

ELIZABETH H KELLOGG

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VISION/GOALS

I have been fascinated by protein structures ever since my first biochemistry class. This fascination, combined with a love of physics, biology, and computer science has led me to pursue one central question during my scientific career: how does protein structure relate to cellular function, and ultimately human health? I will use my unique background to study the proteins whose structures are difficult or impossible to determine using other structural techniques such as x-ray crystallography or NMR. Within the nucleus, chromatin contributes crucially to gene expression patterns; an increasing number of cellular factors have been discovered to play important roles in defining and remodeling chromatin structure and whose malfunction is associated with a wide range of maladies. Similarly, transposases have contributed significantly to the sequence diversity within the genome. I will combine advances in molecular modeling (via Rosetta), high-resolution cryo-EM, and biochemistry to focus on the structure of genomic proteins for which a basic understanding will have significant advance understanding of human health.

My Ph.D. with David Baker established my strong computational background in protein modeling and computational method development. I complemented this training during my postdoc by doing experimental structural biology in the lab of Eva Nogales, a leader in the field of cryo-EM. The synergistic combination of these two approaches has allowed me to approach questions that have long been considered inaccessible, including my recent structural studies of an intrinsically disordered protein, tau, bound to microtubules (MTs).

As an independent investigator, I will probe broad structural questions such as: how is the genome structured? I am deeply interested in important yet difficult to study complexes such as shelterin, a protein complex involved in telomere end protection, and transposases. To this end I have established collaborations with Ahmet Yildiz (UC Berkeley) to study the architecture of shelterin as well as a collaboration with Donald Rio (UC Berkeley) to study the structure and mechanism of the P-element transposase, a representative of a unique class of DNA transposases and an important genome editing tool.

EDUCATION

2013-present	<i>University of California, Berkeley</i> Molecular Biophysics and Integrated Bio-imaging Advisor: Dr. Eva Nogales	
2006-2012	<i>University of Washington</i> Biochemistry Thesis Title: "Assessing and Improving Computational Models of Protein Thermodynamics and Kinetics using Rosetta" Advisor: Dr. David Baker	<i>Ph.D.</i>
2002-2006	<i>University of California, Berkeley</i> Bioengineering	<i>B.S., summa cum laude</i>

FUNDING

awarded June 2017	NIH K99 Pathway to Independence Award "Towards an understanding of telomere end protection: Cryo-EM studies of shelterin structure and function"
2016-2017	Burroughs Wellcome Fund Collaborative Research Travel Grant
2008-2010	NIH F31 Genome Training Grant

SELECTED AWARDS/HONORS

2014	Session Chair "Rosetta and Structural Biology", Rosetta-Conference
2007	NSF fellowship honorable mention
2006	UC Berkeley Bioengineering Department Award Winner Significance: Top honor bestowed on one Bioengineering graduate per year

1. **Kellogg EH***, Hejab N*, Popsel S., Downing K.H., Dimaio F., and Nogales E. “Near-atomic model of microtubule-bound tau interactions” *Science* 360 (6394): 1242-46. June 2018

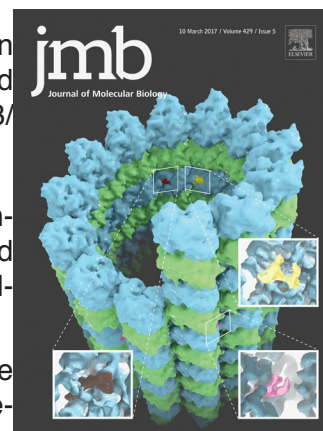
Significance: First high-resolution (3.7 Å) cryo-EM structure of tau reveals details of MT-tau interactions.

Impact:

- a. Highlighted in LBNL news center: <https://newscenter.lbl.gov/2018/05/10/tau-tally-microtubular/>

2. Nogales E., and **Kellogg EH**. “Challenges and opportunities in the high-resolution cryo-EM visualization of microtubules and their binding partners” *Curr. Op. Struct. Biol.* 46:65-70, October 2017

3. Howes SC., Geyer E., LaFrance BJ., Zhang R., **Kellogg EH**, Westermann S., Rice L., and Nogales E., “Structural and functional differences between yeast and mammalian microtubules revealed by cryo-EM” *Journal of Cell Biology* DOI: 10.1083/jcb.201612195, June 2017



4. **Kellogg EH**, Hejab N., Howes S., Northcote P., Miller JH., Diaz FJ., Downing KH. and Nogales E. “Insights into the distinct mechanisms of action of taxane and non-taxane microtubule stabilizers from cryo-EM structures” *Journal of Molecular Biology* 429 (5):633-646, March 2017

Significance: Multiple stabilizing chemotherapeutic drugs are studied in the context of the microtubule lattice and are found to have distinct structural effects, therefore, distinct mechanisms of action.

Impact:

- a. Selected for March 2017 JMB cover volume 429 issue 5.

5. **Kellogg EH***, Howes S.*, Ti SH., Kapoor T., Chacon P., and Nogales E. “Near-atomic cryo-EM structure of PRC1 bound to the microtubule” *PNAS* 113(34):9430-9, August 2016

Significance: Atomic structure of PRC1 on the microtubule elucidates how PRC1 selectively cross-links antiparallel microtubules and identifies novel function of PRC1 in microtubule stabilization.

Impact:

- a. Research highlight in FEBs letter, September 2016. doi: 10.1111/febs.13838

6. Alushin GM.*, Lander GC.*, **Kellogg EH***, Zhang R., Baker D., Nogales E. “High-resolution microtubule structures reveal the structural transitions in $\alpha\beta$ -tubulin upon GTP hydrolysis” *Cell* 157(5):1117-29, May 2014

Significance: The first high-resolution cryo-EM reconstruction of microtubules in different nucleotide states enable atomic flexible-fitting of tubulin to describe, at a detailed level, how nucleotide-hydrolysis induces strain in the microtubule lattice and how chemotherapy drug Taxol relieves this strain.

