

**Name** David W. Taylor

**Address** Department of Molecular Biosciences  
Center for Systems and Synthetic Biology  
University of Texas at Austin  
NHB 4.121  
100 E. 24th St.  
Austin, TX 78712-1597

Office Phone: 512-471-9156  
Email: dtaylor@utexas.edu

**Website** davidtaylorlab.com

### Positions

2022-present Associate Professor, Department of Molecular Biosciences

2016-2022 Assistant Professor and CPRIT Scholar, Department of Molecular Biosciences,  
The University of Texas at Austin

Faculty, LIVESTRONG Cancer Institutes, Dell Medical School

### Post-doctoral Training

2014–2016 California Institute for Quantitative Biosciences  
University of California, Berkeley  
Title: “Structure and Function of CRISPR RNA-guided surveillance complexes in  
bacteria”  
Advisors: Dr. Eva Nogales and Dr. Jennifer A. Doudna

### Education

2013 Yale University Ph.D., *with distinction*  
Molecular Biophysics and Biochemistry  
Advisor: Dr. Hong-Wei Wang

2010 Yale University M.Phil.  
Molecular Biophysics and Biochemistry

2008 Syracuse University B.S., *summa cum laude*  
Biochemistry

### Undergraduate and Graduate Research Experience

2009–2013 Yale University, Department of Molecular Biophysics and Biochemistry  
Dissertation research  
Title: “Structural basis for RNA processing by human Dicer”  
Advisor: Dr. Hong-Wei Wang

2012 Visiting Student Researcher at California Institute for Quantitative Biosciences,  
University of California, Berkeley  
Advisors: Dr. Jennifer A. Doudna and Dr. Eva Nogales

- 2011 NSF East Asia and Pacific Summer Institute Fellow at National Institute for Physiological Sciences, National Institutes of Natural Sciences, Okazaki, Japan  
Title: “Zernike phase-contrast cryo-EM of human Dicer and virus-like particles”  
Advisors: Dr. Kuniaki Nagayama and Dr. Kazuyoshi Murata
- 2009 Yale University, Department of Genetics  
Title: “Alternative miRNA biogenesis pathways in zebrafish”  
Advisor: Dr. Antonio J. Giraldez
- 2008 Yale University, Department of Molecular Biophysics and Biochemistry  
Title: “Structural basis for copper transport by eukaryotic chaperones”  
Advisor: Dr. Vinzenz M. Unger
- 2005–2008 Syracuse University, Department of Chemistry and Department of Biochemistry  
Title: “Development of nucleic acid sensors for pathogenic agents”  
Advisors: Dr. Bruce S. Hudson and Dr. Phillip N. Borer

### Current Research Interests

Understanding the structural basis for RNA-guided adaptive immunity in prokaryotes and developing high-throughput methods for structural biology using cryo-EM

### Awards and Honors

- 2021 ACS Research Scholar, American Cancer Society**
- 2020 College of Natural Sciences Teaching Excellence Award, UT Austin**
- 2020 Faculty Service Award, Natural Sciences Council, CNS student assembly**
- 2020 Teaching Excellence Award, Department of Molecular Biosciences
- 2019 Army Young Investigator, Army Research Office**
- 2016 CPRIT Scholar in Cancer Research, Cancer Prevention and Research Institute of Texas**
- 2015 Division of Biochemistry, Biophysics, and Structural Biology Outstanding Postdoc Award, University of California, Berkeley
- 2015 Damon Runyon Fellow, Damon Runyon Cancer Research Foundation**
- 2014 Mary Ellen Jones Dissertation Prize, Yale University**
- 2011 NSF East Asia and Pacific Summer Institute (EAPSI) Fellow, National Science Foundation
- 2011 Molecular Biophysics and Biochemistry Excellence in Teaching Award, Yale University
- 2010 Yale Scientific Teaching Fellow, Yale University
- 2010 NSF Predoctoral Fellow, National Science Foundation**
- 2008 Research Achievement and Academic Excellence Award, Syracuse University Biology Department
- 2007 Barry M. Goldwater Scholar, Barry M. Goldwater Foundation**
- 2004 Syracuse University Academic Merit Scholar

