Curriculum Vitae – Eva Nogales

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EDUCATION AND TRAINING

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

POSITIONS

8/16 – present	**Head**, Bay Area Cryo-EM Facility (BACEM), Berkeley Site
12/15 – present	**Senior Faculty Scientist,** Molecular Biophysics and Integrative Bioimaging Division, LBNL,
09/15 – present	**Head**, 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 – 11/15	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	LBNL Director's Award for Exceptional Science Achievement
2016	Keith Porter Lecture Award, ASCB
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

2017	Russell Marker Lectures, University of Maryland
2017	Benning Lecturer, University of Utah
2017	Ernest C. Pollard Lecture in Biophysics at Penn State University
2017	Katherine D. McCormick Distinguished Lecture at Stanford University
2016	NCI Distinguished Scientist lecture series speaker
2016	James P. Holland Memorial Lecture, Indiana University
2016	Harvey Lecture, New York
2016	Elected Member of the **American Academy of Arts and Sciences**
2015	Elected Member of the **National Academy of Sciences**
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	Dean's Distinguished Lecture, University of Colorado Medical School
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 SOCIETIES, ADVISORY BOARDS, JOURNALS AND CONFERENCE ORGANIZATION

2016 – present	**Member**, International Academic Advisory Committee for the Beijing Innovation Center for Structural Biology at Tsinghua University.
2016 – present	**Member**, External Advisory Board for the NSF-CREST Center for Cellular and Biomolecular Machines at UC Merced.
2016	Ad hoc scientific advisor for the Beckmann Foundation
2016 – present	**Member**, External Advisory Board for CUNY ASRC-SBI
2015 – present	**Member,** Advisory Council for Princeton's Molecular Biology Department
2015 – present	**Member**, Krios Oversight Committee, OHSU
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 (co-chair since 2017).
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
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 3D Electron Microscopy of Macromolecules
1998	Co-organizer of the workshop “Electron crystallography of biological macromolecules”, Granlibakken.

SERVICE IN FEDERAL AGENCIES and INTERNATIONAL REVIEW PANELS

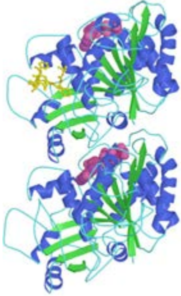
2017	Reviewer for the Villum Fonden, Denmark
2015	NIH special study section panel
2013	CMP study section, ad hoc member
2013	NCSD study section, ad hoc member
2012	MSFC study section, ad hoc member
2005-2009	Macromolecular Structure and Function C Study Section Member

