CURRICULUM VITAE
EVA NOGALES

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EDUCATION AND TRAINING

1988	B.S. in Physics by the Universidad Autónoma de Madrid, Spain
1993	Ph.D. in Biophysics by the Physics Department of Keele University, UK. Advisor: Dr. Joan Bordas, Daresbury Laboratory.
1993 – 95	Postdoctoral training in Biophysics at the Life Science Division, Lawrence Berkeley National Laboratory (LBNL). Advisor: Dr. Kenneth H. Downing.

POSITIONS

09/15 – present	**Chair**, Biochemistry, Biophysics and Structural Biology Division, MCB Department, UC Berkeley.
01/14 – 09/15	Member of the Scientific Advisory Committee for the Life Sciences Division, LBNL
09/13 – 06/15	Chair of Molecular and Cell Biology Undergraduate Affairs, UC Berkeley
01/12 – 06/15	Head of the Biophysics Graduate Program, UC Berkeley
01/10 – 01/14	Deputy Director of the Bioenergy/GTL & Structural Biology Department, Life Science Division, LBNL
11/08 – present	**Senior Faculty Scientist** at LBNL, Life Sciences Division, LBNL
07/06 – present	**Professor** of Biochemistry, Biophysics and Structural Biology, Molecular and Cell Biology Department, UC Berkeley
07/03 – 06/06	Associate Professor of Biochemistry and Molecular Biology, Molecular and Cell Biology Department, UC Berkeley
09/00 – present	**Investigator**, Howard Hughes Medical Institute
07/98 – 10/08	Faculty Scientist, Life Sciences Division, LBNL
07/98 – 06/03	Assistant Professor of Biochemistry and Molecular Biology, Molecular and Cell Biology Department, UC Berkeley
09/95 – 06/98	Staff Scientist, Life Sciences Division, LBNL

AWARDS

2016	Mildred Cohn Award in Biological Chemistry by the American Society for Biochemistry and Molecular Biology
2015	Dorothy Crowfoot Hodgkin Award by the Protein Society
2015	Distinguished Role Model in the Life Sciences, Northwestern University
2005	American Society for Cell Biology Early Career Award
2005	Chabot Science Award for Excellence
2000	Burton Award by the Microscopy Society of America
1998	Outstanding Performance Award, LBNL
1989 – 92	Doctoral fellowships, Spanish Ministry of Education and MRC (U.K.)
1984 – 88	Undergraduate fellowship by the Spanish Ministry of Education

HONORS

2015	Elected Member of the National Academy of Science
2015-present	Member, Advisory Council for Princeton's Molecular Biology Department

2015	Dr. Smith Freeman Endowed Lecture, Chicago Cytoskeleton Meeting
2014 – 2015	Visiting Scholar of the Fundación Jesús Serra (at CNIO, Madrid)
2014	Lamport Lecture, Dept. of Biophysics and Physiology, University of Washington
2014	University of Colorado Medical School Dean's Distinguished Lecture
2013	NIH WALS Lecture
2012	Fitzgerald Lecture, Duke University
2009	Max Birnstiel Lecture at IMP, Vienna
2009	Distinguished Lecture at EMBL, Heidelberg
2007 – 2008	Biomedicine Chair, Foundation BBVA (at CNiO, Madrid)
2006	Annual Hamilton Memorial Lecture, Temple University

PARTICIPATION IN SCIENTIFIC SOCIETIES, JOURNALS AND CONFERENCES (SINCE JULY 1998)

