that these data could be used for fully automated analysis of protein structures from NMR data. This goal, initiated in a collaboration with computer scientists Drs. D. Zimmerman, Y. Huang, and C. Kulikowski in the mid 1990's, was realized with the development of the AutoAssign and AutoStructure (now called ASDP) expert systems for largely automated analysis of NMR resonance assignments and structures. This work continued in collaborations with computer scientist Dr. Y. Huang to develop robust automated NOESY analysis and structure validation tools, and in collaborations with Prof. David Baker (Univ. of Washington) and Chris Sander (Harvard University) to explore hybrid methods combining automated NMR data analysis with sophisticated computational modeling and bioinformatics methods. Montelione also interacts extensively with the global community of participants in the Critical Assessment of Protein Structure Prediction (CASP) experiment, to explore synergies between protein prediction methods and NMR data, and to drive the field of data-guided protein structure prediction using NMR, SAXS, and other experimental data.

a. Zimmerman, D.E.; Kulikowski, C.A.; Huang, Y.J.; Feng, W.; Tashiro, M.; Shimotakahara, S.; Chien, C.; Powers, R.; Montelione, G.T. ***J. Mol. Biol.*** 1997, 269: 592-610. Automated analysis of protein NMR assignments using methods from artificial intelligence.
b. Baran, M.C.; Huang, Y.J.; Moseley, H.N.; Montelione, G.T. ***Chemical Reviews*** 2004, 104: 3451-3555. Automated analysis of protein NMR assignments and structures.
c. Huang, Y.J.; Powers, R.; Montelione, G.T. ***J. Am. Chem. Soc.*** 2005 127: 1665-1674. Protein NMR recall, precision, and F-measure scores (RPF scores): Structure quality assessment measures based on information retrieval statistics.
d. Raman, S.; Lange, O.F.; Rossi, P.; Tyka, M.; Wang, X.; Prestegard, J.; Montelione, G.T.; Baker, D. ***Science*** 2010 327, 1014-8. NMR structure determination for larger proteins using backbone-only data. PMC2909653.
e. Lange, O.F.; Rossi, P.; Sgourakis, N.; Song, Y.; Lee, H.-W.; Aramini, J.M.; Ertekin, A.; Xiao, R.; Acton, T.B.; Montelione, G.T.; Baker, D. ***Proc. Natl. Acad. Sci. U.S.A.*** 2012, 109: 10873 - 10878. Determination of solution structures of proteins up to 40 KDa using CS-Rosetta with sparse NMR data from deuterated samples. PMC3390869
f. Mao, B.; Tejero, R.; Baker, D.; Montelione, G.T. ***J. Amer. Chem. Soc***. 2014, 136: 1893 - 1906. Protein NMR structures refined with Rosetta have higher accuracy relative to corresponding X-ray crystal structures. PMC4129517
g. Montelione, G.T.; Nilges, M.; Bax, A.; Güntert, P.; Herrmann, T.; Richardso J.S.; Schwieters, C.; Vranken, W.F.; Vuister, G.W.; Wishart, D.S.; Berman, H.; Kleywegt, G.J.; Markley, J.L. ***Structure*** 2013, 21: 1563 - 1570. Recommendations of the wwPDB NMR Validation Task Force. PMC3884077.
h. Mao, B.; Guan, R.; Montelione, G.T. ***Structure*** 2011, 19: 757 - 766. Improved technologies now routinely provide protein NMR structures useful for molecular replacement. PMC3612016.

i. Tang, Y.; Huang, Y.P.; Hopf, T.A.; Sanders, C.; Marks, D.S.; Montelione, G.T. ***Nature Methods*** 2015, 12: 751-754. Protein structure determination by combining sparse NMR spectroscopy data with evolutionary couplings. PMC4521990.

2. NMR Pulse sequence design, including Triple Resonance NMR. Montelione's postdoctoral work with Prof. G. Wagner was focused on the creation of new NMR experiments, which have had significant impact in the field of biomolecular NMR. These pulse sequences provide some of the key tools of modern protein NMR, including ZZ-exchange spectroscopy, the J1-resolved E.COSY experiment for measuring scalar coupling constants, and the first ^{1}H,^{13}C,^{15}N triple resonance NMR experiments (HNCH and HCNH) for determining resonance assignments in proteins. This work was followed up at Rutgers by invention of the HCCNH-TOCSY, HcoCCNH-TOCSY experiments, and several other widely used triple-resonance NMR experiments. Triple-resonance NMR is now the standard approach for determining NMR resonance assignments of proteins. This work has had high impact on the field of biomolecular NMR.

