

ROGER LARKEN CHANG, Ph.D.

1301 Morris Park Avenue, Price Center 253A
Department of Systems & Computational Biology
Albert Einstein College of Medicine
Bronx, NY 10461

Roger.Chang@einsteinmed.edu
Phone: 718-678-1251
<https://einsteinmed.edu/labs/roger-chang>

EDUCATION

2012 **Ph.D. Bioinformatics and Systems Biology**, University of California San Diego
Co-Advisors: Bernhard Ø. Palsson, Ph.D. and Philip E. Bourne, Ph.D.
Thesis: Structural Systems Biology Perspective on the Metabolic Impact of Physicochemical Stress

2005 **B.A. Molecular and Cell Biology** (genetics & development emphasis), University of California Berkeley

RESEARCH POSITIONS

Assistant Professor, Albert Einstein College of Medicine 2022-
Department of Systems & Computational Biology

Research associate and associate lab director, Harvard Medical School 2018-2021
Primary Projects:

- Design of intrinsically disordered proteins (IDPs) to induce cryptobiosis in human cells: developed 5-year \$15M proposal, acted as project manager, performed computational analysis and design of IDPs, and enzyme stabilization assays

LSRF postdoctoral research fellow, Harvard Medical School 2013-2018
Advisor: Pamela A. Silver, Ph.D.
Primary Projects:

- Discovery of viral-encoded suppressors of innate immunity in humans: helped develop protein structure-based prediction method to identify immunosuppressors, developed automated gene expression construct design pipeline, advised on development of unsupervised learning analysis of high-throughput microscopy imaging data to establish immune response assay phenotypes, maintained human cell cultures and tested STAT1 nuclear localization assay for innate immune response
- Protein oxidation in *D. radiodurans*: modeled structural proteome, developed 3D feature analysis tools, developed machine learning predictor of protein carbonylation sites, conducted redox proteomic experiments
- Polyploidy in *D. radiodurans*: developed *in vivo* chromosome and plasma membrane fluorescent labeling technique, measured labeled cultures by flow cytometry and microscopy, performed clustering analysis
- RNA nanostructure engineering: developed design pipeline for RNA nanotubes, cloned expression constructs and expressed in *E. coli*, developed riboregulator and FISH tube assembly assays using flow cytometry and microscopy, helped develop super-resolution FISH-DNA-PAINT imaging technique

NSF IGERT & GK-12 graduate student research fellow, University of California San Diego 2007-2012
Co-Advisors: Bernhard Ø. Palsson, Ph.D. and Philip E. Bourne, Ph.D.
Primary Projects:

- Structural systems biology of *E. coli*: reconstructed protein structure-integrated metabolic network, analyzed proteome-wide enzyme thermostability, developed flux balance analysis predictor of thermotolerance, performed nutrient supplementation growth experiments, performed proteome-wide protein-antibacterial interaction prediction, simulated antibacterial mechanisms by flux balance analysis
- Simulation of drug mechanisms: developed model of human renal metabolism, simulated drug response phenotypes by integrating metabolic model with structure-based protein-drug interactions, analyzed clinical hypertensive genotypes in model and predicted genetic predisposition to adverse drug effects

RESEARCH POSITIONS (continued)

- Modeling photosynthetic metabolism: annotated genome of eukaryotic alga *C. reinhardtii*, reconstructed genome-scale metabolic network of *C. reinhardtii*, devised flux balance scheme for simulating different light spectra

NSF IGERT graduate student research fellow, The Scripps Research Institute

2008

Advisor: Stephen P. Mayfield, Ph.D.*Primary Projects:*

- Gene silencing in *C. reinhardtii*: developed design software for gene-specific RNAi constructs, cloned constructs for carotenoid synthesis enzyme knock-downs, generated knock-down strains by chloroplast transformation, validated knock-downs by RT-PCR

Research technician, University of Texas Southwestern Medical Center

2006-2007

Advisor: Richard H. Scheuermann, Ph.D.*Primary Projects:*

- Modular organization of biological networks: developed graph-theoretic algorithms for modularization of protein-protein interaction and genetic interaction networks, studied network sub-structure topology, performed Gene Ontology annotation analysis and helped develop ontology for concepts in network biology
- BioHealthBase Bioinformatics Resource Center: helped develop genomic database, web visualization and analysis tools, and user interface for genomic research of high public health risk pathogens

