

**REMO ROHS, Ph.D.**

Professor of Biological Sciences, Chemistry, Physics & Astronomy, and Computer Science  
Head, Program in Computational Biology and Bioinformatics  
Vice Chair, Department of Biological Sciences  
University of Southern California  
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**EDUCATION AND ACADEMIC DEGREES**

12/2009 Certification of Professional Achievement in Business, Columbia University, New York, NY, USA  
01/2003 Ph.D. in Biochemistry, Department of Biology, Chemistry and Pharmacy, Freie Universität Berlin, Germany  
09/1997 M.Sc. in Physics, Faculty of Natural Sciences, Humboldt Universität Berlin, Germany

**POSITIONS AND APPOINTMENTS**

08/2016-present Full Professor (with Tenure), Molecular and Computational Biology Program, Department of Biological Sciences, University of Southern California, Los Angeles, CA, USA  
01/2016-08/2016 Associate Professor (with Tenure), Molecular and Computational Biology Program, Department of Biological Sciences, University of Southern California, Los Angeles, CA, USA  
2013-present Courtesy appointment, Department of Computer Science, Viterbi School of Engineering, University of Southern California, Los Angeles, CA, USA  
2012-present Courtesy appointment, Department of Physics and Astronomy, University of Southern California, Los Angeles, CA, USA  
2011-present Member, Norris Comprehensive Cancer Center, Keck School of Medicine, University of Southern California, Los Angeles, CA, USA  
2011-present Courtesy appointment, Department of Chemistry, University of Southern California, Los Angeles, CA, USA  
08/2010-01/2016 Tenure-track appointment, Molecular and Computational Biology Program, Department of Biological Sciences, University of Southern California, Los Angeles, CA, USA  
2009-2010 Associate Research Scientist (Advisor: Barry Honig), Howard Hughes Medical Institute, Center for Computational Biology and Bioinformatics, Department of Biochemistry and Molecular Biophysics, Columbia University, New York, NY, USA  
2006-2008 Research Associate (Advisor: Barry Honig), Howard Hughes Medical Institute, Center for Computational Biology and Bioinformatics, Department of Biochemistry and Molecular Biophysics, Columbia University, New York, NY, USA  
2003-2005 Postdoctoral Fellow (Advisor: Zippora Shakked), Department of Structural Biology, Weizmann Institute of Science, Rehovot, Israel

**HONORS AND AWARDS****Personal Awards and Fellowships**

- 2016 USC Mentoring Award in the category Faculty Mentoring Graduate Students, University of Southern California, Los Angeles, CA, USA
- 2016 American Chemical Society OpenEye Outstanding Junior Faculty Award in Computational Chemistry presented at the ACS Spring 2016 National Meeting, San Diego, CA
- 2013 Alfred P. Sloan Research Fellowship, Alfred P. Sloan Foundation, New York, NY
- 2012 Certificate of Appreciation from LCUSD Governing Board for dedication to students of La Cañada High School and supporting the field of science
- 2011 Selected by GenomeWeb as Annual Young Investigator
- 2010 Keynote Address, 2<sup>nd</sup> India-Japan Symposium on Bioinformatics, Indian Institute of Technology, New Delhi, India
- 2005 Postdoctoral Fellowship, Kimmelman Center for Biomolecular Structure and Assembly, Weizmann Institute of Science, Rehovot, Israel
- 2003 Minerva Fellowship, Max Planck Society for the Advancement of Science, Munich, Germany
- 1998 Humboldt Prize for M.Sc. Thesis, Humboldt Universität, Berlin, Germany

**Paper Awards**

- 2016 Dror *et al.* Genome Res. paper received a RECOMB/ISCB Top-10 Paper Award for being one of the ten most influential publications in the fields of regulatory and systems genomics in 2015/16
- 2016 Zhou *et al.* PNAS paper was selected for a Highlight presentation at the RECOMB 2016 conference
- 2015 Zhou *et al.* PNAS paper received a RECOMB/ISCB Top-10 Paper Award for being one of the ten most influential publications in the fields of regulatory and systems genomics in 2014/15
- 2015 Abe *et al.* Cell paper received a RECOMB/ISCB Top-10 Paper Award for being one of the ten most influential publications in the fields of regulatory and systems genomics in 2014/15
- 2014 Yang *et al.* Nucleic Acids Res. paper received a RECOMB/ISCB Top-10 Paper Award for being one of the ten most influential publications in the fields of regulatory and systems genomics in 2013/14
- 2014 Barozzi *et al.* Mol. Cell paper received a RECOMB/ISCB Top-10 Paper Award for being one of the ten most influential publications in the fields of regulatory and systems genomics in 2013/14
- 2013 Yang *et al.* Nucleic Acids Res. paper was selected as NAR Breakthrough Article, a designation received by < 1% of articles published in NAR
- 2013 Gordân *et al.* Cell Rep. paper received a RECOMB/ISCB Top-10 Paper Award for being one of the ten most influential publications in the fields of regulatory and systems genomics in 2012/13
- 2013 Lazarovici *et al.* PNAS paper received a RECOMB/ISCB Top-10 Paper Award for being one of the ten most influential publications in the fields of regulatory and systems genomics in 2012/13
- 2012 Slattery *et al.* Cell paper received the RECOMB/ISCB Top-10 Paper Award for being one of the ten most influential publications in the fields of regulatory and systems genomics in 2011

**PROFESSIONAL ACTIVITIES****Member of Editorial and Professional Boards**

2014-present	Member, Editorial Board, Proteopedia, Israel Structural Proteomics Center, Weizmann Institute of Science, Rehovot, Israel
2012-2014	Member, Academic Advisory Board, zSpace Inc., Sunnyvale, CA
2011-2016	Faculty Member, Faculty of 1000 in Biology (Structural Biology, Section Structure: Transcription and Translation), London, UK
2011-present	Guest Editor, PLOS Computational Biology, Public Library of Science
2010-present	Associate Editor, BMC Bioinformatics, BioMed Central, London, UK
2010-present	Member, Editorial Board, Journal of Biomolecular Structure & Dynamics, Taylor & Francis, Albany, NY