2015-present	**Member of the Editorial Board**, Journal of Cell Biology
2015	Elected Chair, GRC on "3-D Electron Microscopy"
2014	Symposium speaker ASCB meeting, "Cell Structure across Scales"
2015 – present	**Associate Editor** of Journal of Structural Biology
2013	Keynote speaker, GRC on "Proteins"
2012	Co-chair "New Technologies in Imaging", ASCB Annual meeting
2012 – present	**Member of the Editorial Board** of Journal of Molecular Biology
2011	Keynote speaker, GRC on "Motile and Contractile systems"
2011	Keynote speaker, IUCr Annual Meeting, Madrid
2011 – present	**Member of the National Advisory Committee** for the Latin American Fellows Program, PEW Charitable Foundation
2010	Co-organizer, Structural Biology Workshop at Janelia Farm
2009	Member of the Search Committee for the LBNL Director
2009	Chair of the Early Career Selection Committee of the ASCB
2008	Co-organizer of Workshop "Frontiers in Cryo-EM" at Janelia Farm.
2008	Co-organizer of CNIO Cancer Conference "Structure and mechanism of essential complexes for cell survival".
2007	Co-organizer of the "Imaging Techniques" workshop of the GTL-DOE Annual Conference
2007	Co-editor, Macromolecular Section, Current Opinion in Structural Biology
2006	Co-organizer, "Imaging" Mini-symposium ASCB Meeting
2005 – 2009	Member, Macromolecular Structure and Function C Study Section
2004	Co-organizer of HHMI-MPI Workshop on Molecular and Cellular Imaging
2003	Organizer, QB3 Symposium: "Challenges in Biological Imaging: from cells to molecules". Berkeley
2003 – 2005	Elected member of the Biophysical Society Executive Board
2002 – present	**Chair of the Advisory Board** for the National Resource for Automated Molecular Microscopy
2002	Co-organizer of the Biophysical Discussion "Frontiers in structural cell biology ", Biophysical Society
2000 – 2015	Member of the editorial board of Journal of Structural Biology.
1999	Editor of special issue of Journal of Structural Biology on Electron Crystallography

1999	Chair of symposium "Visualizing Function: a new revolution in electron microscopy", Meeting of the American Society for Cell Biology (ASCB).
1999	Chair, session "New Challenges in Data Analysis and Interpretation", GRC on 3-D Electron Microscopy of Macromolecules
1998	Co-organizer of the workshop "Electron crystallography of biological macromolecules", Granlibakken.

SERVICE ON FEDERAL GOVERNMENT ADVISORY COMMITTEES

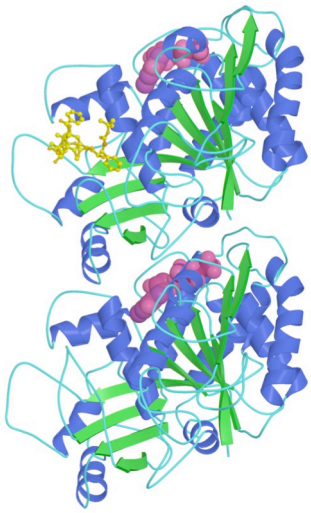
2015	NIH special study section panel
2013	CMP study section, ad hoc member
2013	NCSD study section, ad hoc member
2012	MSFC study section, ad hoc member
2005-2009	Macromolecular Structure and Function C Study Section Member

RESEARCH STATEMENT

My lab is dedicated to the ***visualization of macromolecular function***, using cryo-EM as a main experimental tool. We study two different areas of essential eukaryotic biology: central dogma machinery in the control of gene expression, and cytoskeleton interaction and dynamics in cell division. The unifying principle in our work is the study of macromolecular assemblies as whole units of molecular function by direct visualization of their architecture, functional states, and regulatory interactions.

CONTRIBUTIONS TO SCIENCE

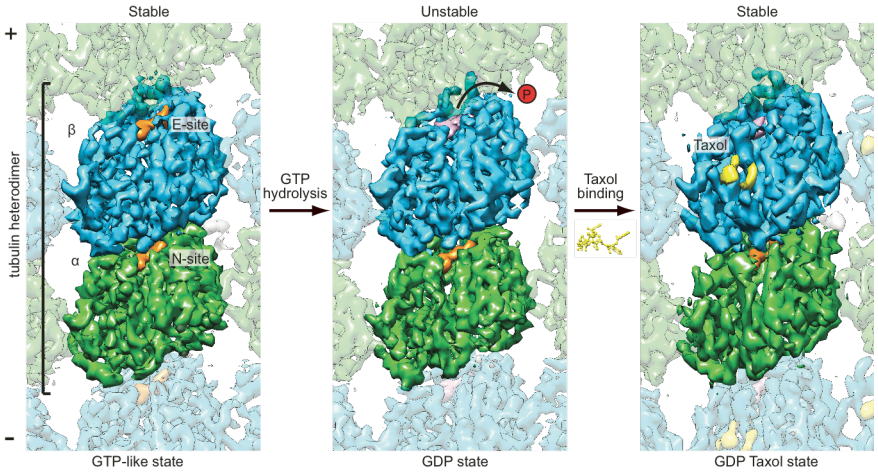
I – Structural Characterization of Tubulin and Microtubule Dynamic Instability



