
BIOGRAPHICAL SKETCH

NAME Bonnie Berger	POSITION TITLE Simons Professor of Mathematics and Electrical Engineering & Computer Science Massachusetts Institute of Technology
eRA COMMONS USER NAME BABERGER	

INSTITUTION and LOCATION	DEGREE	YEAR(s)	FIELD of STUDY
Brandeis University, Waltham, MA	AB	1983	Computer Science
Massachusetts Institute of Technology	SM	1986	Computer Science
Massachusetts Institute of Technology	Ph.D.	1990	Computer Science
Massachusetts Institute of Technology	Postdoc	1990-1992	Applied Mathematics

Advances in modern biology revolve around automated data collection and sharing of the large resulting datasets. I am considered a pioneer in bringing algorithms to the study of biological data, and a founder in this community that I have witnessed grow so profoundly over the last 30 years. I have made major contributions to many areas of computational biology and biomedicine, largely, though not exclusively through mathematical innovations, as demonstrated by over 30,000 citations and an H-index of 79 (H5-index of 61) for my scientific papers and widely used software. I have trained more than 100 undergrad, MEng, PhD students and postdoctoral fellows, many of whom now hold top positions, including tenured Professors: Serafim Batzoglou–Stanford University tenured; Philip Bradley– Fred Hutchinson/U. Washington; Manolis Kellis– MIT; Lior Pachter– UC Berkeley/Caltech; Mona Singh– Princeton University; and Russell Schwartz– CMU. My PhDs with Assistant Professorships include Michael Baym– Harvard; Leonid Chindelevitch– Imperial College London; Hyunghoon Cho– Yale.; Brian Hie– Stanford; Rohit Singh–Duke; Y. William Yu– U Toronto/CMU; and Ellen Zhong– Princeton. In recognition of my success, I was recently the 2019 recipient of the International Society for Computational Biology (ISCB) annual Senior Scientist Award, the pinnacle award in computational biology; and in 2020, received the AWM-SIAM Sonia Kovalevsky Lecture Award and was elected to the National Academy of Sciences

I continually and actively engage in community service and advocating diversity, through my roles as Vice President of ISCB, Head of the RECOMB Steering Committee, and member of the NIH NIGMS and NLM Advisory Councils. I have served as both Proceedings and Conference Chairs for the two top conferences in my field— RECOMB and ISMB. I have headed a workshop at ISMB 2016 on Gender Equality, and been instrumental in including women and diversity as ISCB Fellows and Awards Chair. I have served as an Executive Editor for Journal of Computational Biology, Associate Editor for Bioinformatics, and on editorial boards of PNAS, Annual Reviews for Biomedical Data Science, IEEE/ACM TCBB, Genome Biology, and Cell Systems. I have given keynote addresses and distinguished lectures at SIAM Annual Meeting, RECOMB, ISMB/ECCB, ACM-BCB, RECOMB-RSG; RECOMB-BE, Norway’s Volterra Lecture, Gordon Research Conference, HCA, CSHL, NIH Pi Day, Israeli Bioinformatics Symposium, GenoPri, AMS-MAA Joint Meetings and UCSD’s Rosenblatt Lecture.

A. Positions and Honors

Positions and Employment

1990-1992	NSF Mathematical Sciences Postdoctoral Research Fellowship.
1992-1993	Radcliffe Bunting Institute, Science Scholar.
1992-	Member of Computer Science & Artificial Intelligence Laboratory (CSAIL), MIT.
1992-	Member, Theory of Computation Group, CSAIL, MIT
1992-	Head, Computation and Biology Group, CSAIL, MIT
1992-1997	Assistant Professor of Applied Mathematics, MIT.
1997-1999	Associate Professor of Applied Mathematics, MIT.
1999-2002	Associate Professor of Applied Mathematics, tenured, MIT.

2002- Professor of Applied Mathematics, MIT.
 2004-2012 Affiliated Faculty, Harvard-MIT Health Sciences and Technology (HST).
 2004- Affiliated Faculty, Computational and Systems Biology (CSBi) at MIT.
 2008- Beth Israel Deaconess Board of Overseers and Medical Advisory Committee.
 2010-2020 Joint Appointment, Dept. of Electrical Engineering and Computer Science, MIT.
 2010- Associate Member, Broad Institute of MIT and Harvard.
 2012- Affiliated Faculty, Harvard Medical School.
 2014- Faculty Member, Harvard-MIT Health Science and Technology.
 2015- Member, Center for Microbiome Informatics and Therapeutics.
 2016- Simons Professor of Mathematics, MIT.
 2018-2019 Interim Head of Applied Mathematics, MIT.

Selected Awards and Honors

1990 Ph.D. thesis won MIT George M. Sprowls Prize for best research in computer science.
 1995-1998 NSF Career Award.
 1999 Biophysical Society's Dayhoff Award for research (1 award per year).
 1999 Technology Review's Inaugural TR100 Award for 100 top young innovators for the 21st century.
 2004 Elected as a Fellow of the Association for Computing Machinery (ACM).
 2010 RECOMB Test of Time Award for "Protein folding in the HP model is NP-complete."
 2012 NIH Margaret Pittman Award for Outstanding Scientific Achievement & Lectureship.
 2012 Elected as a Fellow of the International Society for Computational Biology (ISCB).
 2013 Elected to the American Academy of Arts and Sciences.
 2013 Brandeis University Alumni Achievement Award.
 2015 École Polytechnique Fédérale de Lausanne (EPFL) Honorary Doctorate.
 2016 Elected to the American Institute for Medical and Biological Engineering (AIMBE).
 2019 RECOMB Test of Time Award for Isorank algorithm.
 2019 Elected as a Fellow of the American Mathematical Society (AMS).
 2019 ISCB Accomplishments by a Senior Scientist Award (1 per year since 2003).
 2020 AWM-SIAM Sonia Kovalevsky Lecture Award.
 2020 Elected to the National Academy of Sciences (NAS).
 2022 Elected as a Fellow of the Society for Industrial and Applied Mathematics (SIAM)

Other Experience and Professional Service

1995 Organizer for DIMACS Workshop: Sequence-based methods for protein folding.
 1996-2003 BOD for Program in Mathematics and Molecular Biology (PMMB).
 1998 NSF selection panel for the Protein Data Bank (PDB).
 2001- Creator and organizer of MIT Math/CSAIL Bioinformatics Seminar.
 2002- HST Graduate; Bioinformatics & Integrative Genomics; and Curriculum Committees.
 2003-2006 ACM Nominating Committee.
 2003-2014 NIH Scientific Review Group: Comparative modelling, BCMB & BDMA, ad-hoc member.
 2004-2014 Brandeis University Science Advisory Council.
 2006-2015 NIH NCBI Board of Scientific Counselors, 4 time ad-hoc member.
 2008-2014 Beth Israel Deaconess Board of Overseers and Medical Advisory Committee.
 2009-2014 NIH NIGMS Advisory Council, 3 time ad-hoc member.
 2010 RECOMB 2010 Program Chair.
 2010-2016 ISMB Proceedings Chair (2012), Conference Chair (2013) & Steering Committee (2012-13);
 Area Chair (2010, 2012-16).
 2011-2017 Sloan Fellowship Selection Committee, Computational & Evolutionary Molecular Biology.
 2014 Senior Member of ISCB.
 2015-2018 FASEB Excellence in Science Award Committee.
 2015-2018 RECOMB Steering Committee Chair, and member since 2009.
 2015-2016 NIH NIGMS Advisory Council.