**Meeting Organizer, Session Chair, Program and Poster Awards Committee Member**

2017	Program Committee Member, 25 <sup>th</sup> Annual International Conference on Intelligent Systems in Molecular Biology (ISMB)/16 <sup>th</sup> European Conference on Computational Biology (ECCB), Prague, Czech Republic
2015	Co-organizer of Workshop "Rules of protein-DNA recognition: computational and experimental advances", funded by Banff International Research Station for Mathematical Innovation and Discovery, Banff, Canada, and held at Casa Matemática Oaxaca, Mexico
2015	Invited session chair, Keystone Symposia on DNA Methylation and Epigenomics, Keystone, CO, USA
2014	Invited session chair, Symposium "Modeling the effects of water and solvation in biological systems: Developments and applications" at 248 <sup>th</sup> National Meeting, American Chemical Society, San Francisco, CA, USA
2013	Program Committee Member, 21 <sup>st</sup> Annual International Conference on Intelligent Systems in Molecular Biology (ISMB)/12 <sup>th</sup> European Conference on Computational Biology (ECCB), Berlin, Germany
2013	Invited session chair, 18 <sup>th</sup> Conversation on Biomolecular Structure & Dynamics, Albany, NY, USA
2011	Co-organizer of Professor Barry Honig's 70 <sup>th</sup> Birthday Symposium, Columbia University, New York, NY, USA
2009	Co-organizer of symposium "Computer Simulation of Biological Macromolecules", Berlin, Germany
2005	Co-organizer of symposium "New Horizons in Computational Biology", Weizmann Institute of Science, Rehovot, Israel
2000	Chair of organization committee, "Berlin Humboldt School on Structural Biology", Berlin, Germany

**Member of Review Panels, Reviewer of Grants and Manuscripts**

2015	Grant reviewer, Human Frontiers Science Program (HFSP), Strasbourg, France
2015	Grant reviewer, Canada First Research Excellence Fund, NSERC/SSHRC/CIHR granting agencies, Ottawa, Canada
2015	Grant reviewer, Division of Molecular and Cellular Bioscience, National Science Foundation, Arlington, USA
2014	Ad hoc member, NIH study section "Genome, Computational Biology and Technology (GCAT)", National Institutes of Health, Bethesda, USA
2014	Ad hoc reviewer, NSF CAREER awards, National Science Foundation, Arlington, USA
2014-present	Grant reviewer, Biotechnology and Biological Sciences Research Council (BBRC), London, UK

2014	Grant reviewer, Medical Research Council (MRC), London, UK
2014	Grant reviewer, Los Alamos National Laboratory, Los Alamos, NM, USA
2013-present	Member, Standing Committee of External Evaluators, Italian Institute of Technology (IIT), Genova, Italy
2012-2015	Member, HHMI Fellowship Review Panel, Howard Hughes Medical Institute, Chevy Chase, USA (reviewed >100 proposals in 4 years)
2012-present	Grant reviewer, Israel Science Foundation (ISF), Jerusalem, Israel
2011	Reviewer, Banff International Research Station (BIRS), Banff, Canada
2010	Grant reviewer, Wellcome Trust, London, UK
2004-present	Manuscript reviewer for Nature (multiple), Nat. Struct. Mol. Biol. (multiple), Nat. Commun. (multiple), Proc. Natl. Acad. Sci. USA (multiple), Genome Res. (multiple), Dev. Cell, Cell Systems (multiple), Gene, Epigenet. & Chromatin, PLOS Comput. Biol. (multiple), Nucleic Acids Res. (multiple), J. Mol. Biol. (multiple), Bioinformatics (multiple), Protein Sci., PLOS ONE (multiple), BMC Bioinformatics (multiple), FEBS Letters, J. Struct. Biol., Biophys. J. (multiple), Biochemistry (multiple), Biopolymers, Photochem. Photobiol., J. Chem. Theor. Comput., J. Biomol. Struct. Dyn. (multiple), and Curr. Opin. Struct. Biol. (multiple)

### UNIVERSITY SERVICE

2016-present	Vice Chair of Department of Biological Sciences, University of Southern California
2016-present	Head of Computational Biology and Bioinformatics, University of Southern California
2016-present	Member, Science and Engineering Subcommittee of University Committee on Curriculum, University of Southern California
2016-present	Co-chair, Executive Committee for Major in Quantitative Biology, University of Southern California
2016-present	Co-chair, Curriculum Committee, Department of Biological Sciences, University of Southern California
2016-2017	Member, Faculty Search Committee, Multi-scale and data-intensive computing for biology, University of Southern California
2016	Member, Data Science Advisory Board, Michelson Center for Convergent Biosciences, University of Southern California
2015	Member, Dean's advisory committee for department chair selection, Department of Biological Sciences, University of Southern California
2015	Member, Dean's self-study steering/"uber" committee, Department of Biological Sciences, University of Southern California
2015	Member, Self-study subcommittee "undergraduate programs", Department of Biological Sciences, University of Southern California
2015-present	Member, Advisory Board, Women in Science and Engineering (WiSE) Program, University of Southern California
2015-present	Member, Executive Committee for NIH training grant proposal in chemical biology, University of Southern California
2015-2016	Chair, High-performance Computing Committee, Computational Biology and Bioinformatics section, University of Southern California
2015-present	Member, Building Committee, Ray R. Irani Hall, Molecular and Computational Biology section University of Southern California
2014-present	Chair, Space Committee, Computational Biology and Bioinformatics section, University of Southern California
2014-present	Member, Retreat Committee, Molecular and Computational Biology section, University of Southern California
2011-present	Member, Screening Committee, Ph.D. Program in Computational Biology and Bioinformatics, University of Southern California

2011-2013	Organizer, Seminar Series in Computational Biology and Bioinformatics, University of Southern California
2010-2016	Member, Admissions Committee, Ph.D. Program in Computational Biology and Bioinformatics, University of Southern California

## TEACHING AND MENTORING

### Course and Curriculum Development

2016-2017	Developed new major (B.S.) in Quantitative Biology (QBIO), including a new course QBIO 105 Introduction in Quantitative Biology Seminar
2016	Developed new content for and restructured undergraduate course BISC 321 "Science, Technology, and Society"
2014	Co-developed course proposal for new general education course (with F. Sun and M. Waterman)
2012-present	Co-developed new undergraduate level course BISC 481 "Structural Bioinformatics from Atoms to Cells" (with F. Alber)
2011-2014	Initiated and taught "Bioinformatics Institute" at La Cañada High School, La Cañada Flintridge, CA

### Honors and Awards Received by Graduate Students for Work with Rohs

**Tianyin Zhou** (*graduated in 09/2014, was hired by Google as Software Engineer, and promoted to Senior Software Engineer in 10/2016*):