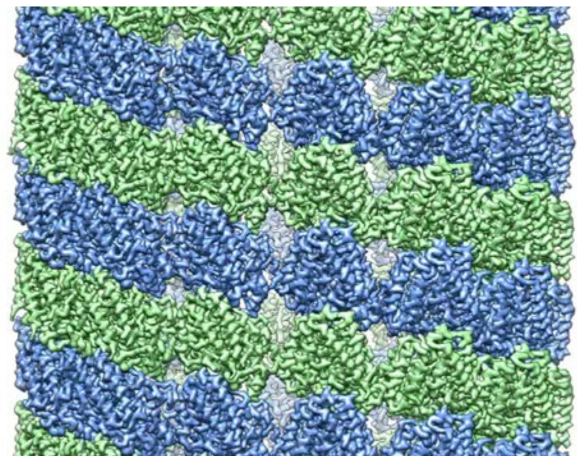
RESEARCH STATEMENT

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

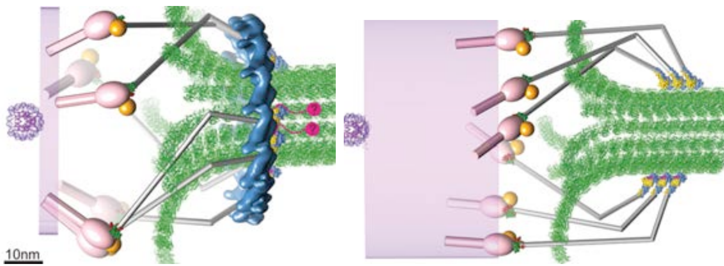
I – Structural Basis of Microtubule Dynamics – We are studying the conformational landscape of tubulin as defined by its nucleotide and assembly states. As a postdoc, I used electron crystallography to produce the first atomic model of tubulin, and established the structural basis of nucleotide exchange, polymerization-coupled hydrolysis, and taxol binding. Later 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. We later 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. These structures 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. More recently we have been able to produced atomic structures of microtubules (~3.5 Å) that illustrate the details of lateral interaction between protofilaments, the mode of binding of the +TIP EB3 and how this protein promote GTP hydrolysis in tubulin.





1. Nogales, E., Wolf, S. G., & Downing, K. H. (1998). Structure of the $\alpha\beta$ 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. Wang, H-W. and Nogales, E. (2005). The nucleotide-dependent bending flexibility of tubulin regulates microtubule assembly, Nature **435**, 911-915.
4. 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 $\alpha\beta$-tubulin upon GTP hydrolysis. Cell **157**, 1117,1129.
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.

II – Interactions of Microtubules with Kinetochore and other Mitotic Proteins- Microtubules dynamics are coupled to the accurate segregation of chromosomes during mitosis via interaction with kinetochores. Our studies of the yeast ***Dam1 kinetochore complex*** showed that it assembles into rings around microtubules that move processively with microtubule ends. We produced the only existing structures of the Dam1 complex and ring around microtubules, defining its subunit organization. We visualized the full-length yeast **Ndc80 complex** and found a dramatic kink at a conserved break in the coiled-coil and proposed its importance 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 and

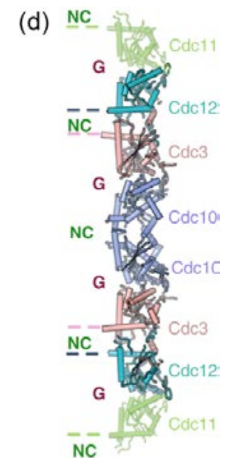


3D models of the budding yeast (left) and vertebrate kinetochore (right)

allows to “probe” the conformational state of the microtubule. Our studies led to a model of how Ndc80’s interaction with MT is tuned by Aurora B phosphorylation of the unstructured N-terminus of Ndc80. 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. In addition to our kinetochore studies we are also interested in the interaction of microtubules with partners important in mitosis. We have recently obtained the structure of the **PRC1** bound to the microtubule. This protein forms antiparallel MT arrays important for setting the spindle midzone and determining the location of the cytokinetic ring. We determined the residues in the spectrin domain of PRC1 contacting the MT and found that PRC1 promotes MT assembly even in the presence of the MT stabilizer taxol. The geometry we visualized, together with molecular dynamic simulations describing the intrinsic flexibility of PRC1, suggests that the MT–spectrin domain interface determines the geometry of the MT arrays cross-linked by PRC1.

1. Westermann, S., Wang, H.-W., Avila-Sakar, A., Drubin, D.G., Nogales, E. and Barnes, G. (2006) The Dam1 kinetochore ring complex moves processively on depolymerizing microtubule ends. Nature **440**, 565-569.
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.
5. Kellogg, E., Howes, S., Ti, S-C., Ramirez-Aportela, E., Kapoor, T., Chacon, P. and Nogales, E. (2016). Near-atomic resolution cryo-EM structure of PRC1 bound to the microtubule. PNAS **113**, 9430-9439.