2015-2021	ISCB Vice President
2013-2022	ISCB Member of Board of Directors, Awards Chair, and Fellows Chair.
2014	ISMB 2016 Gender Equality Workshop Leader.
2016	Cold Spring Harbor Lab's Biological Data Sciences Program Organizer (with 2 others).
2018-2021	Barcelona Supercomputing Center Science Advisory Board.
2018-2020	NIH-NIGMS BDMA Panel.
2019	USC Biology Evaluation Committee.
2019-2022	AAAS Member-at-Large (Mathematics).
2022-2025	NIH NCBI Advisory Council.
2023-	National Academies Board on Mathematical Sciences and Analytics.
2024	RECOMB 2024 Co-Chair of Organizing Committee.

B. Publications (* for corresponding/senior author or † for my student is 1st author)

B1. Selected Annotated Publications

1. B. Berger and J. Rompel. "[Simulating \$\(\log^c n\)\$ -Wise Independence in NC.](#)" *J. of the Association for Computing Machinery* (1991) **38** no. 4:1026-1046. 129 citations.
 - Seminal and ground-breaking paper on removing randomness from parallel algorithms, demonstrating that we can efficiently solve important graph-theoretic problems that are shown to require only poly-logarithmic, rather than full or pairwise, independence of the random variables. 137 citations.
2. B. Berger, P.W. Shor, L. Tucker-Kellogg and J. King *. "[A Local Rule Based Theory of Virus Shell Assembly.](#)" *Proc Nat Acad Sci USA* (1994) **91** no.16:7732-7736. 213 citations.
 - Show that the self-assembly and mis-assembly of viral shells—though seemingly a complex procedure—can be explained purely by local rules that specify the assembly of the desired structure by limiting the combinatorial space of all possible arrangements; over 200 citations to this work.
3. B. Berger, D. B. Wilson, E. Wolf, T. Tonchev, M. Milla and P. S. Kim *. "[Predicting Coiled Coils by Use of Pairwise Residue Correlations.](#)" *Proc Nat Acad Sci USA* (1995) **92** no. 18:8259-8263. 759 citations.
 - First paper to use pairwise correlations for protein structure prediction, and in particular to predict coiled coils; over 1K citations including sequel paper on Paircoil2.
4. E. Wolf †, P. S. Kim * and B. Berger *. "[MultiCoil: A Program for Predicting Two- and Three-Stranded Coiled Coils.](#)" *Protein Science* (1997) **6** no. 6:1179-1189. 851 citations.
First paper to accurately predict oligomerization state of coiled coils using pairwise residue correlations and clustering in higher dimensional space; Markov random field based Multicoil2 (*PLoS ONE* (2011)).
5. B. Berger * and T. Leighton. "[Protein Folding in the Hydrophobic-Hydrophilic \(HP\) Model Is NP-Complete.](#)" *J. of Computational Biology* (1998) **5** no. 1:27-40. 632 citations.
 - Show that the most widely-studied theoretical formulation of protein folding—folding in the hydrophobic-polar lattice model—is NP-complete; many previous papers only were able to show complexity results for limited versions of the problem and not succeeding for the widely-studied case. Received Test of Time Award at RECOMB 2010.
6. S. Batzoglou †, L. Pachter †, J. Mesirov, B. Berger * and E. Lander *. "[Human and Mouse Gene Structure: Comparative Analysis and Application to Exon Prediction.](#)" *Genome Research* **10** no. 7 (2000):950-958. 509 citations.
 - Ground-breaking work on comparative genomics of entire genomes and to predict genes;
7. S. Batzoglou †, D. Jaffe, K. Stanley, J. Butler, S. Gnerre, E. Mauceli, B. Berger †, J. Mesirov and E. Lander. "[ARACHNE: A Whole-Genome Shotgun Assembler.](#)" *Genome Research* (2002) **12** no.1:177-189. 718 citations.
 - Seminal program for whole genome shotgun assembly; used extensively by the Lander group for shotgun sequencing of the human genome.
8. M. Kellis †, N. Patterson, B. Birren, B. Berger * and E. Lander *. "[Methods in Comparative Genomics: Genome Correspondence, Gene Identification, and Motif Discovery.](#)" *J. of Computational Biology* (2004) **11**, nos. 2-3:319-355. 129 citations. (Computational underpinnings of [Nature 2004](#) article).

- Ground breaking work on comparative genomics of entire closely-related genomes, and to identify genes and regulatory motifs.
9. R. Singh †, J. Xu, and B. Berger *. “[Global Alignment of Multiple Protein Interaction Networks with Application to Functional Ortholog Detection.](#)” *Proc Nat Acad Sci USA* (2008) **105** no. 35: 12763-68. 1000 citations with RECOMB 2007 proceedings version. Received 2019 RECOMB Test of Time Award. (Computational underpinnings of [NAR Database Issue 2011](#) article.)
 - Introduced global network alignment and pioneered the use of spectral methods to solve it through Isorank. Led to IsoBase, a database of functionally-related proteins across PPI, as well as genetic interaction, networks, simultaneously incorporating both sequence and network data. Over 1.5K combined citations (with RECOMB and IsoBase database). Many others have since applied our techniques. Received Test of Time Award at RECOMB 2019.
 10. M. Menke, B. Berger * and L. Cowen *, “[Matt: Flexibility Aids Protein Multiple Structure Alignment.](#)” *PLoS Computational Biology* (2008) **4** no.1. Also in *ISMB 2008 Highlights* track. 235 citations.
 - Perform multiple protein structure alignment by innovatively allowing the structures to freely move while they are being aligned and then pastes them back together according to steric constraints; the Matt program has been termed the “most accurate” of its kind by an independent review (Berkalk et al., *Protein Science*, 2009).
 11. P-R. Loh, M. Baym, B. Berger *. “[Compressive Genomics.](#)” *Nature Biotechnology* **30** (2012): 627-630. Most downloaded *Nat Biotech*, July 2012. 139 citations.
 - Introduce compressive genomics, an approach that relies on compressing data in such a way that the desired computation (such as BLAST search) can be performed in the compressed representation. 104 citations.
 12. Y. W. Yu, N. M. Daniels, D. C. Danko and B. Berger *. “[Entropy-Scaling Search of Massive Biological Data.](#)” *Cell Systems* (2015) **1** no. 2:130–140. 57 citations.
 - Develops a compressive algorithmic framework for efficiently searching massive datasets having certain structural properties (i.e. low metric entropy and fractal dimension) common in biology and applies the general framework to chemogenomic, metagenomic, and protein structure data sets.
 13. H. Cho †, D. J. Wu and B. Berger *. “[Secure Genome-Wide Association Analysis Using Multiparty Computation.](#)” *Nature Biotechnology* (2018) **36**: 547-551. Highlighted in [Science](#) (June 8, 2018). 177 citations.
 - Introduce secure crowdsourcing of millions of genomes at scale to perform full GWAS with population stratification correction.
 14. B. Hie †, H. Cho † and B. Berger *. “[Realizing Private and Practical Pharmacological Collaboration.](#)” *Science* (2018) **362** no. 6412: 347-350. Highlighted in *Science*. 51 citations.
 - Invent computational protocol for securely crowdsourcing pharmacological data *at scale*; first demonstration of secure neural networks on large-scale real-world data.
 15. B. Hie †, B. Bryson and B. Berger * “[Efficient Integration of Heterogeneous Single-Cell Transcriptomes using Scanorama.](#)” *Nature Biotechnology* **37** (2019): 685-691. 451 citations.
 - Capitalizing on ideas from panoramas, devised the first method to integrate multiple single-cell data sets across studies and technologies.
 16. B. Hie, E. Zhong, B. Berger * and B. Bryson *. “[Learning the Language of Viral Evolution and Escape](#)” *Science* (2021) **371** no. 6526: 284-288. 163 citations.
 - Leveraging neural language models first brought to protein biology (Berger & Bepler, ICLR 2019), we devised a model that uses grammaticality and semantics to predict viral escape.