2014	Ph.D. Achievement Award in recognition of outstanding academic research, Graduate School, University of Southern California (Rohs as advisor received a Graduate School Mentoring Award)
2014	Harrison M. Kurtz Award given to the most outstanding Ph.D. student in the Biological Sciences, University of Southern California

**Iris Dror** (*joint with Technion, Israel; graduated in 09/2015; joined UCLA as Postdoc in 11/2015*):

2014	Women in Science Fellowship, Israeli Ministry of Science
2013	Paper of the Month Award (with Dror as first and Rohs as last author), Department of Biology, Technion – Israel Institute of Technology
2012	Irwin and Joan Jacobs Fellowship, Graduate School, Technion – Israel Institute of Technology

**Lin Yang** (*graduated in 06/2016 and was hired by Google as Software Engineer*):

2016	Ph.D. Achievement Award in recognition of outstanding academic research, Graduate School, University of Southern California (Rohs as advisor received a Graduate School Mentoring Award)
2015	Dan David Prize Scholarship in the "Future" category Bioinformatics, Dan David Foundation and Tel Aviv University, Tel Aviv, Israel
2015	Harrison M. Kurtz Award given to the most outstanding Ph.D. student in the Biological Sciences, University of Southern California

**Ana Carolina Dantas Machado** (*graduated in 08/2016*):

2016	Harrison M. Kurtz Award given to the most outstanding Ph.D. student in the Biological Sciences, University of Southern California
2015	William E. Trusten Award given to the most outstanding Ph.D. student in the Biological Sciences, University of Southern California
2014	WiSE Merit Fellowship given to Ph.D. students who demonstrate

exceptional work in their field, Women in Science and Engineering Program, University of Southern California

**Tsu-Pei Chiu:**

2017-2018 Manning Endowed Fellowship of the USC Graduate School  
 2016-2017 Research Enhancement Fellowship of the USC Graduate School  
 2016 William E. Trusten Award given to the most outstanding Ph.D. student in the Biological Sciences, University of Southern California

**Beibei Xin**

2017-2018 Research Enhancement Fellowship of the USC Graduate School

**TALKS AND SEMINARS**

**Invited talks at international conferences (08/2010-present; since joining USC)**

1. Symposium on Modeling Water & Solvation in Biochemistry: Developments & Applications, **252<sup>nd</sup> National Meeting, American Chemical Society**, Philadelphia, PA, USA, August 21-25, 2016. Integration of electrostatics and solvation into statistical machine learning approaches for the quantitative modeling of protein-DNA binding.
2. Workshop on Measuring and Modeling Quantitative Sequence-Function Relationships, Banbury Center, **Cold Spring Harbor Laboratory**, NY, USA, July 5-8, 2016. Quantitative modeling of TF-DNA binding: Beyond DNA shape towards biophysical features.
3. Workshop on Healthy Aging, **Japan Science and Technology Agency and Leibniz Association**, Tokyo, Japan, June 20-22, 2016. Transcriptional regulation in the aging genome.
4. Workshop on Regulatory Genomics and Epigenomics, **Simons Institute for the Theory of Computing, University of California at Berkeley**, Berkeley, CA, USA, March 7-10, 2016. Quantitative modeling of transcription factor binding specificities using DNA shape.
5. Workshop on Rules of Protein-DNA Recognition: Computational & Experimental Advances, **Casa Matemática Oaxaca and Banff International Research Station for Mathematical Innovation and Discovery**, Oaxaca, Mexico, June 21-25, 2015. Quantitative modeling of transcription factor binding specificities using DNA shape.
6. **19<sup>th</sup> Conversation on Biomolecular Structure & Dynamics**, Albany, NY, USA, June 9-13, 2015. Quantitative modeling of transcription factor binding specificities using DNA shape.
7. Symposium on Modeling the Effects of Water and Solvation in Biological Systems: Developments and Applications, **248<sup>th</sup> National Meeting, American Chemical Society**, San Francisco, CA, USA, August 10-14, 2014. High-throughput prediction of minor groove electrostatic potential in studies of protein-DNA recognition.
8. **Zing Conference on Protein Folding**, organized by Zing Conferences, Cambridge, UK; held in Punta Cana, Dominican Republic, July 16-19, 2014. Protein family-specific DNA readout mechanisms derived from genomic data using machine learning.
9. Workshop on Rules of Protein-DNA Recognition: Computational & Experimental Advances, **Banff International Research Station for Mathematical Innovation and Discovery**, Banff, Alberta, Canada, June 16-21, 2013. Genome analysis based on the integration of DNA sequence and shape.
10. **DNA @ 60, The 60<sup>th</sup> Anniversary of the Discovery of the DNA Double Helix**, Technion – Israel Institute of Technology, Haifa, Israel, May 26-29, 2013. The structure of the double helix in the genomic era.
11. **International Conference on Biomolecular Forms and Functions, A Celebration of 50 Years of the Ramachandran Map**, Indian Institute of Science, Bangalore, India, January 8-11, 2013. DNA shape in the genomic era.
12. **243<sup>rd</sup> National Meeting, American Chemical Society, Symposium in honor of Professor Andrew McCammon**, San Diego, CA, USA, March 25-28, 2012. Nuance in the double helix: The role of shape in sequence-specific protein-DNA recognition.

13. **Keystone Symposium, Nucleic Acid Therapeutics: From Base Pairs to Bedsides**, Santa Fe, NM, USA, January 10-15, 2012. High-throughput prediction of DNA shape on a genome-wide scale.
14. **Symposium in honor of Professor Barry Honig, Columbia University**, New York, NY, USA, December 15-16, 2011. Genome-wide analysis of DNA shape.
15. **17<sup>th</sup> Conversation on Biomolecular Structure & Dynamics**, Albany, NY, USA, June 14-18, 2011. High-throughput prediction of DNA shape on a genomic scale.
16. **Conference on Modeling Electrostatics in Molecular Biology**, Clemson, SC, USA, April 4-6, 2011. DelPhi in the genomic era: Mapping electrostatic potential as a function of DNA sequence.
17. **6<sup>th</sup> Congress of the Federation of the Israel Societies for Experimental Biology**, Eilat, Israel, February 7-11, 2011. Origins of specificity in protein-DNA recognition.
18. **1<sup>st</sup> Annual Southern California Systems Biology Conference**, Irvine, CA, USA, January 29-30, 2011. Origins of protein-DNA specificity revealed through an integrative approach of structural and systems biology.
19. **4<sup>th</sup> India-Japan Symposium on Cell Engineering and Bioinformatics, Indian Institute of Technology**, New Delhi, India, December 13-14, 2010. The role of DNA shape in protein-DNA recognition.
20. **2<sup>nd</sup> India-Japan Symposium on Bioinformatics, Indian Institute of Technology**, New Delhi, India, December 10-11, 2010. The role of DNA shape in protein-DNA recognition.