### Publications

Citations indices	All	Since 2018	(Google Scholar)
Citations	<b>5601</b>	<b>3289</b>	
h-index	<b>24</b>	<b>23</b>	
i10-index	<b>34</b>	<b>33</b>	

1. McCafferty, C.L., Pennington, E.L., Papoulas, O, Taylor, D.W., Marcotte, E.M. Does AlphaFold2 model proteins' intracellular conformations? An experimental test using cross-linking mass spectrometry of endogenous ciliary proteins. *Communications Biology*, in revision. doi: <https://doi.org/10.1101/2022.08.25.505345>.
2. Roisin E. O'Brien, Jack P.K. Bravo, Delisa Ramos, Grace N. Hibshman, Jacquelyn T.Wright, David W. Taylor. Modes of inhibition used by phage anti-CRISPRs to evade type I-C Cascade. *Mol. Cell*, accepted in principle.
3. Jack P. K. Bravo, Thom Hallmark, Bronson Naegle, Chase L. Beisel, Ryan N. Jackson, David W. Taylor<sup>†</sup>. (2023) RNA targeting unleashes indiscriminate nuclease activity of CRISPR–Cas12a2. *Nature* <https://doi.org/10.1038/s41586-022-05560-w>.  
<sup>†</sup>Corresponding author.
4. Yelland, J.N., Bravo, J.P.K., Black, J.J., Taylor, D.W., Johnson, A.W. (2022) A single 2'-O-methylation of ribosomal RNA gates assembly of a functional ribosome. *Nat. Struct. and Mol. Biol.*, Dec 19. doi: 10.1038/s41594-022-00891-8. Online ahead of print.
5. Caitlyn L. McCafferty, Gabriel Hoogerbrugge, Candice Nichols, Gaia Pigino, David W. Taylor, John B. Wallingford, Edward M.Marcotte. (2022) Integrative modeling reveals the molecular architecture of the Intraflagellar Transport A (IFT-A) complex. *Elife*, Nov 8;11:e81977.
6. Sae-Lee W, McCafferty CL, Verbeke EJ, Havugimana PC, Papoulas O, McWhite CD, Houser JR, Vanuytsel K, Murphy GJ, Drew K, Emili A, Taylor DW, Marcotte EM. (2022) The protein organization of a red blood cell. *Cell Rep.* 40(3): 111103.
7. Bravo JPK, Aparicio-Maldonado C, Nobrega FL, Brouns SJJ, Taylor DW. (2022) Structural basis for broad anti-phage immunity by DISARM. *Nat Commun.* 13(1):2987.
8. Schwartz EA, McBride TM, Bravo JPK, Wrapp D, Fineran PC, Fagerlund RD, Taylor DW. (2022) Structural rearrangements allow nucleic acid discrimination by type I-D Cascade. *Nat Commun.* 13(1):2829.
9. Lucas MJ, Pan HS, Verbeke EJ, Partipilo G, Helfman EC, Kann L, Keitz BK, Taylor DW, Webb LJ. (2022) Cross-Seeding Controls A $\beta$  Fibril Populations and Resulting Functions. *J Phys Chem B.* 126(11):2217-2229.
10. J.P.K. Bravo, M-S. Liu, G.N. Hibshman, T.L. Dangerfield, K. Jung, R.S. McCool, K.A. Johnson, D.W. Taylor. (2022) Structural basis for mismatch surveillance by CRISPR-Cas9. *Nature* 603(7900), 343-347.
11. J.A. Steens, Y. Zhu, D.W. Taylor, J.P.K. Bravo, S.H.P. Prinsen, C.D. Schoen, BJF Keijser, M. Ossendrijver, L.M. Hofstra, S.J.J. Broun, A. Shinkai, J. van der Oost, R.H.J. Staals. (2021) *Nature Communications* 12(1), 5033.
12. C.L. McCafferty, D.W. Taylor<sup>†</sup>, E.M. Marcotte<sup>†</sup>. (2021) Improving integrative 3D modeling into low- to medium- resolution EM structures with evolutionary couplings. *Protein Science* 30(5), 1006-1021. <sup>†</sup>Corresponding authors.