a. Montelione, G.T.; Wagner, G. ***J. Amer. Chem. Soc***. 1989, 111: 3096 - 3098. 2D chemical exchange NMR spectroscopy by proton-detected heteronuclear correlation.
b. Montelione, G.T.; Winkler, M.E.; Rauenbuehler, P.; Wagner, G. ***J. Magn. Resonance*** 1989, 82: 198-204. Accurate measurements of long-range heteronuclear coupling constants from homonuclear 2D NMR Spectra of isotope-enriched proteins.
c. Montelione, G.T.; Wagner, G. ***J. Amer. Chem. Soc***. 1989, 111: 5474 - 5475. Accurate measurements of homonuclear HN-Hα coupling constants in polypeptides using heteronuclear 2D NMR experiments.
d. Montelione, G.T.; Wagner, G. ***J. Magn. Reson***. 1990, 87: 183 - 188. Conformation-independent sequential NMR connections in isotope-enriched polypeptides by ^{1}H-^{13}C-^{15}N triple-resonance experiments.
e. Montelione, G.T.; Lyons, B.A.; Emerson, S.D.; Tashiro, M. ***J. Amer. Chem. Soc***. 1992, 114: 10974 - 10975. An efficient triple resonance experiment using carbon-13 isotropic mixing for determining sequence-specific resonance assignments of isotopically enriched proteins.
f. Emerson, S.D.; Montelione, G.T. ***J. Am. Chem. Soc.*** 1992, 114: 354-356. Accurate measurements of proton scalar coupling-constants using C-13 isotropic mixing spectroscopy.
g. Lyons, B.A.; Montelione, G.T. ***J. Magn. Resonance Series B***. 1993, 101: 206-209. A HCCNH triple-resonance experiment using C-13 isotropic mixing for correlating backbone amide and side-chain aliphatic resonances in isotopically enriched proteins.
h. Shang, Z.G.; Swapna, G.V.T.; Rios, C.B.; Montelione, G.T. ***J. Am. Chem. Soc***. 1997, 119: 9274-9278. Sensitivity enhancement of triple-resonance protein NMR spectra by proton evolution of multiple-quantum coherences using a simultaneous ^{1}H and ^{13}Cconstant-time evolution period.

3. Development of technologies enabling structural genomics. As Director of the Northeast Structural Genomics Consortium (NESG) for 16 years (2000 – 2016), Montelione developed a successful high-throughput pipeline for protein sample and structure production. This program involved extensive efforts in new technology development for protein sample production, as well as for NMR, X-ray, crystallography, and structural bioinformatics. This work resulted in more than 350 peer reviewed publications by the consortium. As part of this project the team targeted large, structurally-uncharacterized domain families, and protein interaction networks involved in human cancer biology. They successfully developed a platform of integrated technology for efficient protein sample and structure production, which has been adopted by industrial structural biology groups. The team developed and refined technologies for codon optimization, construct design and optimization, isotope enrichment using efficient single-protein production systems, automated NMR and X-ray crystallography data analysis, and structure quality assessment metrics. More than 1,300 new structures were deposited in the PDB, and extensive data on protein expression and sample production was archived. More than 500 NMR structures, representing ~ 5% of all NMR structures in the PDB, were determined by the NESG consortium.

a. Montelione, G.T.; Anderson, S. ***Nature Struct. Biology***, 1999, 6: 11-12. Structural genomics: Keystone for a Human Proteome Project;.
b. Montelione, G.T.; Zheng, D.; Huang, Y.J.; Gunsalus, K.C; Szyperski, T. ***Nature Struct. Biol.*** 2000, 7: 982 - 985. Protein NMR spectroscopy in structural genomics.
c. Acton, T.B.; Xiao, R.; Anderson, S.; Aramini, J.M.; … Zhao, L.; Montelione, G.T. ***Meth. Enzymology*** 2011, 493: 21 - 60. Preparation of protein samples for NMR structure, function, and small molecule screening studies. PMC4110644.
d. Montelione, G.T**.** ***F1000 Biology Reports***, 2012, 4: 7. The Protein Structure Initiative: Achievements and visions for the future. DOI: https://doi.org/10.3410/B4-7
e. Koga, N.; Tatsumi-Koga, R.; Liu, G.; Xiao, R.; Acton, T.B.; Montelione, G.T.; Baker, D. ***Nature*** 2012, 491: 222 - 227. Principles for designing ideal protein structures. PMC3705962.
f. Boël, G.; Letso, R.; Neely, H.; Price, W.N.; Wong, K.H.; Su, M.; Luff, J.; Valecha, M.; Everett, J.; Acton, T.B.; Xiao, R.; Montelione, G.T.; Aalberts, D.P.; Hunt, J.F. ***Nature*** 2016, 529: 358 - 363. Codon influence on protein expression in *E. coli* correlates to mRNA levels. PMC5054687

4. Structure – function studies of cancer-associated proteins of the Human Cancer Protein Interaction Network. Montelione has used bioinformatics analysis to characterize networks of protein-protein interactions involved in cancer biology. Several hundred of these cancer-associated proteins were produced by the NESG Protein Production Pipeline, and more than 100 3D structures have been determined and deposited in the PDB. These studies provide novel insights into the structures and functions of oncogenes and tumor suppressors, including structure-function relationships in epidermal growth factor, type-✔ transforming growth factor, and allosteric mechanisms of molecular recognition of HRAS by the RAS-binding domain of the BRAF kinase.

a. Montelione, G.T.; Wüthrich, K.; Nice, E.C.; Burgess, A.W.; Scheraga, H.A. ***Proc. Natl. Acad. Sci. U.S.A.*** 1987**,** 84: 5226-5230. Solution structure of murine epidermal growth factor: determination of the polypeptide backbone chain-fold by nuclear magnetic resonance and distance geometry.
b. Huang, Y.J.; Hang, D.; Lu, L.J.; Tong, L.; Gerstein, M.B.; Montelione, G.T. ***Mol. Cell. Proteomics*** 2008, 7: 2048 - 2060. Targeting the human cancer pathway protein interaction network by structural genomics. PMC2559933
c. Ertekin, A.; Aramini, J.M.; Rossi, P.; Leonard, P.G.; Janjua, H.; Xiao, R.; Maglaqui, M.; Lee, H.-W.; Prestegard, J.H.; Montelione, G.T. ***J. Biol. Chem***. 2012, 287: 16541 - 16549. Human cyclin dependent kinase 2 associated protein 1 is dimeric in its disulfide-reduced state, with natively disordered N-terminal region. PMC3351331.
d. Aramini, J.M.; Vorobiev, S.M.; Tuberty, L.M.; Janjua, H.; Campbell, E.T.; Seethraman, J.; Su, M.; Huang, Y.P.; Acton, T.B.; Xiao, R.; Tong, L.; Montelione, G.T. ***Structure*** 2015, 23: 1 - 12. The RAS-binding domain of human BRAF protein serine/threonine kinase exhibits allosteric conformational changes upon binding HRAS. PMC4963008.
e. Song, F.; Li, M.; Li, G.; Swapna, G.V.T.; Daigham, N.S.; Xia, B.; **Montelione, G.T**.; Bunting, S.F. ***Biochemistry*** 2018 57:6581-6591. Antiparallel coiled-coil interactions mediate homodimerization of the DNA damage repair protein, PALB2.