UCB BFP undergraduate student research fellow, University of California Berkeley

2003-2005

Advisors: Aziz Aboobaker, Ph.D. and Nipam Patel, Ph.D.*Projects:*

- Hox gene evolution in nematodes: evaluated experimental tractability of a variety of nematode species, developed culturing, antibody staining, and RNAi protocols, cloned hox genes for use in RNAi constructs

FELLOWSHIPS AND AWARDS

2014-2017 Moore Foundation Fellow of Life Sciences Research Foundation (full support, postdoctoral)
 2014 NIH NRSA F32 from NIGMS (full support, postdoctoral) (declined)
 2011-2012 NSF GK-12 Socrates Teaching Fellow (full support)
 2010 UCSD Bioinformatics Expo Best Poster Award
 2008-2010 NSF IGERT Plant Systems Biology Fellow (full support)
 2004-2005 UC Berkeley Biology Fellow

PUBLICATIONS

21. Ng T, Olson E, Yoo TY, Weiss HS, Koide Y, Koch P, Rollins N, Mach P, Meisinger T, Bricken T, Chang T, Molloy C, Zürcher J, **Chang RL**, Mitchison T, Glass J, Marks D, Way J, and Silver P. High content screening and computational prediction reveal viral genes that suppress innate immune response. *mSystems* (in press).

20. Veling MT, Nguyen DT, Thadani NN, Oster ME, Rollins NJ, Brock KP, Bethel NP, Lim S, Baker D, Way JC, Marks DS, **Chang RL***, Silver PA*. Natural and designed proteins inspired by extremotolerant organisms can form condensates and attenuate apoptosis in human cells. *ACS Synth Biol.* 2022 Feb 18. doi: 10.1021/acssynbio.1c00572. *Corresponding authors.

19. Lowe NE, **Chang RL***. Making sense of disorder: Investigating intrinsically disordered proteins in the tardigrade proteome via a computational approach. *bioRxiv.* 2022 Jan 31. doi: <https://doi.org/10.1101/2022.01.29.478329>. *Corresponding author.

PUBLICATIONS (continued)