During my postdoc in Ken Downing's lab, I used electron crystallography of zinc-induced sheets of antiparallel protofilaments to produce the first atomic model of tubulin. This model established the structural basis of nucleotide exchange, polymerization-coupled hydrolysis, and taxol binding, and has served as the surrogate for the polymerized/straight state of tubulin. Docking the electron crystallographic structure of the protofilament into lower resolution cryo-EM reconstructions of microtubules has led to pseudo-atomic models of the microtubule of increasing accuracy.

In order to obtain a detailed mechanistic understanding of the process of microtubule dynamic instability we are studying the conformational landscape of tubulin as defined by its nucleotide and assembly states. My lab obtained two structures proposed to mimic intermediates in the assembly and disassembly of microtubules that illustrated the conformational consequences of the nucleotide state and how they relate to longitudinal and lateral assembly. More recently our studies have centered on defining the conformational changes within the microtubule upon GTP hydrolysis. Through the optimization of data

collection and image processing, we produced structures at ~5 Å resolution for three MT states: stable MTs bound to GMPCPP, dynamic MT (where GTP has been hydrolyzed to GDP), and MTs stabilized by taxol. We used Rosetta to generate low energy ensembles to fit each MT map and ultimately generated consensus models that could be compared to define the changes with nucleotide state and taxol binding. We showed that GTP hydrolysis results in a compaction at the interdimer longitudinal interface (by the E-site nucleotide) and a conformational change in a-tubulin that generates strain in the MT lattice. Taxol appears to allosterically inhibit these changes.



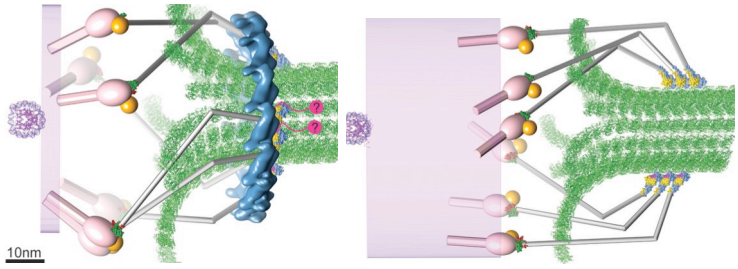
1. Nogales, E., Wolf, S. G., & Downing, K. H. (1998) Structure of the ab tubulin dimer by electron crystallography. Nature **391**, 199-203.
2. Nogales, E., Whittaker, M., Milligan R. A., & Downing, K. H. (1999) High resolution model of the microtubule. Cell **96**, 79-88.
3. Löwe, J., Li, H., Downing, K.H., and Nogales, E. (2001) Refined structure of ab tubulin at 3.5 Å, J. Mol. Biol. **313**, 1083-1095.
4. Wang, H-W. and Nogales, E. (2005) The nucleotide-dependent bending flexibility of tubulin regulates microtubule assembly, Nature **435**, 911-915.
5. Alushin, G.M., Lander, G.C., Kellogg, E.H., Zhang, R., Baker, D. and Nogales, E. (2014) High-resolution microtubule structures reveal the structural transitions in ab-tubulin upon GTP hydrolysis. Cell **157**, 1117,1129.
6. Zhang, R., Alushin, G.M., Brown, A. and Nogales, E. (2015) Mechanistic origin of microtubule dynamic instability and its modulation by EB proteins. Cell **162**, 849-859.

II - Microtubules-Kinetochore Interactions

In the cell the dynamics of microtubules are regulated and made use of by their interaction with different factors. Of special interest is the coupling of microtubules to kinetochores that underlies the accurate segregation of chromosomes during mitosis. Our initial studies of the yeast ***Dam1 kinetochore complex***, in collaboration with the Drubin and Barnes labs (UC Berkeley), showed that this complex assembles into rings around microtubules that move processively with microtubule ends. We used cryo-EM to produce the only existing structures of the Dam1 complex and of its self-assembly around microtubules, defining the subunit organization of Dam1 and characterizing important structural elements for interaction with tubulin.