#### Contributed talks at international conferences (08/2010-present; since joining USC)

21. **Highlight Talk RECOMB 2016 Conference**, Santa Monica, CA, USA, April 17-21, 2016. Quantitative modeling of transcription factor binding specificities using DNA shape.
22. **Cold Spring Harbor Meeting on Systems Biology: Global Regulation of Gene Expression**, Cold Spring Harbor Laboratory, NY, USA, March 15-19, 2016. Deciphering layers of transcription factor-DNA binding on a protein family-specific basis.
23. **Epigenomics 2016 Meeting**, Rio Mar, Puerto Rico, USA, January 31-February 5, 2016. Deciphering layers of transcription factor-DNA binding on a protein family-specific basis.
24. **Keystone Symposia on DNA Methylation and Epigenomics**, Keystone, CO, USA, March 29-April 2, 2015. Modeling of the effect of DNA methylation on DNA shape and protein-DNA binding.
25. **Cold Spring Harbor Meeting on Systems Biology: Global Regulation of Gene Regulation**, held in Rio Mar, Puerto Rico, USA, January 28-February 1, 2015. Quantitative modeling of transcription factor binding specificities using DNA shape.
26. **4<sup>th</sup> Zing Nucleic Acids Conference**, organized by Zing Conferences, Cambridge, UK; held in Cancun, Mexico, December 5-9, 2014. Structural insights into protein-DNA recognition derived from sequencing data using machine learning.
27. **7<sup>th</sup> Annual RECOMB/ISCB Conference on Regulatory and Systems Genomics**, San Diego, CA, USA, November 9-14, 2014. Quantitative modeling of transcription factor binding specificities using DNA shape.
28. **Regulatory Genomics Special Interest Group, 22<sup>nd</sup> Annual International Conference on Intelligent Systems for Molecular Biology (ISMB)**, Boston, MA, USA, July 12, 2014. Quantitative modeling of transcription factor binding specificities using DNA shape.
29. **5<sup>th</sup> Annual RECOMB Conference on Regulatory and Systems Genomics**, San Francisco, CA, USA, November 12-15, 2012. Genome analysis based on the integration of DNA sequence and shape.
30. **Regulatory Genomics Special Interest Group, 20<sup>th</sup> Annual International Conference on Intelligent Systems for Molecular Biology (ISMB)**, Long Beach, CA, USA, July 14, 2012. Genome analysis based on the integration of DNA sequence and shape.
31. **3Dsig, Structural Bioinformatics and Computational Biophysics Satellite Meeting, ISMB**, Long Beach, CA, USA, July 13-14, 2012. Genome-wide analysis of DNA shape.

**Invited departmental seminars (08/2010-present; since joining USC)**

32. Department of Bioinformatics and Genomics, **University of North Carolina, Charlotte**, April 28, 2017. Integrating Genomics and Structural Biology Reveals Mechanisms of Gene Regulation.
33. Department of Chemistry, **University of Utah, Salt Lake City**, April 13, 2017. Integrating Genomics and Structural Biology Reveals Mechanisms of Gene Regulation.
34. Chemical and Structural Biology Division, College of Biological Sciences, **University of Minnesota Twin Cities, Minneapolis**, March 22, 2017. Integrating Genomics and Structural Biology Reveals Mechanisms of Gene Regulation.
35. Program in Quantitative and Computational Biology, **Lewis Sigler Institute for Integrative Genomics, Princeton University**, Princeton, NJ, March 9, 2017. Integrating Genomics and Structural Biology Reveals Mechanisms of Gene Regulation.
1. **Keynote Seminar**, Biozentrum, Faculty of Biology, **Ludwig Maximilians University, Munich**, Germany, December 16, 2016. Revealing mechanisms of gene regulation by integrating genomics and structural biology.
2. Institute Colloquium, **Leibniz Institute on Aging - Fritz Lipmann Institute**, Jena, Germany, July 21, 2016. Deconvolving the mechanisms of transcriptional regulation.
3. Institute of Systems Genetics, **New York University School of Medicine**, New York, NY, USA, June 9, 2016. Revealing mechanisms of gene regulation by integrating genomics and structural biology.
4. Scientific **Symposium "Computational Biology of Aging"**, **Leibniz Institute on Aging - Fritz Lipmann Institute**, Jena, Germany, March 23, 2016. Deconvolving the mechanisms of transcriptional regulation.
5. Bioinformatics and Computational Biology Research Center, **Cedars-Sinai Medical Center**, Los Angeles, CA, January 19, 2016. Quantitative modeling of transcription factor binding specificities using DNA shape.
6. Special Guest Lecture, Azrieli Institute for Systems Biology, **Weizmann Institute of Science**, Rehovot, Israel, May 20, 2015. Quantitative modeling of transcription factor binding specificities using DNA shape.
7. Lecture in Bioinformatics, **Tel Aviv University**, Ramat Aviv, Israel, May 19, 2015. Quantitative modeling of transcription factor binding specificities using DNA shape.
8. Systems Biology Seminar, Program in Bioinformatics, **Boston University**, Boston, MA, USA, April 9, 2015. Quantitative modeling of TF binding specificities using DNA shape.
9. Bioinformatics and Computational Biology Program, **Iowa State University**, Ames, IA, USA, March 25, 2015. Quantitative modeling of transcription factor binding specificities using DNA shape.
10. Dept. of Biochemistry, **New York University School of Medicine**, New York, NY, USA, March 5, 2015. Quantitative modeling of transcription factor binding specificities using DNA shape.
11. Joint Program in Computational Biology, Dept. of Computational and Systems Biology, University of Pittsburgh and Carnegie Mellon University, Pittsburgh, PA, USA, February, 27, 2015. Quantitative modeling of transcription factor binding specificities using DNA shape.
12. Dept. of Computational Molecular Biology **Max Planck Institute for Molecular Genetics**, Berlin, Germany, February 9, 2015. The role of DNA shape in transcription factor-DNA recognition and nucleosome formation.
13. Duke Center for Genomic and Computational Biology, **Duke University**, Durham, NC, USA, November 17, 2014. Quantitative modeling of transcription factor binding specificities using DNA shape.
14. Dept. of Systems Biology, **Columbia University Medical Center**, New York, NY, USA, June 9, 2014. Quantitative modeling of TF binding specificities using DNA shape.
15. Dept. of Systems Biology, **Harvard Medical School**, Boston, USA, May 22, 2014. Quantitative modeling of transcription factor binding specificities using DNA shape.
16. Center for Computational Molecular Biology, **Brown University**, Providence, RI, USA, May 20, 2014. Quantitative modeling of TF binding specificities using DNA shape.