18. Westover C, Najjar D, Meydan C, Grigorev K, Veling MT, Iosim S, Colon R, Yang S, Restrepo U, Chin C, Butler D, Moszary C, Rahmatulloev S, Afshinnkoo E, **Chang RL**, Silver PA, Mason CE. Engineering radioprotective human cells using the tardigrade damage suppressor protein, DSUP. *bioRxiv*. 2020 Nov 10. doi: <https://doi.org/10.1101/2020.11.10.373571>.
17. **Chang RL***, Stanley JA, Robinson MC, Sher JW, Li Z, Chan YA, Omdahl AR, Wattiez R, Godzik A, Matallana-Surget S*. Protein structure, amino acid composition and sequence determine proteome vulnerability to oxidation-induced damage. *EMBO J*. 2020 Oct 19;e104523. doi: 10.15252/embj.2020104523. *Corresponding authors.
16. Brunk E, **Chang RL**, Xia J, Hefzi H, Yurkovich JT, Kim D, Buckmiller E, Wang HH, Cho BK, Yang C, Palsson BO, Church GM, Lewis NE. Characterizing posttranslational modifications in prokaryotic metabolism using a multiscale workflow. *Proc Natl Acad Sci U S A*. 2018 Oct 23;115(43):11096-11101.
15. Chaiboonchoe A, Ghamsari L, Dohai B, Ng P, Khraiweh B, Jaiswal A, Jijakli K, Koussa J, Nelson DR, Cai H, Yang X, **Chang RL**, Papin J, Yu H, Balaji S, Salehi-Ashtiani K. Systems level analysis of the *Chlamydomonas reinhardtii* metabolic network reveals variability in evolutionary co-conservation. *Mol Biosyst*. 2016 Jul 19;12(8):2394-407.
14. Brunk E, Mih N, Monk J, Zhang Z, O'Brien EJ, Bliven SE, Chen K, **Chang RL**, Bourne PE, Palsson BO. Systems biology of the structural proteome. *BMC Syst Biol*. 2016 Mar 11;10:26.
13. MacKellar D, Lieber L, Norman JS, Bolger A, Tobin C, Murray JW, Oksaksin M, **Chang RL**, Ford TJ, Nguyen PQ, Woodward J, Permingeat HR, Joshi NS, Silver PA, Usadel B, Rutherford AW, Friesen ML, Prell J. *Streptomyces thermoautotrophicus* does not fix nitrogen. *Sci Rep*. 2016 Feb 1;6:20086.
12. Ebrahim A, Almaas E, Bauer E, Bordbar A, Burgard AP, **Chang RL**, Dräger A, Famili I, Feist AM, Fleming RMT, Fong SS, Hatzimanikatis V, Herrgård MJ, Holder A, Hucka M, Hyduke D, Jamshidi N, Lee SY, Le Novère N, Lerman JA, Lewis NE, Ma D, Mahadevan R, Maranas C, Nagarajan H, Navid A, Nielsen J, Nielsen LK, Nogales J, Noronha A, Pal C, Palsson BØ, Papin JA, Patil KR, Price ND, Reed JL, Saunders M, Senger RS, Sonnenschein N, Sun Y, Thiele I. Do Genome-scale Models Need Exact Solvers or Clearer Standards? *Mol Syst Biol*. 2015 Oct 14;11(10):831.
11. Chen AH, Lubkowitz D, Yeong V, **Chang RL**, Silver PA. Transplantability of a circadian clock to a noncircadian organism. *Sci Adv*. 2015 Jun 1;1(5):e1500358.
10. **Chang RL**, Xie L, Bourne PE, Palsson BØ. Antibacterial mechanisms identified through structural systems pharmacology. *BMC Syst Biol*. 2013 Oct 10;7:102.
9. O'Brien ET, Lerman JA, **Chang RL**, Hyduke DR, Palsson BØ. Genome-scale models of metabolism and gene expression extend and refine growth phenotype prediction. *Mol Syst Biol*. 2013 Oct 1;9:693.
8. **Chang RL**, Andrews K, Kim D, Li Z, Godzik A, Palsson BØ. Structural systems biology evaluation of metabolic thermotolerance in *Escherichia coli*. *Science*. 2013 Jun 7;340(6137):1220-1223. Selected by Faculty of 1000 (Aug. 2013).
7. Nam H, Lewis NE, Lerman JA, Lee D, **Chang RL**, Kim D, Palsson BO. Network context and selection in the evolution to enzyme specificity. *Science*. 2012, Aug 31;337(6098):1101-1104.
6. **Chang RL**, Ghamsari L, Manichaikul A, Hom EF, Balaji S, Fu W, Shen Y, Hao T, Palsson BØ, Salehi-Ashtiani K, Papin JA. Metabolic network reconstruction of *Chlamydomonas* offers insight into light-driven algal metabolism. *Mol Syst Biol*. 2011, Aug 2;7:518. Thirty-day top downloaded MSB paper and highlighted in *Science* (August 2011).

PUBLICATIONS (continued)

5. **Chang RL**, Xie L, Xie L, Bourne PE, Palsson BØ. Drug off-target effects predicted using structural analysis in the context of a metabolic network model. *PLoS Comput Biol*. 2010, Sep 23;6(9):e1000938. Paper highlighted in *Journal of the American Medical Informatics* (July-August 2011), AMIA Summit on Translational Bioinformatics: Year in Review (March 2011), and selected by Faculty of 1000 (Jan. 2012).
4. **Chang RL**, Luo F, Johnson S, Scheuermann RH. Deterministic graph-theoretic algorithm for detecting modules in biological interaction networks. *Int J Bioinform Res Appl*. 2010;6(2):101-19.
3. Manichaikul A*, Ghamsari L*, Hom EFY*, Lin C*, Murray RR*, **Chang RL***, Balaji S, Hao T, Shen Y, Chavali AK, Thiele I, Yang X, Mello E, Hill DE, Vidal M, Salehi-Ashtiani K, Papin JA. Metabolic network analysis integrated with transcript verification for sequenced genomes. *Nat Methods* 2009, Aug;6(8):589-92. *Equal contribution.
2. Squires B, Macken C, Garcia-Sastre A, Godbole S, Noronha J, Hunt V, **Chang R**, Larsen CN, Klem E, Biersack K, Scheuermann RH. BioHealthBase: informatics support in the elucidation of influenza virus host pathogen interactions and virulence. *Nucleic Acids Res*. 2008, Jan;36(Database issue):D497-503.
1. Luo F, Yang Y, Chen CF, **Chang R**, Zhou J, Scheuermann RH. Modular organization of protein interaction networks. *Bioinformatics* 2007, Jan 15;23(2):207-214.