Our interest in chromosome segregation has led us to study the highly conserved KMN kinetochore network. We visualized the full-length yeast **Ndc80 complex** and found a

dramatic kink within the 560-Å complex localized to a conserved break in the coiled-coil and proposed its important in kinetochore geometry and likely in tension sensing. Using a bonsai human Ndc80 complex, we obtained a subnanometer structure of Ndc80 bound to the microtubule. The binding is coupled to a self-interaction of Ndc80 complexes along protofilaments that explains their cooperativity. Ndc80 binds with a monomeric tubulin repeat, using a minimal "toe-print" that reads highly conserved sequences in tubulin and can "probe" the conformational state of the microtubule. Our studies are consistent with a Hill model where directionality of diffusion by loss of affinity in one direction is coupled to the conformational change into curved protofilaments. Our studies of the unstructured N-terminus of Ndc80, a substrate of Aurora B, led to a model of how Ndc80's interaction with MT is tuned by phosphorylation. In the process, we obtained the only existing structure of the C-terminal tail of tubulin, as it engages the Ndc80 complex in an adjacent protofilament. We have extended our studies to other kinetochore complexes (Mist12 complex, CENP-C). Our work, in the context of additional in vivo studies, has led us to propose models for the organization of both the yeast and the metazoan kinetochore.



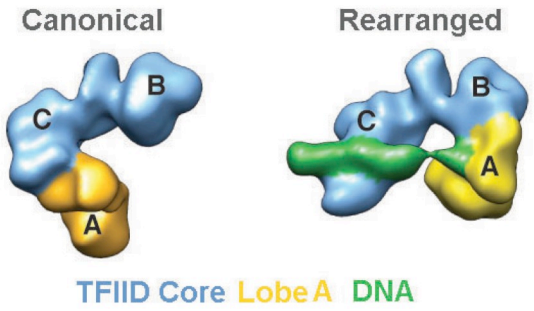
3D models of the budding yeast (left) and vertebrate kinetochore (right) bound to a depolymerizing MT during anaphase.

1. Westermann, S., Avila-Sakar, A., Wang, H-W., Niederstrasser, H., Wong, J., Drubin, D.G., Nogales, E., and Barnes, G. (2005) Formation of a dynamic kinetochore-microtubule interface through assembly of the Dam1 ring complex. Mol. Cell, **17**, 1-20.
2. Wang,H-W., Ramey, V.H., Westermann, S., Leschziner, A., Welburn, J.P.I., Nakajima, Y., Drubin, D.G., Barnes, G. and Nogales, E. (2007) Architecture of the Dam1 kinetochore ring complex: implications for microtubule-driven assembly and force-coupling mechanisms. Nat. Struct. Mol. Biol. **14**, 721-726.
3. Alushin, G., Ramey, V.H., Pasqualato, S., Ball, D., Grigorieff, N., Musacchio, A. and Nogales, E. (2010) The NDC80 complex forms oligomeric arrays along microtubules. Nature **467**, 805-810.
4. Alushin, G. M., Musinipally, V., Matson, D., Tooley, J., Stukenberg P.T. and Nogales, E. (2012) Multimodal microtubule binding by the Ndc80 kinetochore complex. Nature Struct. Mol. Biol. **19**, 1161-1167.

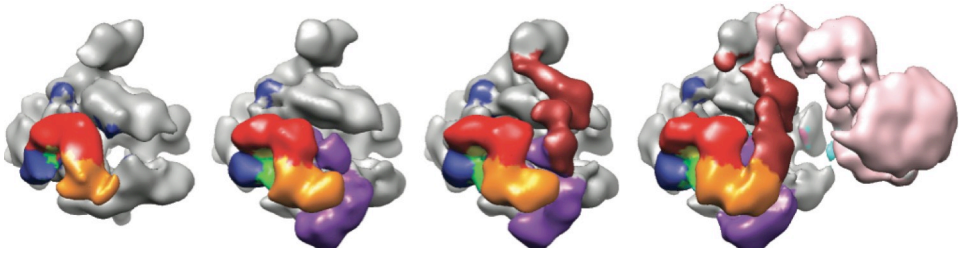
III – Regulation of Gene Expression

Transcription Initiation. The accurate initiation of transcription requires the assembly of a pre-initiation complex (PIC) that include TFIID, TFIIA, TFIIB, TFIIE, TFIIF, TFIIH and RNA pol II. Regulation is achieved by gene specific activators and repressors, cofactor complexes that mediate the interaction of the general machinery with sequence-specific activators, and protein complexes involved in the modification or remodeling of chromatin. The Nogales lab is interested in characterizing the structure of these different components