13. M.J. Schepers, J.N. Yelland, N.A. Moran<sup>†</sup>, D.W. Taylor<sup>†</sup>. (2021) Isolation of the *Buchnera aphidicola* flagellum basal body from the *Buchnera* membrane. *PLoS One*, 16(5) e0245710. <sup>†</sup>Corresponding authors.
14. Y. Zhou, J.P.K. Bravo, H.N. Taylor, J. Steens, R.N. Jackson<sup>†</sup>, R.H.J. Staals<sup>†</sup>, D.W. Taylor<sup>†</sup>. (2021). Structure of a type IV CRISPR-Cas effector. *iScience*, 24, 102201. <sup>†</sup>Corresponding authors.
15. J.P.K. Bravo, T.L. Dangerfield, David W. Taylor<sup>†</sup>, K.A. Johnson<sup>†</sup>. (2021) Remdesivir is a delayed translocation inhibitor of SARS CoV-2 replication. *Mol. Cell* 81(7), 1548-1552.e4. <sup>†</sup>Corresponding authors.
16. C.L. McCafferty, E.M. Marcotte<sup>†</sup>, D.W. Taylor<sup>†</sup>. (2021) Simplified geometric representations of protein structures identify complementary interaction interfaces. *Proteins* 89, 348-360. <sup>†</sup>Corresponding authors.
17. R.E. O'Brien, I.C. Santos, D. Wrapp, J.P.K. Bravo, E.A. Schwartz, J.S. Brodbelt, D.W. Taylor<sup>†</sup>. (2020) Structural basis for assembly of non-canonical small subunits into type I-C Cascade. *Nature Communications* 11, 5931. <sup>†</sup>Corresponding author.
18. T.M. McBride, E.A. Schwartz, A. Kumar, D.W. Taylor, P.C. Fineran, R.D. Fagerlund. (2020) Diverse CRISPR-Cas complexes require independent translation of small and large subunits from a single gene. *Mol. Cell* 80, 971-979.
19. M. Liu, S. Gong, H. Yu, K. Jung, K.A. Johnson<sup>†</sup>, D.W. Taylor<sup>†</sup>. (2020) Basis for discrimination by engineered CRISPR/Cas9 enzymes. *Nature Commun.* 11, 3576. <sup>†</sup>Corresponding authors.
20. M.J. Lucas, H.S. Pan, E.J. Verbeke, L.J. Webb<sup>†</sup>, D.W. Taylor<sup>†</sup>, B.K. Keitz<sup>†</sup>. (2020) Functionalized Mesoporous Silicas Direct Structural Polymorphism of Amyloid- $\beta$  Fibrils. *Langmuir* 36, 7345-7355. <sup>†</sup>Corresponding authors.
21. C.L. McCafferty, E.J. Verbeke, E.M. Marcotte, D.W. Taylor. (2020) Structural Biology in the Multi-Omics Era. *J. Chem. Inf. Model.* 60, 2424–2429.
22. E.J. Verbeke, Y. Zhou, A.P. Horton, A.L. Mallam, D.W. Taylor<sup>†</sup>, E.M. Marcotte<sup>†</sup>. (2019) Separating distinct structures of multiple macromolecular assemblies from cryo-EM projections. *J. Struct. Biol.* 209, 107416. <sup>†</sup>Corresponding authors
23. D.W. Taylor<sup>†</sup>. (2019) The final cut: Cas9 editing. *Nat Struct Mol Biol* 26, 669-670.
24. Y. Zhou, S. Musalgaonkar, A.W. Johnson<sup>†</sup>, D.W. Taylor<sup>†</sup>. (2019) Tightly-orchestrated rearrangements govern catalytic center assembly of the ribosome. *Nature Commun.* 10, 958. <sup>†</sup>Corresponding author.
25. A.J. Simon, V. Ramasubramani, J. Glaser, A. Pothukuchy, J. Gerberich, J. Leggere, B.R. Morrow, J. Golihar, C. Jung, S.C. Glotzer, D.W. Taylor<sup>†</sup>, A.D. Ellington<sup>†</sup>. (2019) Supercharging enables organized assembly of synthetic biomolecules. *Nature Chem.* 11, 204-212. <sup>†</sup>Corresponding author.