17. Dept. of Biochemistry, **University of Wisconsin – Madison**, WI, USA, May 5, 2014. Quantitative modeling of transcription factor binding specificities using DNA shape.
18. **Fred Hutchinson Cancer Research Institute**, Seattle, WA, USA, April 24, 2014. Quantitative modeling of transcription factor binding specificities using DNA shape.
19. Dept. of Genome Sciences, **University of Washington**, Seattle, WA, USA, April 23, 2014. Quantitative modeling of transcription factor binding specificities using DNA shape.
20. Center for Nonlinear Studies, **Los Alamos National Laboratory**, Los Alamos, NM, USA, April 7, 2014. Quantitative modeling of TF binding specificities using DNA shape.
21. Dept. of Genetics, **Washington University**, St. Louis, MO, USA, March 20, 2014. Quantitative modeling of transcription factor binding specificities using DNA shape.
22. Bioinformatics Program, **University of California, Los Angeles (UCLA)**, CA, USA, January 23, 2012. High-throughput prediction of DNA shape on a genome-wide scale.
23. Cell, Molecular, and Developmental Biology Program, **University of California, Riverside**, CA, USA, November 16, 2011. DNA shape is a source of protein-DNA specificity.
24. Center for Theoretical Biological Physics, **University of California, San Diego (UCSD)**, CA, USA, October 7, 2011. DNA shape is a source of protein-DNA specificity.
25. Department of Biochemistry and Molecular Biology, **Tel Aviv University**, Tel Aviv, Israel, February 20, 2011. The role of DNA shape in protein-DNA recognition.
26. Faculty of Biology, **Technion – Israel Institute of Technology**, Haifa, Israel, February 16, 2011. The role of DNA shape in protein-DNA recognition.
27. Dept. of Structural Biology, **Weizmann Institute of Science**, Rehovot, Israel, February 15, 2011. The role of DNA shape in protein-DNA recognition.
28. Dept. of Microbiology and Molecular Genetics, **Hebrew University of Jerusalem**, Jerusalem, Israel, February 14, 2011. The role of DNA shape in protein-DNA recognition.
29. **Sanford-Burnham Medical Research Institute**, San Diego, CA, USA, January 10, 2011. Shape readout mediates specificity in protein-nucleic acid interactions.
30. Dept. of Computational Molecular Biology **Max Planck Institute for Molecular Genetics**, Berlin, Germany, December 7, 2010. The role of DNA shape in transcription factor-DNA recognition and nucleosome formation.
31. **Accelrys, Inc.**, San Diego, CA, USA, November 14, 2010. The role of DNA shape in protein-DNA recognition.

#### Invited USC seminars (08/2010-present; since joining USC)

32. **Keck School of Medicine Seminar**, University of Southern California, Los Angeles, CA, November 21, 2016. Integrating Genomics and Structural Biology Reveals Mechanisms of Gene Regulation.
33. **Bridge@USC Science Faculty Luncheon**, University of Southern California, Los Angeles, CA, November 16, 2016. Transcriptional regulation in the aging genome.
34. **Bridge@USC and Michelson Center for Convergent Biosciences Retreat**, Catalina Island, CA, February 5-7, 2016. Building a bridge between structural biology and Genomics.
35. **The Bridge Institute**, University of Southern California, Los Angeles, CA, February 25, 2015. Building a bridge between structural biology and genomics.
36. **Department of Biological Sciences Intersection Seminar**, University of Southern California, Los Angeles, CA, September 18, 2014. Genome-wide studies of DNA structure, function and evolution.
37. **Symposium “30 Years of Computational Biology at USC”**, University of Southern California, Los Angeles, CA, March 29 - April 1, 2012. Genome-wide analysis of DNA shape.
38. **Department of Physics and Astronomy**, University of Southern California, Los Angeles, CA, February 24, 2012. Physical principles are the basis for molecular mechanisms in biology.
39. **Department of Chemistry**, University of Southern California, Los Angeles, CA, October 6, 2011. DNA shape is a source for protein-DNA specificity.
40. **Bioinformatics Workshop, USC Keck School of Medicine**, University of Southern California, Los Angeles, CA, August 31, 2011. Adding dimensions to linear sequence information.