B2. Other Computational Biology Publications

17. B. Berger. “[Algorithms for Protein Structural Motif Recognition.](#)” *J. of Computational Biology* (1995) **2** no. 1: 125-138. 40 citations.
18. B. Berger and M. Singh. “[An Iterative Method for Improved Protein Structural Motif Recognition.](#)” *J. of Computational Biology* (1997) **4** no. 3:261-273. 48 citations.
19. S. Batzoglou, B. Berger *, D. J. Kleitman, E. S. Lander and L. Pachter. “[Recent Developments in Computational Gene Recognition.](#)” *Documenta Mathematica: Journal der Deutschen Mathematiker-Vereinigung* Extra Volume **ICM I** (1998):649-658. Berger’s invited address. 10 citations.

20. M. Singh †, B. Berger, P. S. Kim, J. M. Berger and A. G. Cochran *. "[Computational Learning Reveals Coiled Coil-Like Motifs in Histidine Kinase Linker Domains.](#)" *Proc Nat Acad Sci USA* (1998) **95** no. 6:2738-2743. 99 citations.
21. B. Berger * and P. W. Shor. "[On the Structure of the Scaffolding Core of Bacteriophage T4 and its Role in Head-Length Determination.](#)" *J. of Structural Biology* (1998) **121** no. 3:285-294. 9 citations.
22. R. Schwartz, P. W. Shor, P. E. Prevelige Jr. and B. Berger *. "[Local Rules Simulation of the Kinetics of Virus Capsid Self-Assembly.](#)" *Biophysical J.* (1998) **75** no.1:2626-2636. 178 citations.
23. M. Singh †, B. Berger * and P. S. Kim *. "[LearnCoil-VMF: Computational Evidence for Coiled-Coil-Like Motifs in Many Viral Membrane Fusion Proteins.](#)" *J. of Molecular Biology* (1999) **290** no. 5:1031-41. 201 citations.
24. B. Berger *, G. W. Hoest, J. Paulson and P. W. Shor. "[On the Structure of the Scaffolding Core of Bacteriophage T4.](#)" *J. of Computational Biology* (1999) **6** no. 1:1-12. 9 citations.
25. L. Pachter, S. Batzoglou, V. Spitzkovsky, E. Banks, E. S. Lander, D. J. Kleitman and B. Berger *. "[A Dictionary Based Approach for Gene Annotation.](#)" *J. of Computational Biology* (1999) **6** no. 3:419-430. 27 citations.
26. S. Batzoglou, B. Berger, J. Mesirov and E. S. Lander *. "[Sequencing a Genome by Walking with Clone-End Sequences: A Mathematical Analysis.](#)" *Genome Research* (1999) **9** no. 12:1163-1174. 37 citations.
27. B. Berger *, J. Kleinberg and T. Leighton. "[Reconstructing a Three-Dimensional Model with Arbitrary Errors.](#)" *J. of the Association for Computing Machinery* (1999) **46** no. 2:212-235. 68 citations.
28. B. Berger *, J. King, R. Schwartz and P. W. Shor. "[Local Rule Mechanism for Selecting Icosahedral Shell Geometry.](#)" *Discrete Applied Mathematics* (2000) **105**(1-3):55-69. 22 citations.
29. R. Schwartz, R. L. Garcea, and B. Berger *. "[Local Rules' Theory Applied to Polyomavirus Polymorphic Capsid Assemblies.](#)" *Virology* (2000) **268** no. 2: 461-470. 50 citations.
30. P. Bradley †, L. Cowen *, M. Menke, J. King * and B. Berger *. "[BETAWRAP: Successful Prediction of \$\beta\$ -Helices from Primary Sequence Reveals an Association with Many Microbial Pathogens.](#)" *Proc Nat Acad Sci USA* (2001) **98** no. 26:14819-14824. 135 citations.
31. L. Cowen, P. Bradley, M. Menke, J. King and B. Berger *. "[Predicting the Beta-Helix Fold from Protein Sequence Data.](#)" *J. of Computational Biology* (2002) **9** no. 2:261-276. 50 citations.
32. P. Bradley, P. S. Kim and B. Berger *. "[Trilogy: Discovery of Sequence-Structure Patterns Across Diverse Proteins.](#)" *Proc Nat Acad Sci USA* (2002) **99** no. 13:8500-8505. 62 citations.
33. A. Coventry, D. J. Kleitman and B. Berger *. "[MSARi: Multiple Sequence Alignments for Statistical Detection of RNA Secondary Structure.](#)" *Proc Nat Acad Sci USA* (2004) **101** no. 33:12102-12107. 114 citations.
34. R. Singh †, N. Palmer, D. Gifford, B. Berger † and Z. Bar-Joseph *. "[Active Learning for Sampling in Time-Series Experiments: with Applications to Gene Expression Analysis.](#)" *Proc 22nd Ann Int'l Conf on Machine Learning* (ICML 2005): 832-839. 24 citations.
35. M. Menke, J. King, B. Berger * and L. Cowen *. "[Wrap-and-Pack: A New Paradigm for Beta Structural Motif Recognition with Application to Recognizing Beta Trefoils.](#)" *J. of Computational Biology* (2005) **12** no. 6:777-795. 17 citations.
36. J. Xu and B. Berger *. "[A Tree Decomposition Approach to Protein Structure Prediction.](#)" *Proc IEEE Computer and Systems Biology* (2005): 247-256. 66 citations.
37. R. Schwartz, P.W. Shor and B. Berger*. "[Local Rule Simulations of Capsid Assembly.](#)" *J. of Theoretical Medicine* (2005) **6** no. 2:81-85. 7 citations.
38. P. Uetz, Y. Dong †, C. Zeretzke, C. Atzler, A. Baiker, B. Berger †, S. Rajagopala, M. Roupelieva, D. Rose, E. Fossum and J. Haas *. "[Herpesviral Protein Networks and their Interaction with the Human Proteome.](#)" *Science* (2006) **311** no.5758:239-242; published online 8 December 2005 (in *Science Express Reports*). 471 citations.
39. R. Singh and B. Berger *. "[ChainTweak: Sampling from the Neighborhood of A Protein Conformation.](#)" *Proc.9th Pacific Symposium on Biocomputing* (2005):52-63. 15 citations.
40. A. V. McDonnell, T. Jiang, A. E. Keating * and B. Berger *. "[Paircoil2: Improved Prediction of Coiled Coils from Sequence.](#)" *Bioinformatics* (2006) **22** no. 3:356-358. 451 citations.
41. M. Junker, C. Schuster, A. V. McDonnell, K. Sorg, M. Finn, B. Berger and P. Clark *. "[Pertactin Beta-Helix Folding Mechanism Suggests Common Themes for the Secretion and Folding of Autotransporter Proteins.](#)" *Proc Nat Acad Sci USA* (2006) **103** no.13:4918-4923. 217 citations.