and how they interact to regulate transcription. A main effort has been to define the structure of the human transcription factor IID (TFIID). Binding of this general factor to the core promoter is the first step in the assembly of the whole transcriptional machinery. In collaboration with Robert Tjian (UC Berkeley) we obtained the first 3-D model of TFIID and showed the existence of significant flexibility within the complex, which we proposed could play a distinct role in directing the formation of an active PIC. We also characterized a cell type-specific TFIID complex containing TAF4b and studied the interaction of TFIID with differential activators. In exciting and recent work in collaboration with James Kadonaga (UCSD), we has shown that TFIID coexists in two predominant states differing dramatically in the location of lobe A (containing TBP and TFIIA) with respect to a more stable BC core. A novel conformation of TFIID, the rearranged state, interacts with promoter DNA in a TFIIA-dependent manner. We found that the downstream region of the SCP is bound by lobe C, while the upstream DNA sequence is bound within lobe A. This has lead us to propose that the dynamic conformational landscape of TFIID may have regulatory consequences by providing specific structural targets that can be recognized by transcriptional activators and repressors. Testing this idea is a major, on going effort.

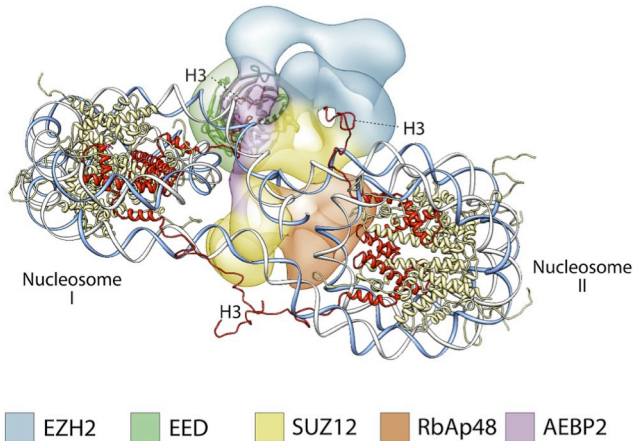


Recently, we have developed an in vitro reconstitution system to describe the stepwise assembly of the human PIC. This study allowed us to describe how TFIIF stabilizes the core promoter DNA along the surface of RNAPII, and how TFIIE addition results in the topological trapping of the DNA on the RNAPII cleft. TFIIE positions TFIIH so that the active ATPase in transcription initiation, XPB, is down stream of the transcription start site. We also used an artificial DNA template that served as a mimic of that generated naturally by the helicase action of TFIIH. The apparent movement of downstream DNA in this structure, together with the positioning of XPB, suggests how XPB would act as a DNA translocase whose activity would push against the stably bound upstream DNA at the TATA box to induce negative supercoiling at the transcription start site.



1. Andel, F., Ladurner, A. G., Inouye, C., Tjian, R. and Nogales, E (1999) Three-dimensional structure of the human TFIID-TFIIA-TFIIB complex. Science **286**, 2153-2156.
2. Liu, W-L., Coleman, R.A., Grob, P., Geles, K.G., King, D.S., Ramey, V.H., Nogales, E. and Tjian, R. (2008) Structural changes in TAF4b-TFIID correlated with promoter selectivity. Mol. Cell **29**, 81-91.
3. Cianfrocco, M.A., Kassevitis, G.A., Grob, P, Fang, J., Juven-Gershon, T., Kadonaga, J.T. and Nogales, E. (2013) Human TFIID binds core promoter DNA in a reorganized structural state. Cell **152**, 120-131.