5. Structure – function studies of the non-structural protein 1 (NS1) from influenza virus. Together with virologist Prof. R. Krug (Univ. of Texas), Montelione made fundamental discoveries regarding structure-function relationships of the NS1 protein, which functions to suppress the host innate immune response to viral infection. The collaboration has provided 3D structures of several critical complexes formed between NS1 and human host proteins using both NMR and X-ray crystallography, and discovered the structural basis for one of the key mechanisms by which NS1 contributes to the unique human / primate host range of influenza B viruses. These studies have provided the basis for the invention of patented approaches for rational design of influenza virus inhibitors and attenuated vaccines. For example, mutations of key RNA-binding residues Arg38 and Ly41 in NS1, first characterized by

Montelione and Krug, provide the basis for live attenuated influenza vaccines that are being evaluated for human clinical trials (Du et al. 2018 Science 359: 290-6)

a. Chien, C.-Y.; Tejero, R.; Huang, Y.; Zimmerman, D.E.; Krug, R.M.; Montelione, G.T. ***Nature Struct. Biol***. 1997, 4: 891 - 895. A novel RNA-binding motif in influenza A non-structural protein 1.
b. Yin, C.; Khan, J.A.; Swapna, G.V.T.; Krug, R.M.; Tong, L.; Montelione, G.T. ***J. Biol. Chem***. 2007, 282: 20584 -20592. Conserved surface features form the double-stranded RNA-binding site of non-structural protein 1 (NS1) from influenza A and B viruses.
c. Das, K.; Ma, L-C.; Xiao, R.; Radvansky, B.; Aramini, J.; Zhao, L.; Marklund, J.; Kuo, R-L.; Twu, K.Y.; Arnold, E.; Krug, R.M.; Montelione, G.T. ***Proc. Natl. Acad. Sci. U.S.A.*** 2008, 105: 13092 - 13097. Structural basis for suppression by influenza A virus of a host antiviral response. PMC2522260.
d. Guan, R.; Ma, L-C; Leonard, P.G.; Amer, B.R.; Sridharan, H.; Zhao, C.; Krug, R.M.; Montelione, G.T. ***Proc. Natl. Acad. Sci. U.S.A.*** 2011, 108: 13468 – 13473. Structural basis for the sequence-specific recognition of human ISG15 by the NS1 protein of influenza B virus. PMC3158222.
e. Aramini, J.M.; Hamilton, K.; Ma, L.C.; Swapna, G.V.; Leonard, P.G.,;Ladbury, J.E.; Krug, R.M.; Montelione, G.T. ***Structure*** 2014, 22: 515-525. ^{19}F NMR reveals multiple conformations at the dimer interface of the nonstructural protein 1 effector domain from influenza A virus.
f. Ma, L-C.; Guan, R.; Hamilton, K.; Aramini, J.; Mao, L.; Wang, S.; Krug, R.M.; Montelione, G.T. ***Structure*** 2016, 24: 1562-1572. A second RNA-binding site in the NS1 protein of influenza B virus.

VII. Editorship of Journals, Review of Manuscripts, Books, Research Proposals, Curating, and Jurying of Exhibitions

Editorial Boards of Scientific Journals

2000 – 2007 Editor, *J. Structural and Functional Genomics*
2007 – 2016 Associate Editor, *J. Structural and Functional Genomics*
2000 – 2007 Associate Editor, *PROTEINS: Structure, Functional, Genetics*
2007 – present Editorial Board Member, *PROTEINS: Structure, Functional, Genetics*
2001 – present Associate Editor, *Faculty of 1000*, Section of Integrative Methods for Structural Biology
2021 – present Editorial Board Member, *Biomolecules*
2021 – 2023 Editorial Board Member, *Current Opinion in Structural Biology – Biophysical Methods*
2021 – 2022 Special Editorial Board Member, *Frontiers in Biomolecular Sciences* (special issue)
2022 – 2023 Special Editorial Board Member, *J Physical Chemistry* (special issue)
2022 – 2023 Special Editorial Board Member, *J Magn Resonance* (special issue)

Reviewer for Scientific Journal Articles

Science, Nature, Proceedings of the National Academy of Science USA, Nature Methods, Nature Communications, Nature Structural Molecular Biology, Structure (Cell Journal), Angewandte Chemie International Edition, Biochemistry, FEBS Letters, Journal of American Chemical Society, Journal of Biological Chemistry, Journal of Biomolecular NMR, Journal of Magnetic Resonance, Journal of Molecular Biology, Protein Science, PROTEINS: Structure, Function, Bioinformatics, J. Structural and Functional Genomics