42. A. McDonnell, M. Menke, N. Palmer, J. King, L. Cowen * and B. Berger *. "[Fold Recognition and Accurate Sequence-Structure Alignment of Sequences Directing Beta-Sheet Proteins.](#)" *Proteins: Structure, Function, and Bioinformatics* (2006) **63**:976-985. 31 citations.
43. J. Waldispühl, B. Berger *, P. Clote * and J. M. Steyaert. "[Predicting Transmembrane \$\beta\$ -barrels and Interstrand Residue Interactions from Sequence.](#)" *Proteins: Structure, Function and Bioinformatics* (2006) **65** no. 1:61-74. 47 citations.
44. J. Waldispühl, B. Berger *, P. Clote * and J. M. Steyaert. "[TransFold: A Web Server for Predicting the Structure and Residue Contacts of Transmembrane \$\beta\$ -barrels.](#)" *Nucleic Acids Research* (2006) (Web Server Issue) **34**:W189-W193. 33 citations.
45. J. Xu and B. Berger *. "[Fast and Accurate Algorithms for Protein Side-Chain Packing.](#)" *J. of the Association for Computing Machinery* (2006) **53** no. 4:1-25. 97 citations.
46. R. Singh, J. Xu and B. Berger *. "[Struct2Net: Integrating Structure into Protein-Protein Interaction Prediction.](#)" *Proc 11th Pacific Symposium on Biocomputing* (2006) **10**:403-414. 78 citations.
47. J. Xu *, F. Jiao and B. Berger *. "[A Parameterized Algorithm for Protein Structure Alignment.](#)" *J. of Computational Biology* (2007) **14** no. 5:564-577. (Also appeared in RECOMB 2006). 65 citations.
48. S. C. Wieland, J.S. Brownstein, B. Berger * and K.D. Mandl *. "[Density-equalizing Euclidean Minimum Spanning Trees for the Detection of All Disease Cluster Shapes.](#)" *Proc of the Nat Acad Sci USA* (2007) **104**:9404-9409. 47 citations.
49. S. C. Wieland, J. S. Brownstein, B. Berger * and K. D. Mandl *. "[Automated Real Time Constant-Specificity Surveillance for Disease Outbreaks](#)" *BMC Medical Informatics and Decision Making* (2007) **7**:15. 27 citations.
50. B. Sterner, R. Singh, and B. Berger *. "[Predicting and Annotating Catalytic Residues: An Information Theoretic Approach](#)". *J. of Computational Biology* (2007) **14** no. 8:1058-1073. 26 citations.
51. R. Singh and B. Berger *. "[Influence Flow: Integrating Pathway-specific RNAi data and Protein Interaction Data.](#)" *Int'l Conference on Intelligent Systems for Molecular Biology* (2007) *PLoS Track*. 2 citations.
52. J. Waldispühl, C. W. O'Donnell, S. Devadas, P. Clote and B. Berger *. "[Modeling Ensembles of Transmembrane Beta-barrel Proteins.](#)" *Proteins: Structure, Function, and Bioinformatics* (2007) **71** no. 3:1097-1112. 35 citations.
53. D. Sontag, R. Singh, and B. Berger *. "[Probabilistic Modeling of Systematic Errors in Two-Hybrid Experiments.](#)" *Proc 12th Pacific Symposium on Biocomputing* (2007) **12**:445-457. 14 citations.
54. R. Singh, J. Xu and B. Berger * "[Pairwise global alignment of protein interaction networks by matching neighborhood topology.](#)" *Proc. of the 11th Annual International Conference on Research in Computational Molecular Biology, Lecture Notes in Computer Science* (2007) **4453**:16-31. 369 citations.
55. V. Pulim, J. Bienkowska *, and B. Berger *. "[LTHREADER: Prediction of Extracellular Ligand-Receptor Interactions Using Localized Threading.](#)" *Protein Science* (2008) **17**:1-14. 16 citations.
56. R. Singh, J. Xu and B. Berger *. "[Global Alignment of Multiple Protein Interaction Networks with Application to Functional Ortholog Detection.](#)" *Proc Nat Acad Sci USA* (2008) **105** no. 35:12763-68. 594 citations.
57. V. Pulim, B. Berger * and J. Bienkowska *. "[Optimal Contact Map Alignment of Protein-Protein Interfaces.](#)" *Bioinformatics* (2008) **24** no. 20:2324-2328. 26 citations.
58. M. Baym, C. Bakal, N. Perrimon and B. Berger *. "[High-resolution Modeling of Cellular Signaling Networks.](#)" *Proc 12th Ann Int'l Conf on Research in Molecular Biology* (2008) *LNCS* **4955**:257-271. 6 citations.
59. M. Menke, B. Berger * and L. Cowen *, "[Matt: Flexibility Aids Protein Multiple Structure Alignment.](#)" *PLoS Computational Biology* (2008) **4** no. 1 (2008). Also in *ISMB 2008 Highlights* track. 248 citations.
60. S.C. Wieland, C. Cassa, K. Mandl * and B. Berger *. "[Revealing the Spatial Distribution of a Disease While Preserving Privacy.](#)" *Proc Nat Acad Sci USA* (2008) **105** no. 46:17608-17613. 68 citations.
61. J. Waldispühl, S. Devadas, B. Berger † and P. Clote *. "[Efficient Algorithms for Probing the RNA Mutation Landscape.](#)" *PLoS Computational Biology* (2008) **4** no. 8:e1000124. 55 citations.
62. M. Schnall-Levin, L. Chindelevitch and B. Berger *. "[Inverting the Viterbi Algorithm: An Abstract Framework for Structure Design.](#)" *Proc 25th International Conference on Machine Learning (ICML 2008)*:904-911. 34 citations.
63. E. Wu, N. Palmer, Z. Tian, A. P. Moseman, M. Galdzicki, X. Wang, B. Berger, H. Zhang and I. S. Kohane. "[Comprehensive Dissection of PDGF-PDGFR Signaling Pathways in PDGFR Genetically Defined Cells.](#)" *PLoS One* (2008) **3** no. 11 e3794. 118 citations.