III – Budding Yeast Septin Assembly and Interactions - We have us ed budding yeast as a model system to explore, both *in vivo* and *in vitro*, essential questions about septin function and the molecular mechanisms that control septin-based cellular structures. We were able to delineate the organization of the yeast septin assembly unit as a rod of Cdc11-Cdc12-Cdc3-Cdc10-Cdc10-Cdc3-Cdc12-Cdc11, and that rods assemble into long filaments via end-on-end interaction of Cdc11 subunits to give rise to apolar filaments. We demonstrated that yeast septins interact specifically with PIP2 and that this interaction results in a distinct filament structure and organization. We demonstrated that the alternative septin Shs1 substitutes for Cdc11, and that Shs1-containing octamers associate laterally into spirals and rings, and that the sporulation specific Spr3 and Spr28 substitute for Cdc12 and Cdc11, respectively. Interestingly, sporulation septins only assemble in vitro in the presence of PIP2-containing membranes. We have also visualized septin organization in the cell using electron tomography and described two sets of orthogonal septin filaments.

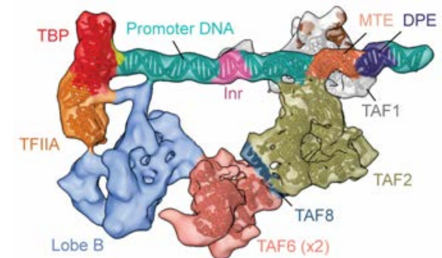


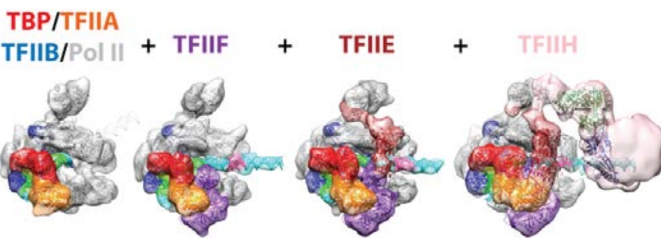
1. Bertin, A., McMurray,M.A., Grob,P., Park, S-S., Garcia, G. III, Patanwala, I., Ng, H-L., Alber, T.C., Thorner, J. and Nogales, E. (2008). Saccharomyces cerevisiae: Supramolecular organization of hetero-oligomers and the mechanism of filament assembly. PNAS **105**, 8274- 8279.

2. Bertin, A., Thai, L., McMurray, M., Garcia, G., Votin, V., Grob, P., Allyn, T., Thorner, J. and Nogales, E. (2010) The phosphoinositide PI(4,5)P2 promotes budding yeast septin filament assembly and organization. J. Mol. Biol. **404**, 711-731.
3. Garcia, G.III, Bertin, A., Li, Z., McMurray, M., Thorner, J. and Nogales, E. (2011). Subunit-dependent modulation of septin assembly: budding yeast septin Shs1 promotes ring and gauze formation. J. Cell Biol. **195**, 993-1004.
4. Bertin, A., MacMurray, M., Pierson, J., Thai, L., MacDonald, K., Zerh, E., Peters, P., Garcia III, G., Thorner, J. and Nogales, E. (2012). Three-dimensional ultrastructure of the septin filament network in Saccharomyces cerevisiae. MBoC **23**, 423-432.
5. Garcia G. III, Finnigan, G.C., Heassley, L.R., Sterling SM, Aggarwal A, Pearson CG, Nogales E, McMurray MA, Thorner (2016). Assembly, molecular organization and membrane-binding properties of developmental-specific septins. J Cell Biol. **212**, 515-29.

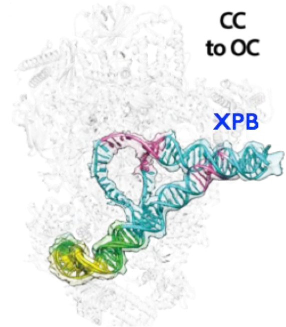
IV – Regulation of Gene Expression

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. Binding of TFIID to the core promoter is the first step. We obtained the first 3-D model of TFIID and showed the existence of significant flexibility within the complex. 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. This has lead us to propose that the dynamic conformational landscape of TFIID may have regulatory consequences. We recently obtained the structure of human TFIID in complex with TFIIA and core promoter DNA at sub-nanometer resolution. We showed that TAF1 and TAF2 mediating major interactions with the downstream promoter and that TFIIA bridges the TBP-TATA complex with lobe B. Superposition of common elements between the two structures provides novel insights into the general role of TFIID in promoter recognition, PIC assembly, and transcription initiation.