26. M. Liu\*, S. Gong\*, H.H. Yu\*, D.W. Taylor<sup>†</sup>, K.A. Johnson<sup>†</sup>. (2019) Kinetic characterization of Cas9 enzymes. *Methods Enzymol.* 616, 289-311. <sup>†</sup>Corresponding author.
27. X. Yi\*, E.J. Verbeke\*, Y. Chang\*, Daniel J. Dickinson<sup>†</sup>, D.W. Taylor<sup>†</sup>. (2018) Snapshots of single particles from single cells using electron microscopy. *J. Biol. Chem.* 294, 1602-1608. <sup>†</sup>Corresponding author.
28. E.J. Verbeke, A.L. Mallam, K. Drew, E.M. Marcotte<sup>†</sup>, D.W. Taylor<sup>†</sup>. (2018) Classification of single particles from human cell extract reveals distinct structures. *Cell Reports* 24, 259-268. <sup>†</sup>Corresponding author.
29. H. Lee, Y. Zhou, D.W. Taylor, D.G. Sashital. (2018) Cas4-dependent prespacer processing ensures high-fidelity programming of CRISPR arrays. *Mol. Cell* 70, 48-49.
30. S. Gong, H.H. Yu, K.A. Johnson<sup>†</sup>, D.W. Taylor<sup>†</sup>. (2018) DNA unwinding is the primary determinant of CRISPR-Cas9 activity. *Cell Reports* 22, 359–371. <sup>†</sup>Corresponding author.
31. M.L. Hochstrasser\*, D.W. Taylor<sup>\*†</sup>, J.E. Kornfeld\*, E. Nogales, J.A. Doudna<sup>†</sup>. (2016) Structure and assembly of a minimal CRISPR-Cascade. *Mol. Cell* 63, 840-851. \*These authors contributed equally to this work. <sup>†</sup>Corresponding author.
32. W.S.V. Kip, H. Shigematsu, D.W. Taylor, S.J. Baserga (2016) Box C/D sRNA stem ends act as stabilizing anchors for box C/D di-sRNPs. *Nucleic Acids Res.* Epub 24 June 2016.
33. F. Jiang\*, D.W. Taylor<sup>\*</sup>, J.S. Chen, J.E. Kornfeld, K. Zhou, A.J. Thompson, E. Nogales, J.A. Doudna. (2016) Structures of a CRISPR-Cas9 R-loop complex primed for DNA cleavage. *Science* 351, 867-871. \*These authors contributed equally to this work.
34. N. Miyazaki\*, D.W. Taylor<sup>\*</sup>, G.S. Hansman, K. Murata. (2016). Antigenic and cryo-electron microscopy structure analysis of a chimeric sapovirus capsid *J. Virol.* 90, 2664-2675. \*These authors contributed equally to this work.
35. R.J. Tomko Jr., D.W. Taylor, Z.A. Chen, H.W. Wang, J. Rappsilber, M. Hochstrasser. (2015) A single  $\alpha$ -helix drives extensive remodeling of the proteasomal lid and completion of regulatory particle assembly. *Cell* 163, 432-444.
36. D.W. Taylor<sup>\*</sup>, Y. Zhu\*, R.H.J. Staals, J.E. Kornfeld, A. Shinkai, J. van der Oost, E. Nogales, J.A. Doudna. (2015) Structures of the CRISPR-Cmr complex reveal mode of RNA target positioning. *Science* 348, 581-585. \*These authors contributed equally to this work.
37. A.V. Wright\*, S.H. Sternberg\*, D.W. Taylor, B.T. Staahl, J.A. Bardales, J.E. Kornfeld, J.A. Doudna. (2015) Rational design of a split-Cas9 enzyme complex. *Proc. Nat. Acad. Sci.* 112, 2984-2989. \*These authors contributed equally to this work.