Impact:

- a. Highlighted by LBNL newscenter, May 2014. <http://bit.ly/2pv1pR2>
- b. Highlighted by Berkeley newscenter, May 2014. <http://bit.ly/2puPRNI>
- c. Highlighted in *Cell*, May 2014. doi: 10.1016/j.cell.2014.05.001

7. Leaver-Fay A., O’Meara M., Tyka M., Jacak R., Song Y., **Kellogg EH**, Thompson J., Davis I., Pache R., Kortemme T., Lyskov S., Gray J., Snoeyink J., Baker D., Kuhlman B. “Scientific Benchmarks for Updating the Rosetta Energy Function” *Methods Enzymol.* 523:109-43, July 2013

8. **Kellogg EH**, Lange OF., Baker D., “Evaluation and optimization of discrete state models of protein folding” *Journal of Physical Chemistry B.* 116(37):11405-13, September 2012

9. Liu Y., **Kellogg EH**, Liang H. "Canonical and Micro-canonical Analysis of Folding of Trpzip2: An All-atom Replica Exchange Monte-carlo Simulation Study" *Journal of Chemical Physics*. 137(4):045103, July 2012
10. **Kellogg EH**, Leaver-Fay A., Baker D., "Role of conformational sampling in computing mutation-induced changes in protein structure and stability" *Proteins: Structure, Function, Bioinformatics*. 29(3):830-8, March 2011
- Significance:** The first computational method in Rosetta to incorporate backbone refinement in order to improve thermodynamic predictions of protein stability with respect to sequence changes.
- Impact:**
- a. Cited ~200 times (Google scholar)
11. Fowler DM., Araya CL., Fleishman SJ., **Kellogg EH**, Stephany JJ., Baker D., Fields S. "High-Resolution Mapping of Protein Sequence-Function Relationships" *Nature Methods*. 7(9):741-6, September 2010
12. Jung HS, Okegawa Y., Shih PM., **Kellogg EH**, Abdel-Ghany SE., Pilon M., Sjolander D., Shikanai T., Niyogi K., "Aradopsis Thaliana PGR7 Encodes a Conserved Chloroplast Protein that is Necessary for Efficient Photosynthetic Electron Transport" *PloS One* 5(7):e11688, July 2010
13. Leung CC., **Kellogg EH**., Kuhnert A., Hanel D., Baker D., Glover JN., "Insights from the Crystal Structure of the Sixth BRCT Domain of Topoisomerase II β Binding Protein 1" *Proteins: Structure, Function, Bioinformatics*. 19(1):162-7, Jan 2010
14. Raman S., Vernon R., Thompson J., Tyka M., Sadreyev R., Pei J., Kim D., **Kellogg EH**., DiMaio F., Lange O., Kinch L., Sheffler W., Kim B, Das R., Grishin N., Baker D. "Structure Prediction for CASP8 with All-Atom Refinement using Rosetta" *Proteins: Structure, Function, Bioinformatics*. 77(S9):89-99, Jul 2009

* Equal contribution

TALKS, WORKSHOPS AND CONFERENCES

2017

Poster Presenter "Cryo-EM Structure of Microtubule-bound Tau", *Understanding Biology Through Structure Symposium*, Santa Fe, NM May 13-17

2016

Poster Presenter "Near-atomic cryo-EM structural studies of microtubules, microtubule-stabilizers, and microtubule-associated proteins" *ASCB*, San Francisco CA, December 2-6

2015

Invited Speaker "Near-atomic cryo-EM structural studies of microtubule stabilizers and microtubule-associated proteins" *Bay area cryo-EM meeting*, UC Berkeley, December 4

Poster Presenter "Microtubule-associated proteins and Microtubule-stabilizing drugs: how they recognize and affect microtubule structure" *HHMI conference*, Bethesda Maryland, November 1-3

Invited Speaker "Insights into the stabilizing mechanism of microtubule-targeting agents at near-atomic resolution using cryo-EM" *Gordon Research Conference 3D EM*, New London NH, June 21-26

Student invited Speaker "High-resolution cryo-EM studies of microtubule-stabilizing agents", Louisiana state university, Baton Rouge LA, May 13

2014

Invited Speaker, "Combining High-Resolution Cryo-EM Rosetta to Study the Effect of Taxol on the Microtubule Lattice", *Rosetta Conference*, Leavenworth Washington, August 1

Invited Speaker "Studying the Structural Origins of Microtubule Dynamic Instability through Combining Computational Modeling and CryoEM" *MCB retreat*, Asilomar CA, Jan 12-14

2013

Invited Speaker, “Studying the Structural Origins of Microtubule Dynamic Instability through Combining Computational Modeling and CryoEM”, Theoretical and Computational Biophysics Group, University of Illinois, Urbana-Champaign Illinois, August 22

Poster Presenter “Studying the structural origins of microtubule dynamic instability through computational modeling and cryoEM”, *GRC 3D EM*, New London NH, June 23-28

2012

Poster Presenter “Evaluation and optimization of discrete state models of protein folding” *Protein Society Meeting*, San Diego CA, August 5 – 8

2009

Invited Speaker, “Predicting $\Delta\Delta G$ s”, *Rosetta Conference*, Leavenworth WA, August 1

TEACHING AND OTHER ACTIVITIES

2016-2017

American Society of Cell Biology, **member**

2013-2014

Biophysical Society, **member**

2007

Graduate Student Instructor, Advanced Biochemistry

2007

Graduate Student Instructor, Intro. to Protein Structure and Intermediary Metabolism

2006

Graduate Student Instructor, General Chemistry