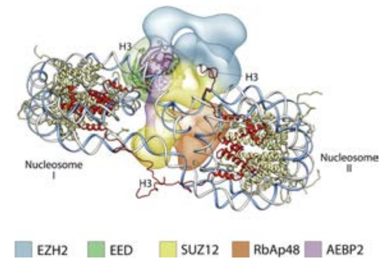
We visualized the stepwise assembly of a human PIC in which TBP substituted for TFIID, and thus defined the relative positions of all the protein components and the DNA. More recently we determined near-atomic resolution structures of the human PIC in a closed state (engaged with duplex DNA), an open state (engaged with a transcription bubble), and an initially transcribing complex (containing six base pairs of DNA-RNA hybrid). Comparison of the different structures has revealed the sequential conformational changes that accompany the transitions from one state to the other throughout the transcription initiation process.



We combined our PIC and TFIID structures by superimposing the common components (TBP, TFIIA and core promoter DNA) to generate a "synthetic" model of the TFIID-based closed PIC (containing nearly 50 polypeptides) (Louder et al., Nature 2016). Overall the two structures fit well with each other, with significant shape complementarity and minimal steric clashes, which are, however, of potential functional relevance.

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. 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.

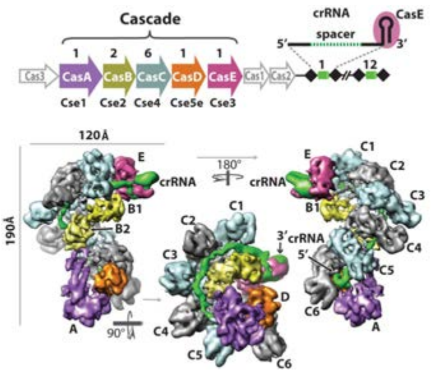


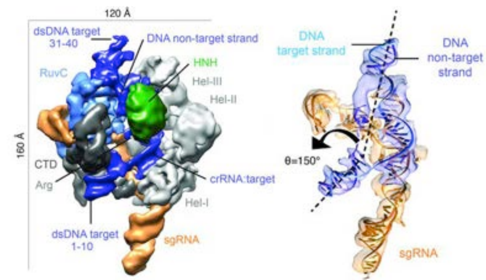
1. Ciferri, C., Lander, G.C., Maiolica, A., Herzog, F., Aebersold, R. and Nogales, E. (2012). Structure of the polycomb represive complex 2 and implications for gene silencing. eLIFE, e00005.
2. Cianfrocco, M.A., Kassevitis, G.A., Grob, P, Fang, J., Juven-Gershon, T., Kadonaga, J.T. and Nogales, E. (2013). Human TFIID binds core promoter DNA in a reorganized structural state. Cell **152**, 120-131.
3. He, Y., Fang, J., Taatjes, D.J., and Nogales, E. (2013) Structural visualization of key steps in human transcription initiation. Nature **495**, 481-486.
4. Louder, R.K., He, Y. Lopez-Blanco, J.R. Fang, J., Chacon, P., and Nogales, E. (2016). Structure of promoter-bound TFIID and insight into human PIC assembly. Nature **531**, 604-609.
5. He, Y., Yan, C., Inouye, C., Tjian, R., Ivanov, I. and Nogales , E. (2016). Near-atomic resolution visualization of human transcription promoter opening. Nature **533**, 359-365.