VIII. Service

A. Service to University

University, School, and Departmental Committees and Dates for Each

Rensselaer Polytechnic Institute

2021 - present Center for Biotechnology and Interdisciplinary Studies (CBIS) Executive Committee.
2022 - present Rensselaer Faculty Senate Procurement Improvement Committee
2023 - present Rensselaer Forward Presidential Committee on Research Infrastructure
2023 - present Rensselaer University Senate Faculty Committee on Promotions and Tenure

Rutgers University and Rutgers Robert Wood Johnson Medical School

2005 – 2012 Director, Cancer Institute of New Jersey Protein Structural Analysis and Modeling Facility
2006 – 2008 Executive Committee, Rutgers University Proteomics Building Planning Committee
2014 – 2018 Rutgers University Committee on Academic Promotions and Tenure (AP&T) – Distinguished Professor Rank
2014 – 2018 Member, Rutgers University Presidential Advisory Committee on Academic Planning and Review (CAPR)
2017 – 2018 Member, CABM Executive Director Faculty Search Committee

Rutgers Graduate School Committees

1998 – 2000 Co-Director, Rutgers Computational Molecular Biology Program
1995 – 2000 Member, NIH Biotechnology Training Program Executive Committee

Departmental Committees - RPI

2021 – present Center for Biotechnology and Interdisciplinary Studies (CBIS) Executive Committee
2022 – present Chemistry Honors Committee

Departmental Committees - Rutgers

2000 – 2019 Center for Advanced Biotechnology and Medicine Computer Committee
2016 – 2019 Center for Advanced Biotechnology and Medicine Peer Evaluation Committee
2019 Molecular Biology and Biochemistry Faculty Recruitment Committee

Undergraduate Student Advising and Counseling

Undergraduate Academic Advisees - Chemistry

1. Chase Alonse
2. Henry Chen
3. Nola Murry
4. John Ricciardi

Undergraduate Research Advisees

1. Chris Damone – Chemical Engineering
2. Nate Antony – Chemistry and Chemical Biology

1. Reena Caplan – Biochemistry, Biophysics and Biology
2. Suren Zakian – Biology

High School Students

1. Ethan Li, Valley Christian High School, San Jose, California. 2022, 2023
2. Anjeli Patel, Montville Township Public Schools, Montville NJ – summer 2022, in person and remote
3. Alex Li, Valley Christian High School, San Jose, California. 2023

Graduate Student Advising and Counseling

Primary Advisor for Ph.D.
1. Rebecca Greene-Cramer – Chemistry and Chemical Biology
2. Laura Spaman – Chemistry and Chemical Biology
3. Tiburon Benavides - Biological Sciences

Rotation Graduate Students
1. Rebecca Greene-Cramer – Chemistry and Chemical Biology
2. Laura Spaman – Chemistry and Chemical Biology
3. John Liu – Chemistry and Chemical Biology
4. Tiburon Benavides - Biological Sciences
5. Darian Topolski - Chemistry

Ph.D. Committees other than primary advisees
1. Adrianne Bunn – Chemistry and Chemical Biology
2. Cody Edson – Chemistry and Chemical Biology
3. Christian Franqiz – Chemistry and Chemical Biology
4. Lauren Gandy – Chemistry and Chemical Biology
5. Noam Hantman – Biological Sciences
6. Aaron Hein – Computer Science, University of South Carolina
7. Patrick Landy – Chemistry and Chemical Biology
8. Rebecca Miceli – Chemistry and Chemical Biology
9. Caitlin Moustouka – Biological Sciences
10. Edgar Peters – Biophysics
11. Brandon Schweibenz – Molecular Biology and Biochemistry, Rutgers University
12. Isha Shah – Chemistry and Chemical Biology
13. Lucas Sutton – Biological Sciences
14. Ellinor Tai – Biological Sciences
15. Jasmine Yang – Chemical Engineering

B. **Professional Societies**

1992 – 1998	Treasurer, Experimental NMR Conference (ENC)
1995 – present	Member, American Association for the Advancement of Science (AAAS)
2000 – present	Member, Biophysical Society
2000 – present	Member, American Chemical Society
2006 – present	Member, International Structural Genomics Organization
2006 – 2014	Treasurer, International Structural Genomics Organization
2019 – present	Member, International Society for HDX with Mass Spectrometry (IS-HDXMS)

C. Community and Public Service

<u>International Grant Reviews</u>

1990	Swedish Research Council for Engineering
2015	START Programme of the Austrian Science Fund (FWF)

2017	Swiss National Science Foundation
2017	Japan Society for the Promotion of Science
2018	KUSCO (Korea-US. Science Cooperation Center), National Research Foundation of Korea
2018	Czech National Science Foundation
2018	The Lise Meitner-Programme of the Austrian Science Fund (FWF)
2020; 2021	Austrian Science Foundation
2021	Biotechnology and Biological Sciences Research Council, United Kingdom

United States National Grant Review Panels

1990 – 2005	NIH Research Resources Program, Ad Hoc
1990 – 2005	NIH, National Cancer Institute, Ad Hoc
1990	The Arthritis Foundation,
1995 – 1999	National Science Foundation Molecular Biophysics Study Section Panel
1997 – present	National Science Foundation Ad Hoc Grant Reviews,
2005	NIH Special Study Section: NIGMS Postdoctoral Fellowship Program
2005	NIH Special Study Section: NIGMS Membrane Protein Structure Initiative,
2010	National Science Foundation Committee of Visitors – Molecular and Cellular Biology,
2011 – 2015	National Science Foundation Advisory Committee for the Biological Sciences Directorate,
2013	National Science Foundation Committee of Visitors – Plant Genomics
2014	National Science Foundation Committee of Visitors – Molecular and Cellular Biology
2017	NIH, National Cancer Institute, Macromolecular Crystallography and Structural Biophysics Intramural Review Committee, NCI Fredrick Maryland Site.
2018	NIH Special Emphasis Panel/Scientific Review Group 2018/05 ZRG1 BCMB-D
2019	NIH Special Study Section: NIGMS Maximizing Investigators' Research Award (R35)
2019	Ralph E Power Faculty Enhancement Awards Review Panel – Oak Ridge Natl Labs
2020	Advisor - White House Office of Science and Technology COVID-19 High Performance Computing Consortium