SELECTED PRESENTATIONS

Chang RL. Unraveling Oxidative Stress Resistance of the Proteome. **Invited talk** at 2019 Molecular Biology Society of Japan Annual Meeting, Fukuoka, Japan.

Chang RL. Structural Model of Vulnerability to Protein Oxidation in Bacteria. **Invited talk** at May 2018 Boston Aging Data Club, Boston, MA.

Chang RL. Understanding Vulnerability to Protein Oxidation in Bacteria. **Invited talk** at 2017 Virginia Tech Biocomplexity Institute – Beyond Sequence Alignment Symposium, Blacksburg, VA.

Chang RL, Robinson MC, Sher JW, Chan YA, Stork DA, Li Z, Silver PA, Matallana-Surget S. Bacterial Proteome Vulnerability to Oxidative Damage. **Poster** at 2017 11th Annual q-bio Conference, New Brunswick, NJ.

Chang RL, Sher JW, Stork D, Silver PA. Structural Analysis of Proteome Vulnerability to Oxidative Damage in *Deinococcus radiodurans*. **Poster** at 2016 ASM Microbe, Boston, MA.

Chang RL, Li Z, Godzik A, Palsson BØ. Structural Reconstruction of the metabolic network of *Escherichia coli* K12. **Poster** at 2011 5th IECA Conference, Riviera Maya, Mexico and 2012 UCSD Bioinformatics Expo, La Jolla, CA.

Chang RL, Xie L, Xie L, Bourne PE, Palsson BØ. Drug off-target effects predicted using structural analysis in the context of a metabolic network model. **Talks** at 2011 UCSD Bioinformatics Expo and 2010 UCSD Dept. of Pharmacology Research Discussions, La Jolla, CA.

Chang RL, Manichaikul A, Santhanam B, Ghamsari L, Hom EFY, Salehi-Ashtiani K, Papin JA. Genome-wide Network Analysis of Metabolism in *Chlamydomonas reinhardtii*. **Posters** at 2010 UCSD Bioinformatics Expo, La Jolla, CA and 2010 DOE GTL meeting, Washington D.C.

Chang RL, Luo F, Johnson S, Scheuermann RH. Deterministic graph-theoretic algorithm for detecting modules in biological interaction networks. **Talk** at BIOT-2008, Dallas, TX.

SELECTED GRANT WRITING

- DARPA Design and Engineering of Biostasis Proteins (DARPA W911NF1920017) 2018
- PIs: Pamela A. Silver, Ph.D., Debora Marks, Ph.D.
 - Conceived, wrote, budgeted, coordinated 7 co-investigators for grant, and managed project
- DARPA Biological Robustness in Complex Settings (DARPA HR0011-15-C-0094) 2015
- PI: Pamela A. Silver, Ph.D.
 - Contributed to portion of grant on computational modeling of bacterial consortia
- DARPA Living Foundries - 1000 Molecules (funded for first phase, finalist for second) 2013-2014
- PI: Pamela A. Silver, Ph.D.
 - Conceived and wrote portions of the grant
 - Presented computational platform to DARPA in Washington D.C.
- NIH R01 - Genome-scale *in silico* model for *E. coli* (funded) 2010
- PI: Bernhard Palsson, Ph.D.
 - Wrote portions of the grant
 - Ranked in 2nd percentile
- NIH R21 - Computational drug development in the context of human metabolic network 2010
- PIs: Bernhard Palsson, Ph.D. & Philip Bourne, Ph.D.
 - Conceived, wrote, and submitted entire grant
- NIH SBIR for GT Life Sciences, Inc., San Diego, CA 2010
- Supervisors: Iman Famili, Ph.D. & Monica Mo, Ph.D.
 - As consultant helped conceive, perform preliminary research for, and write grant