64. Z. Tian, N. Palmer, P. Schmid, H. Yao, M. Galdzicki, B. Berger*, E. Wu*, and I. S. Kohane. "[A Practical Platform for Blood Biomarker Study by Using Global Gene Expression Profiling of Peripheral Whole Blood.](#)" *PLoS One* (2009) **4** no. 4:e5157. 35 citations.
65. A. Bryan Jr., M. Menke, L. J. Cowen, S. L. Lindquist*, and B. Berger*. "[BETASCAN: Probable \$\beta\$ -amyloids Identified by Pairwise Probabilistic Analysis.](#)" *PLoS Computational Biology* (2009) **5** no. 3. 110 citations.
66. D. S. Lun, G. Rockwell, N. J. Guido, M. Baym, J. Kelner, B. Berger, K. Galagan and G. Church*. "[Large-Scale Identification of Genetic Design Strategies using Local Search.](#)" *Nature Molecular Systems Biology* (2009) **5** no. 296. 189 citations.
67. J. Waldispühl, S. Devadas, B. Berger* and P. Clote*. "[RNAmutants: A Web Server to Explore the Mutational Landscape of RNA Secondary Structures.](#)" *Nucleic Acids Research* (2009) **37** no. 46:W281-W286. 15 citations.
68. I. Kaplow †, R. Singh †, A. Friedman, C. Bakal, N. Perrimon*, B. Berger*. "[RNAiCut: Automated Detection of Significant Genes from Functional Genomic Screens](#)" *Nature Methods* (2009) **6** no. 7:476-477. 31 citations.
69. J. Waldispühl, C. W. O'Donnell, S. Will, S. Devadas, R. Backofen and B. Berger*. "[Simultaneous Alignment and Folding of Protein Sequences.](#)" *Proc 13th Ann Int'l Conf on Research in Molecular Biology* (2009) **LNCS 5541**:339-355. 4 citations.
70. C.S. Liao, K. Lu, M. Baym, R. Singh, and B. Berger*. "[IsoRankN: Spectral Methods for Global Alignment of Multiple Protein Networks.](#)" *Bioinformatics* (2009) **25** no. 12:i253 - i258. 432 citations.
71. The ModEncode Consortium, "[Identification of Functional Elements and Regulatory Circuits by Drosophila modENCODE.](#)" *Science* (2010) **330** 6012:1787-1797. 930 citations.
72. P. R. Loh, G. Tucker, M. Yu and B. Berger*. "[Phenotype Prediction Using Regularized Regression on Genetic Data in the DREAM5 Systems Genetics B Challenge.](#)" Winner DREAM5 Challenge 3B Competition. Presented at RECOMB 2010 Systems Biology Satellite Conference. 13 citations.
73. R. Hosur, R. Singh and B. Berger*. "[Sparse Estimation for Structural Variability.](#)" *Algorithms in Bioinformatics Lecture Notes in Computer Science* (2010) **6293**:13-27. 3 citations.
74. R. Singh, D. Park, J. Xu, R. Hosur and B. Berger*. "[Struct2Net: A Web Service to Predict Protein-Protein Interactions Using a Structure-based Approach.](#)" *Nucleic Acids Research* (2010) **38** suppl 2:w508-w515. 117 citations.
75. R. Hosur, J. Xu, J. Bienkowska* and B. Berger*. "[iWRAP: An Interface Threading Approach with Applications to Prediction of Cancer Related Protein-Protein Interactions.](#)" *Journal of Molecular Biology* (2010) **405** no. 5:1295-310. 60 citations.
76. O. Nir, C. Bakal, N. Perrimon and B. Berger*. "[Inference of RhoGAP/GTPase Regulation Using Single-cell Morphological Data from a Combinatorial RNAiScreen.](#)" *Genome Research* (2010) **20**:372-80. 31 citations.
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171. E. Zhong, T. Bepler, J. Davis *, B. Berger *. "[Reconstructing Continuously Heterogeneous Structures from Single Particle cryo-EM with Deep Generative Models.](#)" *Proc. of Intern'l Conf on Learning Representations (ICLR)* (2019). Oral Spotlight Presentation.
172. J. Brasch *, K. M. Goodman *, A. J. Noble, M. Rapp, S. Mannepalli, F. Bahna, V. P. Dandey, T. Bepler, B. Berger, T. Maniatis, C.S. Potter, B. Carragher, B. Honig and L. Shapiro. "[Visualization of Clustered Protocadherin Neuronal Self-Recognition Complexes.](#)" *Nature* (2019) **569**:280–283. 73 citations.
173. B. Hie, B. Bryson and B. Berger * "[Efficient Integration of Heterogeneous Single-Cell Transcriptions using Scanorama.](#)" *Nature Biotechnology* (2019) **37**:685-691. 285 citations.
174. B. Hie, H. Cho, B. DeMeo, B. Bryson and B. Berger *. "[Geometric Sketching Compactly Summarizes the Single-Cell Transcriptomic Landscape.](#)" *Cell Systems* (2019) **8** no. 6:483-493.e7. (June, 2019; cover art) Featured Report from RECOMB 2019. 75 citations.
175. H. Cho, B. DeMeo, J. Peng, and B. Berger *. "[Large-Margin Classification in Hyperbolic Space.](#)" *AISTATS Proceedings* (2019). 34 citations.
176. A. Narayan, H. Cho and B. Berger *, "[Density-Preserving Visualization of Single Cells.](#)" *Nature Biotechnology* (2021). Also accepted for oral presentation at ISMB/ECCB (2019). 69 citations.
177. T. Bepler and B. Berger *. "[Learning Protein Sequence Embeddings using Information from Structure.](#)" *Proc. of ICLR* (2019). 257 citations.
178. B. DeMeo and B. Berger *. "[An Unsupervised Learning Approach for Sketching Single-Cell Data.](#)" *International Conference on Machine Learning* 2019. Oral presentation.
179. L. Hutchison, B. Berger * and Z. Kohane *. "[Meta-analysis of Caenorhabditis elegans single-cell developmental data reveals multi-frequency oscillation in gene activation.](#)" *Bioinformatics* (2020) **36** no. 13:4047–4057 (preprint first posted online Mar. 5, 2017).
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181. A. Shajii †, I. Numanagic †, R. Baghdadi, S. Amarasingh * and B. Berger *. "[Seq: A High-Performance Language for Bioinformatics.](#)" *Proc. OOPSLA 2019*. ISMB/ECCB 2019 poster. 18 citations.
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183. DeMeo and B. Berger *. "Hopper: A Mathematically Optimal Algorithm for Sketching Biological Data." *Bioinformatics* (2020) **36** Supplement:i236-i241. Also ISMB 2020.
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185. B. Hie †, J. Peters, S. Nyquist, A. Shalek, B. Berger †, and B. Bryson *. “[Computational Methods for Single-Cell RNA Sequencing](#)”. *Annual Reviews of Biomedical Data Science*. **3**:339-364. 74 citations.
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187. H. Cho † *, S. Simmons †, R. Kim † and B. Berger *. “[Privacy-Preserving Biomedical Database Queries with Optimal Privacy-Utility Trade-offs](#).” *Cell Systems* (2020) **10** no. 5:408-416.e9.
188. C. G. K. Ziegler †, S. J. Allon †, S. K. Nyquist †, I. M. Mbanjo †, V. N. Miao, C. N. Tzouanas, Y. Cao, A. S. Yousif, J. Bals, B. M. Hauser, J. Feldman, C. Muus, M. H. Wadsworth II, S. W. Kazer, T. K. Hughes, B. Doran, G. J. Gatter, M. Vukovic, F. Taliaferro, B. E. Mead, Z. Guo, J. P. Wang, D. Gras, M. Plaisant, M. Ansari, J. M. S. Sucre, C. J. Taylor, B. Lin, A. Waghray, V. Mitsialis, D. F. Dwyer, K. M. Buchheit, J. A. Boyce, N. A. Barrett, T. M. Laidlaw, S. L. Carroll, L. Colonna, V. Tkachev, C. W. Peterson, A. Yu, H. B. Zheng, H. P. Gideon, C. G. Wenchell, P. L. Lin, C. D. Bingle, S. B. Snapper, J. A. Kropski, F. J. Theis, H. B. Schiller, L-E., Zaragosi, P. Barbry, B. Berger †, A. Leslie, H-P. Kiem, J. L. Flynn, S. M. Fortune, R. W. Finberg, L. S. Kean, M. Garber, A. Schmidt, D. Lingwood, A. K. Shalek, J. Ordovas-Montanes. “[SARS-CoV-2 receptor ACE2 is an interferon-stimulated gene in human airway epithelial cells and is detected in specific cell subsets across tissues](#).” HCA Lung Biological Network. *Cell* (2020) **181** no. 5:1016-1035.e19. 2094 citations.
189. M. Gui, M. Ma, E. Sze-Tu, X. Wan, F. Koh, E. D. Zhong, B. Berger, J. H. Davis. S. K. Dutcher, R. Zhang and A. Brown. “[Structures of Radical Spokes and Associated Complexes Important for Ciliary Motility](#)”. *Nature Structural & Molecular Biology* (2020) **28**:29-30. 53 citations.
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192. E. Berger, D. Yorukoglu, L. Zhang, S. Nyquist, A. Shalek, M. Kellis, I. Numanagić, and B. Berger *. “[Improved Haplotype Inference by Exploiting Long-range Linking and Allelic Imbalance in RNA-seq Datasets](#).” *Nature Communications* (2020) **11**:4662. 18 citations.
193. B. Hie †, B. Bryson *, B. Berger *. “[Leveraging Uncertainty in Machine Learning Accelerates Biological Discovery and Design](#)”. *Cell Systems* (2020) Published October 15, 2020. 93 citations.
194. B. Berger *, M. S. Waterman and Y. William Yu *. “[Levenshtein Distance, Sequence Comparison and Biological Database Search](#).” *IEEE Transactions on Information Theory* (2021) **67** no. 6:3287-3294. 47 citations.
195. A. Narayan †, B. Berger * and H. Cho *. “[Assessing Single-cell Transcriptomic Variability through Density-preserving Data Visualization](#).” *Nature Biotechnology* (2021) **39**:765–774. 58 citations.
196. E. Zhong, T. Bepler, B. Berger * and J. Davis *. “[CryoDRGN: Reconstruction of Heterogeneous cryo-EM Structures Using Neural Networks](#).” *Nature Methods* (2021) **18**:176-185. 268 citations.
197. M. A. Sherman, R. E. Rodin, G. Genovese, C. Dias, A. R. Barton, R. E. Mukamel, B. Berger, P. J. Park, C. A. Walsh, and P-R Loh. “[Large Mosaic Copy Number Variations Confer Autism Risk](#)”. *Nature Neuroscience* (2021) **2**:197-203. Epub Jan 11. 31 citations.
198. B. Hie, E. Zhong, B. Berger * and B. Bryson *. “[Learning the Language of Viral Evolution and Escape](#)” *Science* (2021) **371** no. 6526:284-288. 163 citations.
199. R. Singh, B. Hie, A. Narayan, and B. Berger *, “[Schema: metric learning enables interpretable synthesis of heterogeneous single-cell modalities](#).” *Genome Biology* (2021) **22** no. 131. 24 citations
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202. S. Sledzieski, R. Singh, L. Cowen * and B. Berger *. “[D-SCRIPT translates genome to phenome with sequence-based, structure-aware, genome-scale predictions of protein-protein interactions](#).” *Cell Systems* (2021) **12** no. 6:969-982.e6. 47 citations.