38. R.H.J. Staals\*, Y. Zhu\*, D.W. Taylor\*, J.E. Kornfeld, K. Sharma, A. Barendregt, J.J. Koehorst, M. Vlot, N. Neupane, K. Varossieau, K. Sakamoto, T. Suzuki, N. Dohmae, S. Yokoyama, P.J. Schaap, H. Urlaub, A.J.R. Heck, E. Nogales, J.A. Doudna, A. Shinkai, J. van der Oost. (2014) RNA Targeting by the Type III-A CRISPR-Cas Csm Complex of *Thermus thermophilus*. *Mol. Cell* 56, 518-530. \*These authors contributed equally to this work.
39. M.L. Hochstrasser\*, D.W. Taylor\*, P. Bhat, C.K. Guegler, S.H. Sternberg, E. Nogales, J.A. Doudna. (2014) CasA mediates Cas3-catalyzed target degradation during CRISPR RNA-guided interference. *Proc. Nat. Acad. Sci.* 111, 6618–6623. \*These authors contributed equally to this work.
40. M. Jinek\*, F. Jiang\*, D.W. Taylor\*, S.H. Sternberg\*, E. Kaya, S.H. Sternberg, E. Ma, C. Anders, M. Hauer, K. Zhou, S. Lin, M. Kaplan, A.T. Iavarone, E. Charpentier, E. Nogales, J.A. Doudna. (2014) Structures of Cas9 Endonucleases Reveal RNA-Mediated Conformational Activation. *Science* 343, 1247997. \*These authors contributed equally to this work.
41. R.H.J. Staals\*, Y. Agari\*, S. Maki-Yonekura\*, Y. Zhu, D.W. Taylor, E. van Duijn, A. Barendregt, M. Vlot, J.J. Koehorst, K. Sakamoto, A. Masuda, N. Dohmae, P.J. Schaap, J.A. Doudna, A.J.R. Heck, K. Yonekura, J. van der Oost, A. Shinkai. (2013) Structure and activity of an RNA-targeting Type III-B CRISPR-Cas complex in *Thermus thermophilus*. *Mol. Cell* 52, 135-145. \*These authors contributed equally to this work.
42. S.L. Wolin, C. Belair, X. Chen, S. Sim, D.W. Taylor, H.W. Wang. (2013) Noncoding Y RNAs as Tethers and Gates: Insights from Bacteria. *RNA Biol.* 10, 1602-1608.
43. D.W. Taylor\*, E. Ma\*, H. Shigematsu\*, M.A. Cianfrocco, C.N. Noland, K. Nagayama, E. Nogales, J.A. Doudna, H.W. Wang. (2013) Substrate-specific structural rearrangements of human Dicer. *Nat. Struct. Mol. Biol.* 20, 662-670. \*These authors contributed equally to this work.
44. X. Chen, D.W. Taylor, C.C. Fowler, J.E. Galan, H.W. Wang, S.L. Wolin. (2013) An RNA degradation machine sculpted by Ro autoantigen and noncoding RNA. *Cell* 153, 166-177.
45. K.R. Bower-Phipps, D.W. Taylor, H.W. Wang, S.J. Baserga. (2012) The box C/D sRNP dimeric architecture is conserved across domain Archaea. *RNA* 18, 1553-1562.
46. G.S. Hansman, D.W. Taylor, J.S. McLellan, T.J. Smith, I. Georgiev, J.R.H. Tame, S.Y. Park, M. Yamazaki, F. Gondaira, M. Miki, K. Katayama, K. Murata, P.D. Kwong. (2012) Structural basis for broad detection of genogroup II noroviruses by a monoclonal antibody that binds to a site occluded in the viral particle. *J. Virol.* 86, 3635-3646.
47. M.F. Roberts, D.W. Taylor, V.M. Unger. (2011) Two modes of interaction between the membrane-embedded TARP stargazin's C-terminal domain and the bilayer visualized by electron crystallography. *J. Struct. Biol.* 174, 542-551.

48. D. Cifuentes, H. Xue, D.W. Taylor, H. Patnode, Y. Mishima, S. Cheloufi, E. Ma, S. Mane, G.J. Hannon, N.D. Lawson, S.A. Wolfe, A.J. Giraldez. (2010) A novel miRNA processing pathway independent of Dicer requires Argonaute2 catalytic activity. *Science* 328, 1694-1698.
49. H.W. Wang, C. Noland\*, B. Siridechadilok\*, D.W. Taylor\*, E. Ma, K. Felderer, J.A. Doudna, E. Nogales. (2009) Structural insights into RNA processing by the human RISC-loading complex. *Nat. Struct. Mol. Biol.* 16, 1148-1153. \*These authors contributed equally to this work.

