

ELIZABETH H KELLOGG

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VISION/GOALS

My vision is to combine computational protein modeling with cryo-EM structure determination to address questions related to genome structure.

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). Recently, I obtained a high-resolution (3.5 Å) of MT-bound tau that reveals the detailed atomic interactions between tau and microtubules. Tau adopts a well-defined structure between the interface of two tubulin dimers, establishing a model in which tau stabilizes microtubules by 'stapling' together tubulin dimers along MT protofilaments.

As an independent investigator, I will probe broad structural questions uniquely addressable using my training such as: how is the genome structured? I am deeply interested in important yet difficult to study complexes. To this end I have established collaborations with professors at UC Berkeley to study questions of relevance on the molecular determinants of genome structure.

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
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
2006	UC Berkeley Bioengineering Department Citation Winner Significance: <i>highest honor bestowed by department</i>

1. **Kellogg EH.***, Hejab N*, Popsel S., Dimaio F., and Nogales E. “New insights into tau’s structure and mechanism using cryo-EM” *in preparation*

Significance: First high-resolution (3.5 Å) cryo-EM structure of tau reveals details of MT-tau interactions.

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

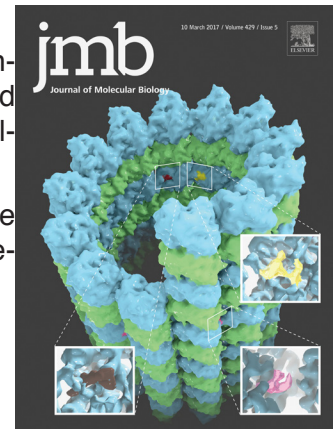
3. Howes SC., Geyer E., LaFrance BJ., Zhang R., **Kellogg EH.**, Westermann S., Rice L., and Nogales E., “Structural and functional differences between yeast and mammalian microtubules revealed by cryo-EM” *Journal of Cell Biology* DOI: 10.1083/jcb.201612195, June 2017

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

* co-first author

TALKS, WORKSHOPS AND CONFERENCES

2017

Poster Presenter “High-resolution cryo-EM structure of microtubule-bound tau”, *Innovations in imaging for the life sciences symposium*, Seattle WA, August 30

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*, Berkeley CA, 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

MENTORING

2017 – current	Graduate student in Molecular and Cellular Biology	Lisa Eshun-Wilson
2017 (spring)	Rotation student in Molecular and Cellular Biology	Christopher Hoel
2015 – 2016	Graduate student in Comparative Biochemistry	Nisreen Hejab
2014 – 2016	Undergraduate student in Molecular and Cellular Biology	Conner Lambden