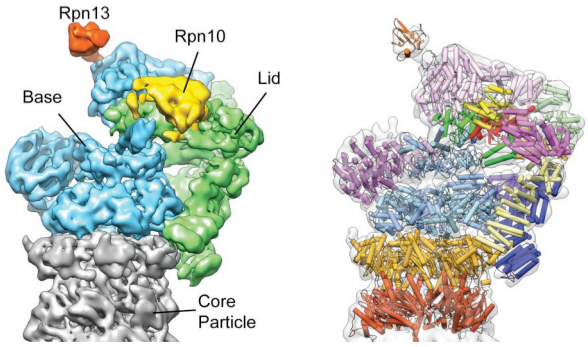
4. He, Y., Fang, J., Taatjes, D.J., and Nogales, E. (2013) Structural visualization of key steps in human transcription initiation. Nature **495**, 481-486.



Gene silencing. Polycomb Repressive Complex 2 (PRC2) is essential for gene silencing, establishing transcriptional repression of specific genes by tri-methylating Lysine 27 of histone H3. PRC2 function is essential, and aberrant PRC2 activity has been shown to affect tumor development and metastasis, making it a promising target of cancer therapy. In spite of its biological importance, little was known about PRC2 architecture and subunit organization. We reconstituted a tetrameric human PRC2 complex (Ezh2/EED/Suz12/RbAp48) with its cofactor AEBP2 and obtained the only available structural description of the complex (20 Å resolution). We used a tagging strategy to position all functional domains within the complex that showed that the Ezh2's SET domain forms a core with the two activity-controlling elements, the WD40 domain of EED and the VEFS domain of Suz12. This analysis allowed us to propose models for its engagement with nucleosomal substrates and for its regulation by epigenetic markers.

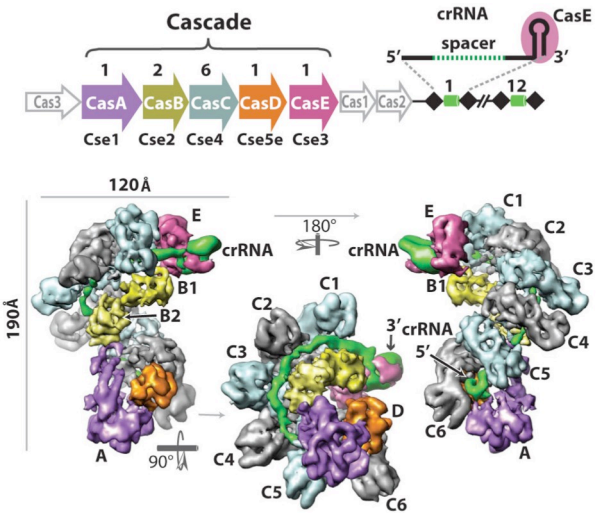
1. Ciferri, C., Lander, G.C., Maiolica, A., Herzog, F., Aebersold, R. and Nogales, E. (2012) Structure of the polycomb represive complex 2 and implications for gene silencing. eLIFE, e00005.

IV – Recent Collaborations of Special Notice



Proteosome (with Andreas Martin). The ubiquitin-proteasome system is the major pathway for selective protein degradation. The proteasome contains over 30 different subunits that form a barrel-shaped 20S proteolytic core, capped by 19S regulatory particles composed of a lid and base subcomplexes required for substrate recognition, deubiquitination, unfolding, and translocation. We obtained a subnanometer resolution structure of the budding yeast 26S proteosome. By defining the structure of the lid in isolation, and labeling each component of both the lid and base, we were able to localized each protein and propose a model of how recognition of ubiquitinated samples, removal of ubiquitin chains and threading of the polypeptide chain into the translocase channel and the proteolytic chamber are coordinated. The deubiquitinase Rpn11, directly above the pore in the base leading to the 20S chamber, is surrounded by the ubiquitin receptors Rpn10 and 13. This work provides a structural framework for the mechanistic understanding of ubiquitin-dependent protein degradation.

CRISPR/Cas Systems (with long-term collaborator Jennifer Doudna). The bacteria and archaea adaptive immunity is a nucleic acid– based system in which short fragments of foreign DNA are integrated into clustered regularly interspaced short palindromic repeats (CRISPRs)[3]. In type I and III CRISPR/Cas systems, CRISPR transcripts are processed into short crRNAs that are incorporated into a large ribonucleoprotein surveillance complex. We determined the first sub-nanometer structure of Cascade, the type I surveillance complex in E. coli. The seahorse-shaped Cascade displays the crRNA along a helical arrangement of CasC subunits that protect the crRNA from degradation, while maintaining availability for base pairing. Cascade engages invading nucleic acids through high-affinity base pairing near the 5' end of the crRNA. Base pairing extends along the crRNA resulting in short helical segments that trigger a concerted conformational change. Our structures of the dsDNA-bound Cascade with Cas3 showed that the CasA subunit is essential to recognize DNA target sites and to position Cas3 adjacent to the PAM to ensure cleavage.