Service on Major National and International Committees

International

2003 – 2016	Advisory Board, International Structural Genomics Organization (ISGO)
2006 – present	NMR Advisory Committee, Worldwide Protein Data Bank (wwPDB)
2007 – 2010	Advisory Committee, International BioMagResDataBase (BioMagResDB)
2007 – 2016	Advisory Committee, European E-NMR International Computational Grid Project
2011 – present	co-Chair, wwPDB Task Force on NMR Structure Validation
2012 – present	Advisor and Assessor, Critical Assessment of Protein Structure Prediction (CASP)

National

1999 – 2003	Advisory Committee, National Magnetic Resonance Facility Madison WI (NMRFAM)
2017 - 2022	Scientific Advisory Board, Seattle Structural Genomics Center for Infectious Disease (SSGCID) and Midwest Center for Structural Genomics of Infectious Diseases (CSGID)

IX. Professional and Public Lectures

(List invited and contributed papers and lectures, giving title, organization, and dates.)

Prof. Montelione has presented approximately 70 invited lectures since 2000, including:

Invited Speaker, "Structural and Functional Genomics in Pharmaceutical Design". Princeton, NJ, October 24 - 25, 2001.

Invited Speaker, "International Keystone Meeting: Structural Genomics: From Gene Sequence to Function". Breckenridge CO. January 5 - 10, 2002.

Invited Speaker, "Workshop in Protein Production for Structural Genomics". NIGMS, NIH, Bethesda, MD, March 7 – 8, 2002.

Invited Speaker, "Workshop in NMR and Structural Genomics". University of Wisconsin at Madison, Madison, WI, June 22, 2002.

Invited Speaker, "Second International Conference in Structural Genomics". International Structural Genomics Organization (ISGO) Conference, Berlin, GERMANY, October 10 – 13, 2002.

Invited Speaker, "Bruker NMR Technology Development Group". Bruker BioSpin, Karlsruhe, GERMANY, October 15, 2002.

Invited Speaker, "International Meeting for European High Field NMR Network". Montecatteni, ITALY, October 17, 2002.

Invited Speaker, "Alberta Synchrotron Institute Meeting in Structural Genomics". Banff, Alberta, CANADA, October 24, 2002.

Invited Speaker, "Workshop on Protein Production and Crystallization for Structural Genomics". NIGMS, NIH, Bethesda, MD, April 9 - 11, 2003.

Invited Speaker, "European Science Foundation: NMR in Structural Biology", Strousbourg, FRANCE. Sept. 7 – 12, 2003.

Invited Speaker, "CABM Symposium: Functional Genomics". Piscataway, NJ. October, 2003.

Invited Speaker, "International Keystone Meeting: Frontiers of NMR in Structural Biology". Taos. New Mexico, USA January, 2003.

Invited Speaker, "International Keystone Meeting: Structural Genomics: From Gene Sequence to Function". Snowbird, Utah, USA. April 13-20, 2004.

Invited Speaker, "International Keystone Meeting: Frontiers of NMR in Structural Biology". Banff, British Columbia, CANADA. January 29 – Feb 5, 2005.

Invited Speaker, "International Symposium on Cell Free Protein Production". Matsayama, JAPAN. October 22 – 25, 2005.

Invited Speaker, "International Keystone Meeting: Structural Genomics: From Gene Sequence to Function" Keystone, Colorado, USA. January 28 – February 4, 2006.

Invited Speaker, “12th Bijvoet Symposium: Protein Structure in relation to dynamics and interactions” Utrecht, THE NETHERLANDS. April 6 – 7, 2006.

Invited Speaker, University of Florence, Florence, ITALY, September 23, 2006.

Invited Speaker, “Computational Aspects – “Biomolecular NMR Gordon Research Conference”, Aussois, FRANCE September 24-29, 2006

Invited Speaker, “CABM Symposium: Molecular Aspects of Human Disease”. Piscataway, NJ, USA. October 16, 2006.

Invited Speaker, “International Structural Genomics Organization Workshop on Automated Methods for Protein NMR Data Analysis”. Yokohama, JAPAN. October 18, 2006.

Invited Speaker, “Third International Conference on Structural Genomics”. Beijing, PEOPLES REPUBLIC OF CHINA, October 18 – 22, 2006.

Invited Speaker, “Jiangnan University”, Wuxi, PEOPLES REPUBLIC OF CHINA. October 30, 2006.

Invited Speaker, “Eastern Analytical Society”, Somerset, NJ, USA. November 13, 2006.

Invited Speaker, “NIH Protein Structure Initiative Annual Meeting”, Bethesda, Maryland, USA. December 7, 2006.

Invited Speaker, “Keystone Meeting on Frontiers of NMR in Structural Biology”. Snowbird, Utah, USA. January 4 – 11, 2007.