## PUBLICATIONS

## Peer-reviewed journal articles (08/2010-present; since joining USC)

1. N.S. Tangprasertchai, R. Di Felice\*, X. Zhang, I.M. Slaymaker, C. Vazquez Reyes, W. Jiang, **R. Rohs**, and P.Z. Qin. CRISPR-Cas9 mediated DNA unwinding detected using site-directed spin labeling. **ACS Chem. Biol.** In press (2017).  
*\*Di Felice was a research faculty member associated with the Rohs lab.*
2. J.M. Sagendorf\*, H.M. Berman, and **R. Rohs**. DNAProDB: an interactive tool for structural analysis of DNA-protein complexes. **Nucleic Acids Res.** In press (2017).  
*\*Sagendorf is Rohs' PhD student. Rohs was a corresponding author.*
3. L. Yang\*<sup>#</sup>, Y. Orenstein<sup>#</sup>, A. Jolma, Y. Yin, J. Taipale, R. Shamir, and **R. Rohs**. Transcription factor family-specific DNA shape readout revealed by quantitative specificity models. **Mol. Syst. Biol.** 13, 910 (2017).  
*\*Yang was Rohs' PhD student. \*Yang and Orenstein contributed equally. Rohs was a corresponding author.*
4. S. Schwörer, F. Becker, C. Feller, A.H. Baig, U. Köber, H. Henze, J.M. Kraus, B. Xin\*, A. Lechel, D.B. Lipka, C.S. Varghese, M. Schmidt, **R. Rohs**, R. Aebersold, K.L. Medina, H. A. Kestler, F. Neri, J. von Maltzahn, S. Tümpel, and K.L. Rudolph. Epigenetic stress responses induce muscle stem-cell ageing by Hoxa9 developmental signals. **Nature** 540, 428-432 (2016).  
*\*Xin is Rohs' PhD student.*  
*Commentary:* S. Eliazer and A.S. Brack. Cause and consequence in aged-muscle decline. **Nature** 540, 349-350 (2016).
5. S. Schöne, M. Jurk, M.B. Helabad, I. Dror\*, I. Lebars, B. Kieffer, P. Imhof, **R. Rohs**, M. Vingron, M. Thomas-Chollier, and S.H. Meijnsing. Sequences flanking the core-binding site modulate glucocorticoid receptor structure and activity. **Nat. Commun.** 7, 12621 (2016).  
*\*Dror was Rohs' PhD student.*
6. A. Mathelier, B. Xin\*, T.P. Chiu\*, L. Yang\*, **R. Rohs**, and W.W. Wasserman. DNA shape features improve transcription factor binding site predictions *in vivo*. **Cell Syst.** 3, 278-286 (2016).  
*\*Xin and Chiu are and Yang was Rohs' PhD student. Rohs was a corresponding author.*  
*This paper was selected as Highlight presentation at the ECCB Conference 2016.*  
*Commentary:* G.D. Stormo and B. Roy. DNA structure helps predict protein binding. **Cell Syst.** 3, 216-218 (2016).
7. G. Kuzu, E.G. Kaye, J. Chery, T. Siggers, L. Yang\*, J. Dobson, S. Boor, J. Bliss, W. Liu, G. Jogl, **R. Rohs**, N.D. Singh, M.L. Bulyk, M.Y. Tolstorukov, and E. Larschan. Expansion of GA dinucleotide repeats increases the density of CLAMP binding sites on the X-chromosome to promote *Drosophila* dosage compensation. **PLOS Genet.** 12, e1006120 (2016).  
*\*Yang was Rohs' PhD student.*
8. I. Dror\*, **R. Rohs**, and Y. Mandel-Gutfreund. How motif environment affects transcription factor search dynamics: finding a needle in a haystack. **BioEssays** 38, 605-612 (2016).  
*\*Dror was Rohs' PhD student.*
9. T.P. Chiu\*<sup>#</sup>, F. Comoglio<sup>#</sup>, T. Zhou\*, L. Yang\*, R. Paro, and **R. Rohs**. DNashapeR: an R/Bioconductor package for DNA shape prediction and feature encoding. **Bioinformatics** 32, 1211-1213 (2016).  
*\*Chiu is and Zhou and Yang were Rohs' PhD students. #Chiu and Comoglio contributed equally. Rohs was the corresponding author.*
10. G.E. Zentner, S. Kasinathan, B. Xin\*, **R. Rohs**, and S. Henikoff. ChEC-seq kinetics discriminates transcription factor binding sites by DNA sequence and shape. **Nat. Commun.** 6, 8733 (2015).  
*\*Xin is Rohs' PhD student.*

11. I. Dror\*, T. Golan, C. Levy, **R. Rohs**, and Y. Mandel-Gutfreund. A widespread role of the motif environment in transcription factor binding across diverse protein families. **Genome Res.** 25, 1268-1280 (2015).  
*\*Dror was Rohs' PhD student. Rohs was a corresponding author.*  
*This paper was selected as **Highlight** presentation at the ECCB Conference 2016.*
12. Z. Deng, Q. Wang, Z. Liu, M. Zhang, A.C. Dantas Machado\*, T.P. Chiu\*, C. Feng, Q. Zhang, L. Yu, L. Qi, J. Zheng, X. Wang, X.M. Huo, X. Qi, X. Li, W. Wu, **R. Rohs**, Y. Li, and Z. Chen. Mechanistic insights into metal ion activation and operator recognition by the ferric uptake regulator. **Nat. Commun.** 6, 7642 (2015).  
*\*Dantas Machado was and Chiu is Rohs' PhD student. Rohs was a corresponding author.*
13. F. Comoglio, T. Schlumpf, V. Schmid, **R. Rohs**, C. Beisel, and R. Paro. High-resolution profiling of *Drosophila* replication start sites reveals a DNA shape and chromatin signature of metazoan origins. **Cell Rep.** 11, 821-834 (2015).
14. N. Abe, I. Dror\*, L. Yang\*, M. Slattery, T. Zhou\*, H.J. Bussemaker, **R. Rohs**, and R.S. Mann. Deconvolving the recognition of DNA sequence from shape. **Cell** 161, 307-318 (2015).  
*\*Dror, Yang, and Zhou were Rohs' PhD students. Rohs was a corresponding author.*  
*This article received a **RECOMB/ISCB Top-Paper Award** for being one of the **most influential papers** in 2014/15 in the fields of Regulatory & Systems Genomics, and was highlighted by a **commentary in Nat. Rev. Genet.** and USC news release.*  
*Commentary:* Burgass D.J. DNA elements: Shaping up transcription factor binding. **Nat. Rev. Genet.** 16, 258-259 (2015).
15. M. Levo, E. Zalckvar, E. Sharon, A.C. Dantas Machado\*, Y. Kalma, M. Lotan-Pompan, A. Weinberger, Z. Yakhini, **R. Rohs**, E. Segal. Unraveling determinants of transcription factor binding outside the core-binding site. **Genome Res.** 25, 1018-1029 (2015).  
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*Research Highlight:* Faial, T. Fine-tuning of transcription factor binding. **Nat. Genet.** 47, 429 (2015).
16. T. Zhou\*<sup>#</sup>, N. Shen<sup>#</sup>, L. Yang\*, N. Abe, J. Horton, R.S. Mann, H.J. Bussemaker, R. Gordân, and **R. Rohs**. Quantitative modeling of transcription factor binding specificities using DNA shape. **Proc. Natl. Acad. Sci. USA** 112, 4654-4659 (2015).  
*\*Zhou and Yang were Rohs' PhD students. <sup>#</sup>Zhou and Shen contributed equally. Rohs was a corresponding author.*  
*This article received a **RECOMB/ISCB Top-Paper Award** for being one of the **most influential papers** in 2014/15 in the fields of Regulatory & Systems Genomics, and was highlighted by a **commentary in PNAS**, a USC news release, and the **Faculty of 1000**.*  
*This paper was selected as **Highlight** presentation at the RECOMB Conference 2016.*  
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*\*Yang was Rohs' PhD student.*
18. T.P. Chiu\*<sup>#</sup>, L. Yang\*<sup>#</sup>, T. Zhou\*, B.J. Main, S.C.J. Parker, S.V. Nuzhdin, T.D. Tullius, and **R. Rohs**. GBshape: a genome browser database for DNA shape annotations. **Nucleic Acids Res.** 43, D103-D109 (2015).  
*\*Chiu is and Yang and Zhou were Rohs' Ph.D. students. <sup>#</sup>Chiu and Yang contributed equally. Rohs was the corresponding author.*
19. A.C. Dantas Machado\*<sup>#</sup>, T. Zhou\*<sup>#</sup>, S. Rao\*<sup>#</sup>, P. Goel\*<sup>#</sup>, C. Rastogi<sup>#</sup>, A. Lazarovici, H.J. Bussemaker, and **R. Rohs**. Evolving insights on how cytosine methylation affects protein-DNA binding. **Brief. Funct. Genomics** 14, 61-73 (2015).