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204. T. Bepler and B. Berger. [“Learning the Protein Language: Evolution, Structure and Function.”](#) *Cell Systems* (2021) **12** no. 6, 654-669.e3. 159 citations
205. J. Chen, M. Edupalli, B. Berger * and H. Cho *. [“Secure and federated linear mixed model association tests.”](#) bioRxiv (posted May 24, 2022).
206. R. Wu, F. Ding, R. Wang, R. Shen, X. Zhang, S. Lao, C. Su, Z. Wu, Q. Xie, B. Berger *, J. Ma *, J. Peng *. [“High-resolution *de novo* structure prediction from primary sequence.”](#) bioRxiv (posted July 22, 2022.)
207. H. Cho, D. Froelicher, J. Chen, M. Edupalli, A. Pyrgelis, J. Troncoso-Pastoriza, J-P Hubaux * and B. Berger *. [“Secure and Federated Genome-Wide Association Studies for Biobank-Scale Datasets.”](#) bioRxiv (posted December 02, 2022). Under review.
208. M. Cyrus Maher, I. Bartha, S. Weaver, J. Di Iulio, E. Ferri, L. Soriaga, F. Lempp, B. Hie, B. Bryson, B. Berger, D. Robertson, G. Snell, D. Corti, H. Virgin, S. Kosakovsky Pond and A. Telenti. [“Predicting the mutational drivers of future SARS-CoV-2 variants of concern.”](#) *Science Translational Medicine* (Jan 11 2022) **14** no. 633. 78 citations.
209. A. P. Wu, R. Singh and B. Berger *. [“Granger causal inference on DAGs identifies genomic loci regulating transcription.”](#) *Proc. of International Conference on Learning Representations* (2022).
210. S. Shan, S. Luo, Z. Yang, J. Hong, Y. Su, F. Ding, L. Fu, C. Li, P. Chen, J. Ma, X. Shi, Q. Zhang, B. Berger, L. Zhang and J. Peng. [“Deep learning guided optimization of human antibody against SARS-CoV-2 variants with broad neutralization.”](#) *Proceedings of the National Academy of Sciences* (March 1, 2022) **119** no. 11:e212295419.
211. S. Nyquist, P. Gao, T. Haining, M. Retichin, Y. Golan, R. Drake, K. Kolb, B. Mead, N. Ahituv, M. Martinez, A. Shalek, B. Berger and B. Goods. [“Cellular and transcriptional diversity over the course of human lactation.”](#) *Proceedings of the National Academy of Sciences* (2022) **119** no. 15:e2121720119.
212. H. Gideon, T. Hughes, C. Tzouanas, M. Wadsowrth, A.A. Tu, T. Gierahn, J. Peters, F. Hopkins, J-R Wei, C. Kummerlowe, N. Grant, K. Nargan, J.Y Phuah, H. Jacob Borish, C. Ganchua, A. Myers, K. Patel, C. Ameen, C. Cochran, S. Ibrahim, J. Tomko, L. frye, J. Rosenberg, A. Shih, M. Chao, E. Klein, C. Scanga, J. Ordovas-Montanes, B. Berger, J. Mattila, R. Madansein, J.C Love, P. Ling Lin, A. Leslie, S. Behar, B. Bryson, J. Flynn, S. Fortune, A. Shalek. [“Multimodal profiling of lung granulomas in macaques reveals cellular correlates of tuberculosis control.”](#) *Immunity* (2022) **55**:827–846. 48 citations.
213. H. Smaljovic, A. Shajii, B. Berger, H. Cho and I. Numanagic. [“Segure: a high-performance framework for rapid development of secure bioinformatics pipelines.”](#) *Proc. 2022 IEEE Intern’l Parallel and Distributed Processing Symposium Workshops (IPDPSW)* (2022).
214. M. Sherman, A. Yaari, O. Priebe, F. Dietlin, P.R Loh and B. Berger *. [“Genome-wide Mutation Rate Modeling Identifies Novel Driver Mutations.”](#) *Cancer Discovery* (2022), **12** no. 8; 1837.
215. R. Singh, K. Devkota, S. Sledzieski, B. Berger and L. Cowen. [“Topsy-Turvy: integrating a global view into sequence-based PPI prediction.”](#) *Bioinformatics* (2022) **38** Issue Supplement 1:i264–i272
216. D. Vasyliuk, J. Felt, E. Zhong, B. Berger, J. Davis and C. Yip. [“Conformational landscape of the yeast SAGA complex as revealed by cryo-EM.”](#) *Scientific Reports* **12**, no. 12306 (2022).
217. E. Zhong, A. Lerer, J. Davis and B. Berger *. [“CryoDRGN2: Ab Initio Neural Reconstruction of Dynamic Protein Complexes.”](#) *Microscopy and Microanalysis* (2022) **28** Supplement S1.
218. T. Jivanjee, S. Ibrahim, S. Nyquist, G. James Gatter, J. Bromley, S. Jaiswal, B. Berger, S. Behar, J.C Love and A. Shalek. [“Enriching and Characterizing T Cell Repertoires from 3’ Barcoded Single-Cell Whole Transcriptome Amplification Products.”](#) *Methods in Molecular Biology* (2022) **2574**.
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221. R. Singh, A. P Wu and B. Berger. [“Granger causal inference on DAGs identifies genomic loci regulating transcription”.](#) *Proc. of International Conference on Learning Representations* (2022).
222. R. Fardoos, S. Nyquist, O. Asowata, S. Kazer, A. Singh, A. Ngoepe, J. Giandhari, N. Mithabela, D. Ramjit, S. Singh, F. Karim, S. Buus, F. Anderson, J.Z Porterfield, A. Sibiya, R. Bipath, K. Moodley, W.