Invited Speaker, “NIH Workshop on Overcoming Bottlenecks in Structural Genomics”. Bethesda, Maryland, USA. March 19 - 20, 2007

Invited Speaker. “NIH Protein Structure Initiative, Annual Meeting”. Bethesda, Maryland, USA December 5 – 6, 2007.

Invited Speaker, “Keystone Meeting on Structural Genomics in Biology and Medicine”. Steamboat Springs, Colorado, USA. January 7 – 11, 2008.

Invited Speaker, “PSI Workshop on Functional Annotation for Structural Genomics”, San Diego, California, USA, March 7 – 8, 2008.

Invited Speaker, “PSI Workshop on Homology Modeling for Biology”, San Francisco, California, USA, July 10 – 12, 2008.

Organizer and Speaker, “PSI Workshop on Visions for Structural Genomics”, Bethesda, Maryland, USA, July 28 - 29, 2008

Invited Speaker, ”5th International Meeting in Structural Genomics”, Oxford, England, UNITED KINGDOM, September 20 - 23, 2008.

Invited Speaker, Department of Biochemistry, Cambridge, England, United Kingdom, September 24, 2008.

Invited Speaker. “NIH Protein Structure Initiative, Annual Meeting”. Bethesda, Maryland, USA, December 10 – 12, 2008.

Invited Speaker, “ENMR Workshop on Automated Structure Analysis”. Florence, Italy. May 4, 2009.

Invited Speaker, “Structural Genomics in Drug Discovery”. Tsin-Jin, Peoples Republic of China. June 2009.

Invited Speaker, “NIH Protein Structure Initiative, Annual Meeting”. Bethesda Maryland, USA, December 9-10, 2009.

Invited Speaker, “2nd Annual ENMR Workshop on Automated Structure Analysis”. Florence, ITALY. May 6, 2010.

Invited Speaker, “International Structural Genomics Conference”. Toronto, Canada. May 9 – 13, 2011.

Invited Speaker, “Gordon Research Conference in Computational Methods for NMR Spectroscopy”. Barga, Italy. May 29 – June 2, 2011.

Invited Speaker, “Functional Roles of Intrinsic Dynamics in Proteins: Some Lessons from Structural Genomics”. University of Michigan, Ann Arbor, Michigan, USA. October 11, 2011.

Invited Speaker, “Structural Genomics”. Cornell University, Ithaca, New York, USA. October 19, 2011.

Invited Speaker. “Template-based Modeling Assessment”. Critical Assessment of Protein Structure Prediction CASP10 International Meeting. Gaeta, Italy. December 9 - 12. 2012

Invited Speaker, “Evolutionary Couplings in Protein NMR”. Gordon Research Conference in Computational Methods for NMR. Mt. Snow, Vermont, USA. June 2-7, 2013.

Invited Speaker, Structural Life Science 7th International Conference on Structural Genomics, Sapporo, JAPAN. July 29, 2013.

Invited Speaker, “Function Discovery by Structural Genomics”. Inauguration Symposium for Princeton Chemistry Department NMR Laboratory, Princeton University, Princeton, New Jersey, USA. September 26, 2013.

Invited Speaker, “A Structure-Based Inhibitor Discovery Process Applied to Influenza Non-structural Protein 1 (NS1)” ICMol, University of Valencia, Valencia, SPAIN. October 8, 2014.

Keynote Speaker, "Developing NMR for Studies of Larger Proteins and Enzymes. Application to R. chinensis Lipase". 2014 Symposium on Lipase Biotechnology and it Application Trends. School of Biotechnology. Jiangnan University. Wuxi, PEOPLES REPUBLIC OF CHINA. Oct 23, 2014.

Invited Speaker, “Sparse NMR Contacts for Modeling Protein Structures”. Critical Assessment of Protein Structure Prediction CASP 11 International Meeting. Pairaso Mayo, Playa de Carmen, MEXICO. December 1 - 7, 2014.

Invited Speaker, “Hybrid Approaches for Protein Structure Determination Combining Computational Modeling with Sparse NMR Restraints”. 56th Experimental NMR Meeting (ENC). Asilomar, California, USA. April 19 – 24, 2015.

Keynote Speaker. “Hybrid Approaches for Protein Structure Determination Combining Computational Modeling with Sparse NMR Restraints”. 14th Upstate New York NMR and Structural Biology Symposium. Syracuse, New York, USA. October 20, 2015.

Invited Speaker. “Hybrid Approaches for Protein Structure Determination Combining Computational Modeling with Sparse NMR Restraints”. Symposium on Enzymes for Chirality: Protein Engineering and Molecular Design, School of Biotechnology, Jiangnan University, Wuxi, PEOPLES REPUBLIC OF CHINA. November 6, 2015.

Invited Speaker. “Protein Structure Determination Combining Computational Modeling with Sparse NMR Restraints”. Eastern Analytical Symposium. Somerset, New Jersey, USA. November 16-18, 2015.

Invited Speaker. “Synergies of Molecular Modeling Calculations and Protein NMR Spectroscopy”. National Science Foundation / Rice University Workshop in Modeling and Dynamics in Molecular Biophysics. Arlington, Virginia, USA. January 27-28, 2016.

Invited Speaker. “Hybrid Approaches for Protein Structure Determination Combining Computational Modeling with Sparse NMR Restraints”. Gordon Research Conference on Molecular Structure Elucidation. Mt. Snow, Vermont, USA. August 12-17, 2016.

Invited Speaker. “Protein NMR Structure Validation: Model vs Data Validation Metrics”. wwPDB Protein NMR Validation Task Force Meeting. Osaka, JAPAN. August 26-27, 2016.