Cas9, the hallmark protein of type II CRISPR/Cas systems, is a dual RNA-guided DNA endonuclease that cleaves foreign DNA at specific sites and is being used as an RNA- programmed genome editing tool. Our EM studies showed its two structural lobes undergo guide RNA-induced reorientation to form a central channel where DNA substrates can bind, thus implicating guide RNA loading as a key step in Cas9 activation.

We have also characterized two type III CRISPR systems, which recognize and cleave single-stranded RNA. Our structure of the Thermus thermophilus type III-A Csm complex is composed of two intertwined filaments, one of repeating Csm3 subunits, and a smaller one of Csm2 subunits, capped by Csm5 and a foot-like base contains Csm. We have now obtained near-atomic resolution reconstructions (~4.5 Å) of the Thermus thermophilus type III-B Cmr complex that show thumb-like β-hairpins of Cmr subunits intercalating between segments of duplexed crRNA:target RNA to facilitate cleavage of the target phosphodiester backbone at 6-nt intervals. Remarkable architectural similarity to the CRISPR-Cascade complex suggests divergent evolution of these systems from a common ancestor.

1. Lander, G.C., et al., *Complete subunit architecture of the proteasome regulatory particle.* Nature, 2012. **482**(7384): p. 186-91.
2. Wiedenheft, B., et al., *Structures of the RNA-guided surveillance complex from a bacterial immune system.* Nature, 2011. **477**(7365): p. 486-9.
3. Jinek, M., et al., *Structures of Cas9 endonucleases reveal RNA-mediated conformational activation.* Science, 2014. **343**(6176): p. 1247997.
4. Taylor, D.W., Zhu, Y., Staals, R.H.J., Kornfield, J.E., Shinkai, A., vander Oost, J., Nogales, E. and Doudna, J.A. (2015) Structures of the CRISPR-Cmr complex reveal mode of RNA target positioning. Science **348**, 581-585.

PUBLICATIONS (REVERSE CHRONOLOGICAL ORDER)