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*\*Zhou, Yang, and Dantas Machado were Rohs' Ph.D. student, and #contributed equally. Rohs was a corresponding author.  
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*\*Yang was Rohs' PhD student.  
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23. L. Yang\*, T. Zhou\*, I. Dror\*, A. Mathelier, W.W. Wasserman, R. Gordân, and **R. Rohs**. TFBSshape: a motif database for DNA shape features of transcription factor binding sites. **Nucleic Acids Res.** 42, D148-D155 (2014).  
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*This paper was **highlighted on journal cover** of NAR throughout 2014.*
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*\*Zhou and Dantas Machado were Rohs' Ph.D. students, and Lu was Rohs' postdoc.*

*<sup>#</sup>These authors contributed equally. Rohs was a corresponding author.*

*This publication received a **RECOMB/ISCB Top-10 Paper Award** for being one of the ten **most influential papers** in 2012/13 in the fields of Regulatory & Systems Genomics.*

*This paper was selected as **Highlight** presentation at the ISMB Conference 2014.*

30. R. Gordân, N. Shen<sup>#</sup>, I. Dror\*<sup>#</sup>, T. Zhou\*<sup>#</sup>, J. Horton, **R. Rohs**, and M.L. Bulyk. Genomic regions flanking E-box binding sites influence DNA binding specificity of bHLH transcription factors through DNA shape. **Cell Rep.** 3, 1093-1104 (2013).

*\*Dror and Zhou were Rohs' Ph.D. students. <sup>#</sup>These authors and Shen contributed equally. Rohs was a corresponding author.*

*This publication received a **RECOMB/ISCB Top-10 Paper Award** for being one of the ten **most influential papers** in 2012/13 in the fields of Regulatory & Systems Genomics.*

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*\*Dantas Machado was Rohs' Ph.D. student.*

33. M. Slattery, T. Riley, P. Liu, N. Abe, P. Gomez-Alcala, I. Dror\*, T. Zhou\*, **R. Rohs**, **B. Honig**, **H.J. Bussemaker**, and **R.S. Mann**. Cofactor binding evokes latent differences in DNA binding specificity between Hox proteins. **Cell** 147, 1270-1282 (2011).

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*Commentary: H. Stower. Gene Regulation: Resolving transcription factor binding. **Nat. Rev. Genet.** 13, 71 (2012).*

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34. E.P. Bishop<sup>#</sup>, **R. Rohs**<sup>#</sup>, S.C.J. Parker<sup>#</sup>, S.M. West, P. Liu, R.S. Mann, B. Honig, and **T.D. Tullius**. A map of minor groove shape and electrostatic potential from hydroxyl radical cleavage patterns of DNA. **ACS Chem. Biol.** 6, 1314-1320 (2011).

*<sup>#</sup>Rohs contributed equally as a co-first author.*

*This article was **highlighted on the cover** of the journal's December 2011 issue.*

#### **Peer-reviewed journal articles (until 08/2010; before joining USC)**

35. **R. Rohs**<sup>#</sup>, X. Jin<sup>#</sup>, S.M. West, R. Joshi, B. Honig, and R.S. Mann. Origins of specificity in protein-DNA recognition. **Ann. Rev. Biochem.** 79, 233-269 (2010).

*<sup>#</sup>Rohs was the first author and contributed equally to Jin.*

*This article was highlighted by the Faculty of 1000.*

36. M. Kitayner<sup>#</sup>, H. Rozenberg<sup>#</sup>, **R. Rohs<sup>#</sup>**, O. Suad, D. Rabinovich, B. Honig, and Z. Shakked. Diversity in DNA recognition by p53 revealed by crystal structures with Hoogsteen base pairs. **Nat. Struct. Mol. Biol.** 17, 423-429 (2010).  
*#Rohs contributed equally as a co-first author.*  
*This publication was highlighted by a News & Views article in **Nat. Struct. Mol. Biol.***  
*Commentary:* S. Chitayat and C.H. Arrowsmith. Four p(53)s in a Pod. **Nat. Struct. Mol. Biol.** 17, 390 (2010).
37. S.M. West, **R. Rohs**, R.S. Mann, and B. Honig. Electrostatic interactions between arginines and the minor groove in the nucleosome. **J. Biomol. Struct. Dyn.** 27, 861-866 (2010).  
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38. **R. Rohs<sup>#</sup>**, S.M. West<sup>#</sup>, A. Sosinsky, P. Liu, R.S. Mann, and B. Honig. The role of DNA shape in protein-DNA recognition. **Nature** 461, 1248-1253 (2009).  
*#Rohs was the first author and contributed equally to West.*  
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*Commentary:* T.D. Tullius. Structural Biology: DNA binding shapes up. **Nature** 461, 1225-1226 (2009).
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*#Rohs contributed equally as a co-second author.*  
*This publication was highlighted by a News & Views article in **Nat. Struct. Mol. Biol.***  
*Commentary:* S.C. Harrison. Three-dimensional intricacies in protein-DNA recognition and transcriptional control. **Nat. Struct. Mol. Biol.** 14, 1118-1119 (2007).
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42. **R. Rohs**, I. Bloch, H. Sklenar, and Z. Shakked. Molecular flexibility in ab initio drug docking to DNA: binding-site and binding-mode transitions in all-atom Monte Carlo simulations. **Nucleic Acids Res.** 33, 7048-7057 (2005).  
*\*Rohs was the corresponding author.*
43. **R. Rohs**, H. Sklenar, Z. Shakked. Structural and energetic origins of sequence-specific DNA bending: Monte Carlo simulations of papillomavirus E2 protein-DNA binding sites. **Structure** 13, 1499-1509 (2005).  
*\*Rohs was the corresponding author.*  
*Commentary:* T. Siggers, T. Silkov, and B. Honig. Bending in the right direction. **Structure** 13, 1400 (2005).
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*\*Rohs was the corresponding author.*
45. **R. Rohs** and H. Sklenar. Methylene blue binding to DNA with alternating GC base sequence: continuum treatment of salt effects. **Indian J. Biochem. Biophys.** 38, 1-6 (2001).
46. **R. Rohs**, H. Sklenar, R. Lavery, and B. Röder. Methylene blue binding to DNA with alternating GC base sequence: a modeling study. **J. Am. Chem. Soc.** 122, 2860-2866 (2000).