## Patents

“Structure-Guided Methods of Cas9-Mediated Genome Engineering,” U.S. Patent No. 9,963,689

## Talks, Workshops, and Conferences

- 2021 Invited talk at Oklahoma State University, June 2021
- 2021 Invited talk at University of Virginia, June 2021
- 2021 Invited talk at University of Maryland, February 2021
- 2020 Invited talk at Biophysical Society Annual Meeting, San Diego, CA, February 15, 2020.  
Invited talk at Cornell University, Ithaca, NY, postponed due to COVID.  
Invited talk at Oklahoma State University, Oklahoma, NB, postponed due to COVID.
- 2019 Invited talk at Bayer Pharmaceuticals, Austin, TX. July 10, 2019.  
Invited talk at CRISPR 2019, Quebec, Canada. June 16, 2019.  
Invited talk at Emory University, Atlanta, GA. March 3, 2019.  
Invited Talk at American Chemical Society National Meeting, Boston, MA. August 19, 2018.
- 2018 Invited talk, Mechanisms of CRISPR-Cas9, Emerging Science, National Academies of Science, Washington, D.C., January 2018  
Invited talk, Mechanisms of CRISPR-Cas9, Continuing education course, Society of Toxicology, San Antonio, March 2018
- 2017 Invited talk, Cryo-EM for structure determination, DNA23, Austin, TX, September 2017  
Invited talk, Hierarchical assembly of CRISPR-Cas complexes and biological materials, Foundations of Nanoscience, Snowbird, Utah, April 2017.  
Invited talk, Structures of CRISPR-Cas surveillance complexes, Texas A&M, F.A. Cotton Award Symposium, April 28, 2017.
- 2016 Invited talk, R-loop formation by CRISPR-Cas surveillance complexes, Trinity University, October 2016.  
Structures of a minimal CRISPR-Cascade, poster at 3D EM Gordon Conference in Hong Kong, June 2016.  
Structures of a minimal CRISPR-Cascade, poster at CRISPR conference in Tel Aviv, Israel, May 2016.
- 2015 Student invited talk at Tufts University, Boston, MA, October 2015.

Structures of RNA-guided CRISPR-Cas surveillance complexes, invited talk at Bay Area Cryo-EM meeting at UCSF, June 2015.

Structures of the CRISPR-Cmr complex reveal mode of target positioning, poster at CRISPR conference in New York City, NY, June 2015.

2014 Structures of the CRISPR-Cmr complex reveal mode of target positioning, invited talk at UC, Berkeley Biophysics Retreat at Marconi Conference Center, October 2014.

RNA-induced structural activation of the RNA-guided endonuclease Cas9, invited talk at Beijing area cryo-EM meeting at Tsinghua University in Beijing, China, January 2014

## Teaching Experience and Career Development

- F2022          Structure and Function of Molecular Machines (BCH 339M) at UT Austin  
CES score: 4.8 (out of 5)  
Science of Monsters (NSC 110H) at University of Texas at Austin  
CES score: 4.8 (out of 5)
- F2021          Physical Methods of Biochemistry (BCH 370) at University of Texas at Austin  
CIS score: 4.9 (out of 5.0)  
Science of Monsters (NSC 110H) at University of Texas at Austin  
CIS score: 4.8 (out of 5)
- S2020          Science of Monsters (NSC 110H) at University of Texas at Austin  
CIS score: 5.0 (out of 5.0)
- F2019          Physical Methods in Biochemistry (BCH 370) at University of Texas at Austin  
CIS score: 5.0 (out of 5.0)  
CRISPR: Science or Science Fiction? (NSC 110H) at University of Texas at Austin  
CIS score: 5.0 (out of 5.0)
- F2018          Physical Methods in Biochemistry (BCH 370) at University of Texas at Austin  
CIS score: 4.9 (out of 5.0)
- F2017          Physical Methods in Biochemistry (BCH 370) at University of Texas at Austin  
CIS score: 4.9 (out of 5.0)
- 2009–2010    Theory and Practice of Scientific Teaching I and II (with Dr. Jo Handelsman)
- 2008–2009    Fundamentals of Teaching Science Course at Yale University