III – Recent Collaborations of Special Notice

*Proteosome (with Andreas Martin)***.** The proteasome contains a barrel-shaped 20S proteolytic core and a 19S regulatory particle composed of a lid and base subcomplexes that are required for substrate recognition, deubiquitination, unfolding, and translocation. We obtained a subnanometer resolution structure of the budding yeast 26S proteasome, localized each protein, and proposed 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. This work provided 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). 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., Estrin, E., Matyskiela, M.E., Bashore, C., Nogales, E. and Martin, A. (2012) Complete subunit architecture of the proteosome regulatory particle. Nature **482**,186-191.
2. Wiedenheft, B., Lander, G.C., Zhou, K., Jore, M.M., Brouns, S.J.J., van der Oost, J., Doudna, J.A., and Nogales, E. (2011) Structures of the RNA-guided surveillance complex from a bacterial immune system. Nature **477**, 486-489.
3. 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.
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.
5. Jiang, F., Taylor, D.W., Chen, J.S., Kornfeld, J.E., Zhou, K., Thompson, A.W., Nogales, E. and Doudna, J.A. (2016). Structures of a CRISPR-Cas9 R-loop complex primed for DNA cleavage. Science **351**, 867-871.

PUBLICATIONS

1. Howes, S.C., Geyer, E.A., LaFrance, B., Zhang, R., Kellogg, E.H., Westermann, S., Rice, L.M. and Nogales, E. (2017) Structural differences between yeast and mammalian microtubules revealed by cryo-EM. JCB, in press.
2. Jiyung Shin, J., Jiang, F., Liu, J-J., Bray, N.L., Rauch, B.J., Baik, S.H., Nogales, E., Bondy-Denomy, J., Corn, J.E., and Doudna, J.A. Disabling Cas 9 by anti-CRISPR DNA mimic. Science Advances, in press.
3. Nogales, E. and Kellogg, E.H. (2017) Challenges and opportunities in the high-resolution cryo-EM visualization of microtubules and their binding partners. COSB, Epub ahead of print.
4. Nogales, E, Patel, A. and Louder R.K. (2017) Towards a Mechanistic Understanding of Core Promoter Recognition from Cryo-EM Studies of Human TFIID, COSB, Epub ahead of print.
5. Xu, C.S., Hayworth, K.J., Lu, Z., Grob, P., Hassan, A., Garcia Cerdan, J.G., Niyogi, K.K., Nogales, E., Weinberg, R.J. and Hess, H.F. (2017) Enhanced FIB-SEM systems for large-volume 3D imaging. eLife **6**, e25916.
6. Nogales E., Louder R.K. and He Y. (2017) Structural Insights into the Eukaryotic Transcription Initiation Machinery. Ann. Rev. Biophys **46**, 59-83.
7. Kellogg, E., Hejab, N.M.A., Howes, S., Northcote, P, Miller, J.H., Diaz, J.F., Downing, K.H. and Nogales, E. (2017). Insights into the distinct mechanisms of action of taxane and non-taxane microtubule stabilizers from cryo-EM studies. J. Mol. Biol. **429**, 633–646. Cover in that issue.
8. Nogales, E, Fang, J. and Louder R.K. (2017) Structural dynamics and DNA interaction of human TFIID. Transcription **8**, 56-60.
9. Booth, E.A, Sterling, S.M., Dovala, D., Nogales, E. and Thorner, J. (2016) Effects of Bni5 Binding on Septin Filament Organization. J.Mol. Biol. **428**, 4962-4980.
10. Nogales, E. (2016) Dear microtubule, I see you. Mol. Bol. Cell **27**, 3202-3204.
11. Hurley, J.H. and Nogales, E. (2016) Next-generation electron microscopy in autophagy research. Curr. Opin. Struct. Biol. **41**, 211-216.
12. Nogales E., Louder R.K., He Y. (2016) Cryo-EM in the study of challenging systems: the human transcription pre-initiation complex. Curr Opin Struct Biol. **40**, 120-127.
13. Hochstrasser M.L., Taylor D.W., Kornfeld J.E., Nogales E., Doudna J.A. (2016) DNA targeting by a minimal CRISPR RNA-guided Cascade. Mol Cell. 63,840-851.
14. Kellogg, E., Howes, S., Ti, S-C., Ramirez-Aportela, E., Kapoor, T., Chacon, P. and Nogales, E. (2016) Near-atomic resolution cryo-EM structure of PRC1 bound to the microtubule. PNAS 113, 9430-9439.
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