- Kuhn, B. Berger, S. Nguyen, T. De Oliveria, T. Ndung'u, P. Goulder, A. Shalek, A. Leslie and H. Kløverpris. "HIV specific CD8+ TRM-like cells in tonsils express exhaustive signatures in the absence of natural HIV control." *Frontiers in Immunology* (2022) **13** no. 912038.
223. B. Berger, D. Tian, W. Li, M. El-Kebir, A. Tomescu, R. Singh, N. Beerenwinkel, Y. Li, C. Boucher and Z. Bar-Joseph. "What are the keys to succeeding as a computational biologist in today's research climate?" *Cell Systems* (2022) **13** no. 10:P781-785.
224. A. P. Wu, T. Markovich, B. Berger, N. Hammerla, R. Singh. "Causally-guided Regularization of Graph Attention Improves Generalizability." (2022).
225. M. Sherman, A. Yaari, O. Priebe, F. Dietlien, PR. Loh *, B. Berger *. "Genome-wide mapping of somatic mutation rates uncovers drivers of cancer." *Nature Biotechnology* (2022) **40**:1634–1643.
226. L. Kinman, B. Powell, E. Zhong *, B. Berger * and J. Davis *. "Uncovering structural ensembles from single-particle cryo-EM data using cryoDRGN." *Nature Protocols* (2022) **18**:319-339.
227. B. Berger and Y. Yu. "Navigating bottlenecks and trade-offs in genomic data analysis." *Nature Reviews Genetics* (2022) **24**:235-250.
228. D. Froelicher, H. Cho, M. Edupalli, J. Sa Sousa, J-P Boussuat, A. Pyrgelis, J. Treoncoso-Pastoriza, B. Berger * and J-P Hubaux *. "Scalable and Privacy-Preserving Federated Principal Component Analysis." *Proc. of IEEE Symposium on Security and Privacy (SP)* (2023).
229. "[Codon: A Compiler for High-Performance Pythonic Applications and DSLs.](#)" *Proc. of 32nd ACM SIGPLAN International Conference on Compiler Construction* (2023):191-202.
230. S. Zaman, S. Sledzieski, B. Berger, Y. Wu and M. Bansal. "virDTL: Viral Recombination Analysis Through Phylogenetic Reconciliation and Its Application to Sarbecoviruses and SARS-CoV-2." *Journal of Computational Biology* (2023). **30** no. 1:3-20.
231. J. E. Otto, O Ursu, A. P. Wu, E. B. Winter, M. S. Cuoco, S. Ma, K. Qian, B. C. Michel, J. D. Buenrostro, B. Berger, A. Regev, and C. Kadoch. "[Structural and functional properties of mSWI/SNF chromatin remodeling complexes revealed through single-cell perturbation screens.](#)" *Molecular Cell* (2023) **83** no. 8:1350-1367.e7
232. Y. Kim, C. Worby, S. Acharya, L. Dijik, D. Alfonsetti, Z. Gromko, P. Azimzadeh, K. Dodson, G. Gerber, S. Hultgren, A. Earl, B. Berger * and T. Gibson *. "Strain Tracking with Uncertainty Quantification." bioRxiv (Posted Jan. 26, 2023).
233. H. Smaljovic, A. Shajii, B. Berger *, H. Cho * and I. Numanagic *. "Secure: a high-performance framework for secure multiparty computation enables biomedical data sharing." *Genome Biology* (2023) **24** no. 5.
234. D. Pellow, L. Pu, B. Ekim, L. Kotlar, B. Berger, R. Shamir, Y. Orenstein. "Efficient minimizer orders for large values of k using minimum decycling sets." *Genome Research* (2023). RECOMB 2023 special issue.
235. B. Ekim, K. Sahlin, P. Medvedev, B. Berger * and R. Chikhi *. "mapquik: Efficient low-divergence mapping of long reads in minimizer space." *Genome Research* (2023). RECOMB 2023 special issue.
236. S. Sadhuka, D. Friedman, B. Berger * and H. Cho *. "Accurate Assessment of transcriptomic re-identification risks using discriminative sequence models." *Genome Research* (2023). RECOMB 2023 special issue.
237. R. Singh, A. P. Wu, A. Mudide and B. Berger *. "Unraveling causal gene regulation from the RNA velocity graph using Velorama." *Cell Systems* (2023). Focus on RECOMB special issue.
238. B. Ewen-Campen, H. Luan, J. Xu, R. Singh, N. Joshi, T. Thakkar, B. Berger, B. H. White, N. Perrimon. "split-intein Gal4 provides intersectional genetic labeling that is fully repressible by Gal80." *Proceedings of the National Academy of Sciences* (June 6, 2023).
239. S. Sledzieski, R. Singh, B. Bryson, L. Cowen * and B. Berger *. "[Contrastive learning in protein language space predicts interactions between drugs and protein targets.](#)" *Proceedings of the National Academy of Sciences* (2023) **120** no. 24: e2220778120. Also Neurips 2022.

B3. Other Graph Algorithms Publications

240. B. Berger and J. Rompel. "[A Better Performance Guarantee for Approximate Graph Coloring.](#)" *Algorithmica* (1990) **5** no. 1-4:459–466. 83 citations.
241. B. Awerbuch, B. Berger, L. Cowen and D. Peleg. "[Low Diameter Graph Decomposition is in NC.](#)" *Random Structures and Algorithms* (1994) **5** no. 3:441–452. 27 citations.