TEACHING, MENTORSHIP, AND OUTREACH

- Sys Bio Undergrad Outreach and Internship Workgroup, Harvard Medical School** 2020-2021
- Role:* founding member
 - Activities:* expanding research opportunities/mentorship for minorities; assembled kit to facilitate NIH diversity supplement application; developed/piloted secondary mentor program for interns; developed proposal for post-bacc program; advised summer interns on end-of-summer presentations
- Authentic Science Research Program, Byram Hills High School, Armonk, New York** 2020-2021
- Role:* research mentor *Student:* Nora Lowe
 - Activities:* remotely mentored student on wet/dry tardigrade protein research; biweekly meetings/assignments
- Northeastern University Co-op Program** 2019-2020
- Role:* research mentor *Student:* Julian Stanley
 - Activities:* supervised masters student in protein modeling and analysis of protein oxidation properties
- Harvard-Amgen Scholars Program** 2017
- Role:* research mentor *Student:* Ashton Omdahl
 - Activities:* trained an undergraduate research intern in computational systems biology, protein modeling and analysis, and viral genome analysis
- Harvard Systems Biology Department Rotation Student Mentor** 2016-2020
- Role:* research mentor *Students:* Devon Stork, Tobyn Branck, Katrina Warner
 - Activities:* trained and supervised 3 graduate students in wet/dry lab projects

TEACHING, MENTORSHIP, AND OUTREACH (continued)**Harvard FAS Center for Systems Biology Undergraduate Summer Research Program** 2014-2016

- *Role:* research mentor *Students:* Ziyou Ren, Joel Sher, Matthew Robinson
- *Activities:* trained undergraduate research interns in computational systems biology and bench experimental techniques for molecular biology and microbiology

Biology and Chemistry, Patrick Henry High School, San Diego 2011-2012

- *Role:* NSF GK-12 teaching fellow
- *Partner teacher:* Autumn Ross
- *Activities:* lectures, ran learning exercises, designed lessons introducing bioinformatics, pharmacogenomics, structural biology, biochemistry, evolution, and bioethics; organized/ran booth at San Diego Science and Engineering Festival 2012; 3-month formal training in pedagogy and lesson plan development
- *Published lesson plan:* Genomics, Bioinformatics, and Health
(<http://sciencebridge.ucsd.edu/programs/socrates/projects/biology/genomics-bioinformatics-health.html>)

Structural Bioinformatics Data & Analysis, University of California San Diego 2009

- *Role:* graduate teaching assistant
- *Professor:* Philip Bourne
- *Topics:* macromolecular structure data, experimental techniques for structure determination, biological data classification, protein structure alignment, protein-protein and protein-ligand interactions
- *Activities:* prepared and graded homework assignments and exams, held regular office hours and individual tutoring sessions, aided in course redesign, guest lecturer (2010, 2011, 2012)

Systems Biology and Bioengineering, University of California San Diego 2009

- *Role:* graduate teaching assistant
- *Professor:* Bernhard Palsson
- *Topics:* network reconstruction, constraint-based modeling, linearization, SVD, omics data analysis
- *Activities:* developed slides, gave lectures, prepared and graded homework assignments and exams, held regular office hours and individual tutoring sessions, contributed to new textbook, maintained course website

PROFESSIONAL MEMBERSHIPS

- American Society for Microbiology (ASM) 2010-present
- American Association for the Advancement of Science (AAAS) 2013-present
- Society for the Advancement of Chicanos and Native Americans in Science (SACNAS) 2021-present

EDITORIAL ACTIVITIES

- **Textbook contribution:** Palsson BO. Systems Biology: Constraint-based Reconstruction and Analysis. Cambridge University Press, 2015.
- Peer reviewer for ISMB Program Committee (2010)
- Peer reviewer for scientific journals:

<i>Journal of Proteomics</i> (2021-)	<i>Nucleic Acids Research</i> (2011-)
<i>BMC Bioinformatics</i> (2021-)	<i>Nature Reviews Microbiology</i> (2011-)
<i>Nat Commun</i> (2020-)	<i>Cell Reports</i> (2011-)
<i>The Plant Journal</i> (2018-)	<i>Metabolic Engineering</i> (2010-)
<i>Scientific Reports</i> (2016-)	<i>Nature</i> (2009-)
<i>ACS Synthetic Biology</i> (2015-)	<i>BioEssays</i> (2009-)
<i>Molecular BioSystems</i> (2013-)	<i>PLoS Comp Biol</i> (2009-)
<i>Cell</i> (2013-)	