Invited Speaker. “Protein NMR”. 16th Korean Institute for Advanced Study (KIAS) Protein Folding Winter School. Seoul, Korea. January 16 – 20, 2017. Three lectures.

Invited Speaker. “Protein NMR Structure Validation”. 61st Annual Meeting of the Biophyscial Society. New Orleans, USA. February 11-15, 2017.

Lead Organizer and Speaker. “Protein NMR Structure Validation”. wwPDB Protein NMR Validation Task Force Meeting. Newby, Maine, USA. June 17, 2017.

Plenary Lecture. “Hybrid Approaches for Protein Structure Determination Combining Computational Modeling with Sparse NMR Restraints”. 17th KIAS Conference on Protein Structure and Function. Korean Institute for Advanced Study, Seoul, SOUTH KOREA. September 22, 2017.

Invited Speaker. “Structural Biology of Innate Immune Suppression by Influenza Viruses”. i3D Retreat Rutgers New Jersey Medical School, Newark, NJ USA October 25, 2017

Plenary Lecture. "Hybrid Methods for Protein Structure Determination Combining NMR Data, Evolutionary Co-Variance Data, and Conformational Modeling." 4th International Conference on Protein and RNA Structure Prediction. Montego Bay, JAMAICA, WEST INDIES. December 6, 2017.

Invited Speaker. "Hybrid Methods for Protein Structure Determination Combining NMR Data, Evolutionary Co-Variance Data, and Conformational Modeling." 2018 Biophysical Society Meeting: Memorial Symposium to Honor Dr. Kamal Shukla. San Francisco, California, USA. February 16, 2018.

Invited Speaker. “Structural Biology of Innate Immune Suppression by Influenza Viruses”. Lawrence Berkeley National Laboratories. Berkeley, California. USA. February 22, 2018.

Invited Speaker. "Hybrid Methods for Protein Structure Determination Combining Computational Modeling with Evolutionary Co-Variance and NMR Data". Gordon Research Conference on Structure Elucidation in Pharmaceutical Industry. Newby, Maine, USA. August 13, 2018.

Invited Speaker. "Proteins Flex to Function: The Role of Conformational Plasticity in Molecular Recognition". Department of Biological Sciences, Rensselaer Polytechnic Institute. Troy, New York, USA. October 11, 2018

Invited Speaker. "Proteins Flex to Function: The Role of Conformational Plasticity in Molecular Recognition". Centro di Risonanze Magnetiche CERM, University of Florence, Sesto Fiorentino, Italy. October 22, 2018.

Plenary Speaker. "Proteins Flex to Function: The Role of Conformational Plasticity in Molecular Recognition". 2018 Symposium on Protein Engineering and Molecular Design of Industrial Enzymes. School of Biotechnology, Jiangnan University, Wuxi, PEOPLES REPUBLIC OF CHINA. November 7, 2018.

Plenary Speaker. "Proteins Flex to Function: The Role of Conformational Plasticity in Molecular Recognition". The 18th KIAS Conference on Protein Structure and Function. Korean Institute for Advanced Study, Seoul, South Korea. November 16, 2018

Plenary Speaker. "Data-Assisted Protein Prediction in CASP13". Critical Assessment of Protein Structure Prediction CASP 13 International Meeting. Pairaso Mayo, Playa de Carmen, Mexico. December 3, 2018.

Invited Speaker. "Proteins Flex to Function: The Role of Conformational Plasticity in Molecular Recognition". Institute for Bioscience and Biotechnology Research, National Institutes of Standard and Technologies, Rockville, Maryland USA. February 4, 2019.

Invited Speaker. "The wwPDB NMR Structure Validation Project". Biophysical Society Satellite Workshop: Working Towards Federated Structural Models". Baltimore Maryland USA. March 1, 2019.

Invited Speaker. "Proteins Flex to Function: The Role of Conformational Plasticity in Molecular Recognition". University of Calgary, Calgary, Canada. May 21, 2019.

Invited Speaker. "HDX-MS in CASP – Critical Assessment of Protein Structure Prediction" Second International Meeting in Biomolecular Hydrogen-Deuterium Exchange with Mass Spectroscopy. Banff, CANADA. May 23, 2019.

Sabbatical Lectures in Bioinformatics and Protein NMR. University of Florence, Florence, ITALY. November and December 2019.

Invited Speaker. "Proteins Flex to Function: The Role of Conformational Plasticity in Molecular Recognition". University of Florida, Gainesville, Florida, USA. February 3, 2020.

Invited Speaker. "The Hepatitis C Virus Protease Inhibitor Grazoprevir Synergizes with SARS-CoV2 Polymerase Inhibitor Remdesivir to Suppress Virus Replication". Western New York American Chemical Society. New York, USA (Zoom) November 11, 2020

Invited Speaker. "Assessment of prediction methods for protein structures determined by NMR in CASP14" International Critical Assessment of Protein Structure Prediction Meeting (Zoom). December 9, 2020.

Invited Speaker. “Proteins Flex to Function: The Role of Conformational Plasticity in Molecular Recognition”. Center for Quantitative Biology (formally Center for Theoretical Biology). Peking University, Beijing PEOPLES REPUBLIC OF CHINA (Zoom). December 14, 2020.

Invited Speaker. “Proteins Flex to Function: The Role of Conformational Plasticity in Molecular Recognition”. Wesleyan University, Middletown, Connecticut USA. March 27, 2021.

Invited Speaker. “Assessment of prediction methods for protein structures determined by NMR in CASP: Impact of AlphaFold2”. Gruppo Italiano Discussione Risonanze Magnetiche (GIRDM). University of Pisa, Pisa, ITALY (Zoom). September 8 – 10, 2021.