## Mentoring

### Current:

- 1 Lab manager: Helen Chen, Ph.D.
- 2 Postdoctoral fellows: Jack P.K. Bravo, Ph.D., Isabel Strohkendl, Ph.D.
- 4 Graduate students: Evan Schwartz, Roisin O'Brien, Caitie McCafferty, Jamie Yelland
- 2 Research technicians: Delisa Ramos and Catherine Moy

1 Undergraduate student: Shashwat Limbasia

Former:

Postdoctoral fellows

Yi Zhou, Ph.D (2016-2018), currently Scientist (cryo-EM Director) at Regeneron Pharmaceuticals, NY, NY

Shanzhong Gong, Ph.D. (2016-2018), currently Scientist I at Tango Therapeutics, Boston, MA

Mu-Sen Liu, Ph.D. (2018-2020), currently Lead Discovery (Structural Biology) at Rheos Medicines, Cambridge, MA

Zhongwu Zhou, Ph.D. (2019-2021), currently EM director, UMass, MA

Graduate Students

Eric Verbeke, Ph.D. (2016-2021), currently postdoctoral fellow at Princeton University, NJ

Matthew Schepers, M.A. (2016-2020), currently at Beckman Coulter

**Service and Community Outreach**

**2022-present Vice Chair, University General Faculty Standing Committee on Educational Policy**

**2022 Co-chair, Dean's Task Force on Graduate Student Mentoring, College of Natural Sciences**

2021-2022 Member, University General Faculty Standing Committee on Educational Policy

2020-present Member, Interdisciplinary Life Sciences (ILS) Executive Committee, UT Austin

**2019-present Advisor, Biochemistry Graduate Program**

2019-present Member, Diversity and Inclusion Committee, Department of Molecular Biosciences

2018-2019 Member, Biochemistry Undergraduate Curriculum Redesign Committee, College of Natural Sciences

2019-2020 Member, ILS Seminar Committee, UT Austin

**2019-2020 Co-Chair, Provost's Task Force for Student Feedback, UT Austin**

2018-2020 Member, University General Faculty Standing Committee on Educational Policy

**2018-2019 Chair, University General Faculty Standing Committee on Responsibilities, Rights, and Welfare of Graduate Student Academic Employees Committee**

**Current Research Support**

American Cancer Society (RSG-21-050-01-DMC) Structures of human DNA repair complexes; Total costs \$795,000; 2021-2025.

NIH R35 1R35GM138348-01, NIGMS (2020-2025; \$1,250,000). Imaging macromolecular machines in gene regulation.

Medical Research Grant, Robert J. Kleberg, and Helen C. Kleberg Foundation (2019-2022; \$673,828). Structure and Function of CRISPR/Cas9 enzymes.

Welch Research Grant, Welch Foundation (2020-2023; \$240,000). F-1938-20170325.

Cancer Prevention and Research Institute of Texas, CPRIT Scholar in Cancer Research (2016-2020; \$2,000,000). RR160088. This CPRIT award is for Recruitment of First-Time, Tenure-Track Faculty Members and takes the place of university start-up funds

### **Completed Research Support**

Army Young Investigator Award, Army Research Office (2019-2022; \$2,749,981). W911NF-19-1-0021. Harnessing the architecture of natural biological modules for templated assembly

Research Grant, Army Research Office (2018-2022; \$429,175). W911NF-15-0120. Design of protein biomaterials through tailored shape and packing strategies of patchy particles (co-PI).

Welch Research Grant, Welch Foundation (2017-2020; \$195,000). F-1938-20170325.

Damon Runyon Cancer Research Foundation, Damon Runyon Fellow (2014-2018; \$208,000). DRG-2218-15.

National Science Foundation, East Asia and Pacific Summer Institute Fellow (2011; \$5,000). This NSF award allowed for summer research in Japan.

National Science Foundation, Graduate Research Fellow (2010-2012; \$138,000).

Barry M. Goldwater Foundation, Goldwater Scholar (2007-2008; \$7,500).