47. **R. Rohs**, C. Etchebest, and **R. Lavery**. Unraveling proteins: a molecular mechanics study. **Biophys. J.** 76, 2760-2768 (1999).

#### Invited News & Views articles (08/2010-present; since joining USC)

48. **R. Rohs**, A.C. Dantas Machado\*, and L. Yang\*. Exposing the secrets of sex determination. **Nat. Struct. Mol. Biol.** 22, 437-438 (2015).  
*\*Dantas Machado and Yang were Rohs' Ph.D. students. Rohs was the corresponding author.*
49. **B. Honig** and **R. Rohs**. Biophysics: flipping Watson and Crick. **Nature** 470, 472-473 (2011).  
*Rohs was a corresponding author.*

#### Peer-reviewed book chapters (08/2010-present; since joining USC)

50. N.S. Tangprasertchai, X. Zhang, Y. Ding, K. Tham, **R. Rohs**, I.S. Haworth, and **P.Z. Qin**. Integrated Spin-Labeling/Computational-Modeling Approaches for Mapping Global Structures of Nucleic Acids. **Methods Enzymol.** 564, 427-453 (2015).
51. R. Harris<sup>#</sup>, T. Mackoy<sup>#</sup>, A.C. Dantas Machado\*<sup>#</sup>, D. Xu, **R. Rohs**, and **M.O. Fenley**. Opposites attract: Shape and electrostatic complementarity in protein-DNA complexes. Chapter 3, vol. 2 in T. Schlick, editor. **Innovations in Biomolecular Modeling and Simulation**. 53-80 (2012). Biomolecular Sciences series, Royal Society of Chemistry, RCS Publishing, London, UK.  
*\*Dantas Machado was Rohs' Ph.D. student and <sup>#</sup>contributed equally as co-first author. Rohs was a corresponding author.*

#### Educational peer-reviewed publication (08/2010-present; since joining USC)

52. A.C. Dantas Machado\*, S.B. Saleebyan\*<sup>#</sup>, B.T. Holmes\*<sup>#</sup>, M. Karelina\*<sup>#</sup>, J. Tam\*<sup>#</sup>, S.Y. Kim\*<sup>#</sup>, K.H. Kim\*<sup>#</sup>, I. Dror\*, E. Hodis, E. Martz, P.A. Compeau, and **R. Rohs**. Proteopedia: 3D visualization and annotation of transcription factor-DNA readout modes. **Biochem. Mol. Biol. Educ.** 40, 400-401 (2012).  
*\*Dantas Machado and Dror were Rohs' Ph.D. students. <sup>#</sup>High-school students mentored by Rohs contributed equally. Rohs was the corresponding author.*

## GRANTS AND RESEARCH SUPPORT

### Current research support

Role: PI

Project/Proposal Title: Genome analysis based on the integration of DNA sequence and shape

Source of Support: NIH/NIGMS (R01)

Total Award Period Covered: 02/01/2014 – 01/31/2018

Role: PI

Project/Proposal Title: Alfred P. Sloan Research Fellowship

Source of Support: Alfred P. Sloan Foundation

Total Award Period Covered: 09/15/2013 – 09/14/2017

Role: PI (multi-PI with Nuzhdin, DePace, and Marjoram)

Project/Proposal Title: Multi-scale modeling of genetic variation in a developmental network

Source of Support: NIH/NIGMS (U01)

Total Award Period Covered: 09/30/2013 – 06/30/2017

Role: co-I (PI XJ Chen)

Project/Proposal Title: Structural Basis of APOBEC Functions and Interactions with HIV-Vif

Source of Support: NIH/NIGMS (R01)

Total Award Period Covered: 09/15/2016 – 06/30/2020

Role: co-I (PI Bussemaker)

Project/Proposal Title: Inferring gene regulatory circuitry from functional genomics data

Source of Support: NIH/NHGRI (R01)

Total Award Period Covered: 07/15/2013 – 06/30/2017

Role: PI

Project/Proposal Title: Collaborative Research: Experimental and computational studies of DNA binding by human paralogous transcription factors

Source of Support: NSF/MCB

Total Award Period Covered: 09/15/2014 – 08/31/2017

Role: PI (multi-PI with Fraser and Roberts)

Project/Proposal Title: Bridging gene regulation from molecules to organisms

Source of Support: Bridge@USC Institute

Total Award Period Covered: 07/01/2016 – 06/30/2017

Gift for research activities, zSpace, Inc., Sunnyvale, CA

Gift for research activities, NVIDIA Corp., Santa Clara, CA

#### **Previous Research Support** (*since joining USC*)

Role: PI

Project/Proposal Title: Deciphering molecular mechanisms of p53-DNA recognition

Source of Support: American Cancer Society

Total Award Period Covered: 07/01/2012 – 06/30/2013

Role: PI

Project/Proposal Title: Molecular dynamics simulations of p53-DNA complexes

Source of Support: National Research Council (NRC) and D.E. Shaw Research

Total Award Period Covered: 11/01/2012 – 07/31/2013

#### **Meeting Support for International Workshop**

Role: Co-applicant (with Bussemaker)

Project/Proposal Title: Workshop “Rules of protein-DNA recognition: computational and experimental advances” at Oaxaca/Mexico in June 2015

Source of Support: Banff International Research Station for Mathematical Innovation and Discovery, Canada

#### **Other Research Support**

Gift for USC-Technion Visiting Fellows Program