Chair and Co-organizer, Biophysical Society Celebration of 50 Yrs of Protein Data Bank. Web-based International Symposium. October 6, 2021.

Session Chair and Co-organizer. NJ American Chemical Society Annual Symposium. Web Based International Symposium. October 18, 2021.

Invited Speaker. “Enabling Drug Discovery by Structural Bioinformatics”. Rensselaer Polytechnic Institute – Center for Biotechnology and Interdisciplinary Studies, Troy, NY, USA. October 27, 2021.

Plenary Speaker. “AlphaFold Models of Small Proteins Rival the Accuracy of Experimental NMR Structures”. New York Structural Biology Laboratory and Columbia University, New York, NY. June 17, 2022.

Plenary Speaker. “Guiding NMR Data Analysis with AlphaFold Models”. CCPN NMR Software Workshop, Bath, United Kingdom. July 20, 2022.

Plenary Speaker. “Guiding analysis of experimental NMR data with AlphaFold models”. EMBO Workshop: When predictions meet experiments: The future of structure determination”. Palermo, ITALY, September 5 – 8, 2022.

Invited Speaker. “Non-Structural Protein 1 of Influenza B Binds 5’-Triphosphorylated dsRNA to Suppress RIG-I Activation and Enhance Viral Virulence”. Department of Pharmaceutical Chemistry, University of Bologna. Bologna, ITALY. September 15, 2022.

University Lecturer. “Proteins, Protein Design, and Their Impact on Humanity”. Institute of Advanced Studies of the Alma Mater Studiorum - University of Bologna. Bologna Italy, September 20, 2022

Invited Speaker. “Guiding analysis of experimental NMR data with AlphaFold models”. Department of Biochemistry, Weill Medical School of Cornell University, November 3, 2022.

Invited Speaker. “Multiple Conformational Modeling in CASP”. International Meeting of Critical Assessment of Protein Structure Prediction, Antalya, TURKEY, December 11, 2022.

Session Chair and Co-organizer. CASP Special Interest Group in Modeling of Conformational Ensembles”. International Meeting of Critical Assessment of Protein Structure Prediction, Antalya, TURKEY, December 11, 2022.

Invited Speaker. “SARS Corona Virus PLpro Protease Inhibitor Design”. Annual Meeting of Antiviral Drug Discovery (AViDD) Center for Pathogens of Pandemic Concern. Scripps Research Institute. La Jolla, CA. March 7, 2023

X. Honors and Awards

1981 – 1984	National Science Foundation Graduate Fellowship, National Science Foundation,
1981 – 1982	Sage Graduate Research Fellowship, Cornell University, Ithaca NY,
1987	Outstanding Chemistry Graduate Student, Cornell University, Ithaca NY,
1988 – 1989	Damon Runyon-Walter Winchell Cancer Research Fund Postdoctoral Fellowship
1989	Searle Scholar Award Searle Scholars Program,
1990	Johnson & Johnson Research Discovery Award, Johnson & Johnson, New Brunswick NJ,
1992, 1994	American Cyanamid Award in Physical and Analytical Chemistry, American Cyanamid Company, Wayne NJ,
1993 – 1998	National Science Foundation Young Investigator Award, National Science Foundation,
1994 – 1997	Proctor and Gamble Young Investigator Award, The Proctor & Gamble Fund
1995 – 1997	Camille and Henry Dreyfus Teacher-Scholar Award
1995	Rutgers University Board of Trustees Award for Research and Scholarly Excellence
1999	Michael and Kate Bárány Young Investigator Award of the Biophysical Society
2006	Elected Fellow, American Association for the Advancement of Science
2010	Appointed Jerome and Lorraine Aresty Endowed Chair by Rutgers Board of Trustees
2014	Rutgers Football Award for Academic Excellence
2019	Appointed Rensselaer Polytechnic Institute Constellation Chair in Structural Bioinformatics
2022	Elected Visiting Fellow, Institute for Advanced Study, University of Bologna, Bologna, Italy

XI. Sabbatical Leaves, Off-Campus Study Programs, Foreign Professional Travel

(Give dates and topics.)

1993	Visiting Scientist, Pharmacia, A.B., Stockholm, Sweden
1997	Visiting Professor, Department of Physical Chemistry, University of Valencia, SPAIN
2019	Visiting Professor, University of Florence, Florence ITALY

XII. Other Activities

(List other relevant activities such as consulting (include name of company and days per year), expert witness, or significant activities not included in previous categories.)

1990 – 1997	Consultant, Pharmacia, A.B., Stockholm, Sweden
1990 – 1999	Consultant, Chiron Corp., Emeryville, CA
1993	Visiting Scientist, Pharmacia, A.B., Stockholm, Sweden
1993 – 1999	Consultant, Wyeth-Ayerst Research Laboratories, Princeton, NJ
1995 – 2003	Consultant, Novartis Pharmaceutical Corp., East Hanover, NJ
1996 – 1999	Consultant, Eli Lilly and Co., Indianapolis, IN
2000 – 2002	Scientific Advisory Board and Consultant, GeneFormatics, San Diego, CA
2006 – 2008	Scientific Advisory Board and Consultant, Influmedics, Philadelphia, PA
2007 – present	Scientific Advisory Board and Founder, Nexomics Biosciences, NJ. 1 day / month

XIII. In addition to the above information, include if pertinent, concrete evidence of teaching ability and any unusual contributions to university affairs, such as curriculum advising or development, continuing education participation, etc.

None noted