242. B. Berger, J. Rompel and P. W. Shor. "[Algorithms for Set Cover with Applications to Learning and Geometry](#)." *J. of Computer and System Science* (1994) **3**:454–477, in special issue of the best papers from FOCS '89. 323 citations.
243. B. Berger and L. Cowen. "[Scheduling with Concurrency-Based Constraints](#)." *J. of Algorithms* (1995) **18** no. 1:98–123. 3 citations.
244. B. Berger, M. Brady, D. Brown, and T. Leighton. "[Nearly Optimal Algorithms and Bounds for Multilayer Channel Routing](#)." *J. of the Association for Computing Machinery* (1995) **42** no. 2:500–542. 103 citations.
245. B. Awerbuch, B. Berger, L. Cowen and D. Peleg. "[Fast Distributed Network Decomposition](#)." *J. of Parallel and Distributed Computing* (1996) **39** no. 2:105–114. 70 citations.
246. L. W. Hobbs, A. N. Sreeram, C. E. Jesurum and B. Berger. "[Structural Freedom, Topological Disorder, and the Irradiation-Induced Amorphization of Ceramic Structures](#)." *Nuclear Instruments and Methods in Physics Research* (1996) **116** no. 1-4:18-25. 172 citations.
247. C. E. Jesurum, V. Pulim, B. Berger and L. Hobbs. "[Topological Modeling of Topologically-Disordered Tetrahedral Structures Using Local Approaches](#)." *Materials Science Forum* (1997) **239**:37–40. 18 citations.
248. B. Berger and P. W. Shor. "[Tight Bounds for the Maximum Acyclic Subgraph Problem](#)." *J. of Algorithms* (1997) **25**, no. 1:1–18. 33 citations.
249. B. Berger. "[The Fourth Moment Method](#)." *SIAM J. on Computing* (1997) **26**, no. 4:1188–1207. 36 citations.
250. B. Awerbuch, B. Berger, L. Cowen and D. Peleg. "[Near-Linear Cost Construction of Sparse Neighborhood Covers](#)." *SIAM J. on Computing* (1998) **28** no. 1:263–277. 113 citations.
251. L. W. Hobbs, C.E. Jesurum, V. Pulim and B. Berger *. "[Local Topology of Silica Networks](#)." *Philosophical Magazine A* (1998) **78** no. 3:679–711. 102 citations.
252. L. W. Hobbs, C. E. Jesurum, V. Pulim and B. Berger *. "[Local rules switching mechanism for viral shell geometry](#) ." *Material Science and Engineering* (1998) **253** no. 1–2:16–29.18 citations.

C. Selected Keynotes and Distinguished Addresses

Calculating the Secrets of Life

USC Computational Biology Symposium in honor of Mike Waterman's 80th, Invited Address, 2022

Learning Regulatory Control from Multi-omic Dynamics

Human Cell Atlas Meeting, Keynote, 2022

Biomedical Data Sharing and Analysis at Scale

Joint Mathematics Meeting, Invited Address, 2020

UCSD Volterra Lecture, 2020

Learning the Language of Viral Evolution and Escape

AICures Drug Discovery Conference, Invited Address, 2020

Biomedical Data Sharing with Privacy

ECCB, Keynote, Athens, Greece, 2018

Volterra Lecture, Distinguished Address, Trondheim, Norway, 2018

Israeli Symposium on Bioinformatics, International Keynote, Haifa, Israel, 2018

ISMB, Vari SIG Keynote, Chicago, Illinois, 2018

ISMB/ECCB2019 Senior Scientist Keynote, 2019

GenoPri Keynote, 2019

Computational biology in the 21st century: making sense out of massive data

Margaret Pittman Lecture at NIH, Keynote, Bethesda, 2015

SIAM Annual Meeting, Keynote, 2014

ISMB/ECCB, Keynote, Vienna, Austria, 2013

Transposing Yeast to Human Networks: Insights into Neurodegenerative Diseases

EMBL-EBI Industry Programme Workshop, Keynote, Cambridge, MA, 2017

SNVs and Copy Number Variations in Complex Diseases

Gordon Research Conference on SNPs and Disease, Mount Holyoke College, MA, 2016

Computational biology in the 21st century: algorithms that scale

NIH PI Day, Keynote, 2017

RECOMB, Keynote, Warsaw, Poland, 2015

RECOMB/ISCB Regulatory & Systems Genomics, Keynote, 2015

ACM-BCB & WABI, Joint Keynote, Atlanta, Georgia, 2015

UC San Diego, Distinguished Address, San Diego, CA 2015

Compressive Genomics: Scaling Faster than Light

Stanford Biomedical Data Science, Distinguished Address, Palo Alto, CA, 2015

RECOMB-Bioinformatics Education (contributed a MOOC), Bethesda, 2015

Microsoft CABI meeting, Cambridge, MA, 2015

EPFL, Honorary Doctorate, Lausanne, Switzerland, 2015

Compressive Metagenomics

Center for Microbiome Informatics & Therapeutics, Keynote, Cambridge, MA 2017

Mathematical Challenges in Molecular Biology

AMS/MAA Joint Meeting, Joint Keynote, Phoenix, Arizona, 2005

International Congress of Mathematicians, Berlin, Germany, 1998

E. Edited Books

B. Berger, editor, *ISMB Proceedings*, *Bioinformatics* Editorial volume **28** (2012).

B. Berger and J. Waldispühl, *Novel Perspectives on Protein Structure Prediction*, *The Problem Solving Handbook for Computational Biology and Bioinformatics*, Heath, Lenwood S.; Ramakrishnan, Naren (Eds.)(2010).

B. Berger, editor, [*Research in Computational Molecular Biology, 14th Annual International Conference, RECOMB 2010*](#), volume 6044 of *Lecture Notes in Computer Science*, Springer (2010).

F. Mentorship

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MEng: Eric Banks (Broad Institute); Jeffrey T. Chen (MosaicML); Ryan Chung; Eric Eisner (Google); George Homsey (Atair Aerospace); Chiho Im (Stanford); Shreyan Jain; Matt Menke (Google); Daniel K. Park (Biogen); Vinay Pulim (Start-up); Maria Rodriguez; Eben Scanlon (McKinsey & Co); Prof. Russell Schwartz (CMU); Val SpitkovskyStanford/Google; Jason Trigg (Arch); Timothy F. Truong; Andy Tso (Hudson River Trading); Yuhao Wang; and Michael Yu (TTI, Chicago).

Recent Postdocs: Prof. Jerome Waldispuhl (McGill); Prof. Sebastian Will (Ecole Polytechnique, France); Prof. Jinbo Xu (TTI-C/U Chicago); Luke Hutchison (Google); Hadar Benyamini (Hebrew University); Prof. Jian Peng (UIUC); Prof. Noah Daniels (URI); Prof. Yaron Orenstein (Ben Gurion Univ.); Sepehr Ehsani (U. of Toronto); Sean Simmons (Broad Institute); Andrew Morin (Startup); Prof. Ibrahim Numanagić (Simon Fraser); Tristan Bepler (NY Structural Biology Center); Prof. Amy Keating (MIT); and Prof. David Brudno (Toronto).