1. Bertin, A. and Nogales, E. (2015) Characterization of Septin Ultrastructure in Budding Yeast Using Electron Tomography. Methods Mol. Biol., in press.
2. Nogales, E. (2015) An Electron Microscopy Journey in the Study of Microtubule Structure and Dynamics. Protein Science, Epub ahead of print.
3. Zhang, R. and Nogales, E. (2015) Finding the Lattice Seam to Improve Cryo-EM Reconstructions of Microtubules. JSB, Epub ahead of print.
4. Ciferri, C., Lander, G.C. and Nogales, E. (2015) Protein Domain Mapping by Internal Labeling and Single Particle Electron Microscopy. JSB, Epub ahead of print.
5. Zhang, R., Alushin, G.M., Brown, A. and Nogales e. (2015) Mechanistic origin of microtubule dynamic instability and its regulation by EB proteins. Cell **162**, 849-859.
6. Nogales, E. and Scheres, S.H.W. (2015) Cryo-EM: a unique tool for the visualization of molecular complexity. Mol. Cell 58, 677-689..
7. Taylor, D.W., Zhu, Y., Staals, R.H.J., Kornfield, J.E., Shinkai, A., vander Oost, J., Nogales, E. and Doudna, J.A. (2015) Structures of the CRISPR-Cmr complex reveal mode of RNA target positioning. Science 348, 581-585.
8. Baskaran, S., Carlson, L.-A., Stjepanovic, G., Young, L.N., Kim, D.J., Grob, P., Stanley, R.E., Nogales, E., Hurley, J.H. (2014) Architecture and dynamics of the autophagic phosphatidylinositol 3-kinase complex. eLife 2014;10.7554/*eLife*.05115
9. Staals, R.H.J., Zhu, Y., Taylor, D.W., Kornfeld, J.E., Sharma, K., Barendregt, A., Koehorst, J.J., Vlot, M., Neupane, N, Varossieau, K., Sakamoto, K., Suzuki, T., Dohmae, N., Yokoyama, S., Schaap, P.J., Urlaub, H., Heck, A.J.R., Nogales, E., Doudna, J.A., Shinkai, A.,van der Oost, J. (2014) RNA Targeting by the Type III-A CRISPR-Cas Csm Complex of Thermus thermophilus. Mol Cell **56**, 518-539.
10. Nakamura M, Chen L, Howes SC, Schindler TD, Nogales E, Bryant Z. (2014) Remote control of myosin and kinesin motors using light-activated gearshifting. Nat Nanotechnol. **9**, 693-697.
11. Onoa, B., Schneider A.R., Brooks, M.D., Grob, P., Nogales, E., Geissler, P.L., Niyogi, K.K., Bustamante, C. (2014) Atomic Force Microscopy of Photosystem II and Its Unit Cell Clustering Quantitatively Delineate the Mesoscale Variability in Arabidopsis Thylakoids. PLoS One: e101470.
12. Clausen, C.H., Brooks, M.D., Li, T.-D., Grob, P., Kemalyan, G., Nogales, E., Niyogi, K.K. and Fletcher D.A. (2013) Dynamic mechanical responses of Arabidopsis thylakoid membranes during PSII specific illumination. Biophys. J. **106**, 1864-1870.
13. Alushin, G.M., Lander, G.C., Kellogg, E.H., Zhang, R., Baker, D. and Nogales, E. (2014) High-resolution microtubule structrues reveal the structural transitions in ab-tubulin upon GTP hydrolysis. Cell **157**, 1117,1129. Preview in Cell; News and Views in NSMB (Jun 4).
14. Hochstrasser ML, Taylor DW, Bhat P, Guegler CK, Sternberg SH, Nogales E, Doudna JA. (2014) CasA mediates Cas3-catalyzed target degradation during CRISPR RNA-guided interference. PNAS **111**, 6618-6623.
15. Jinek, M., Jiang, F., Taylor, D.W., Sternberg, S.H., Kaya, E., Ma, E., Andres, C., Hauer, M., Zhou, K., Lin, S., Kaplan, M., Iavarone, A.T., Charpentier, E., Nogales, E. and Doudna, J.A. (2014) Structures of Cas9 endonucleases reveal RNA-mediated conformational activation. Science **343**, 1247997.
16. Howes, S.C., Alushin, G.M., Shida, T., Nachury, M.V. and Nogales, E. (2014) Effects of tubulin acetylation and tubulin acetyltransferase binding on microtubule structure. Mol Biol Cell, **25**, 257-266.
17. Bleichert F., Balasov M., Chesnokov I., Nogales E., Botchan MR., Berger JM (2013) A Meier-Gorlin syndrome mutation in a conserved C-terminal helix of Orc6 impedes origin recognition complex formation,eLife 2014; 10.7554/eLife.00882.
18. Musinipally, V., Alushin, G.M. and Nogales, E. (2013) The Microtubule Binding Properties of CENP-F and of CENP-E's C-terminus, J Mol Blol. **425**, 4427-4441.
19. Cianfrocco, M.A. and Nogales, E. (2013) Regulatory interplay between TFIID's conformational transitions and its modular interaction with core promoter DNA. Transcription, Transcription **4**,

120-126.

20. Sun, C., Querol-Audi, J., Mortimer, S.A., Arias-Palomo, E., Doudna, J.A., Nogales, E. and Cate, J.H.D. (2013) Two RNA-binding motifs in eIF3 direct HCV IRES-dependent translation. Nucleic Acids Res. 41, 7512-7521.
21. Kassube, S.A., Fang, J., Grob, P., Yakovchuk, P., Goodrich, J.A. and Nogales, E. (2013) Structural insights into transcriptional repression by ncRNAs that bind to Human Pol II. J. Mol. Biol. **425**, 3639-3648.
22. de Val, N., McMurray, M.A, Lam, L.H., Hsiung, C. C.-S., Bertin, A., Nogales, E. and Thorner, J. (2013) Native cysteine residues are dispensable for the structure and function of all five yeast mitotic septins. Proteins **81**, 1964-1979.
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