

Name David W. Taylor
Born: February 28, 1986 in Hershey, PA

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Center for Systems and Synthetic Biology
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Positions

2022- 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 Molecular Biophysics and Biochemistry Advisor: Dr. Hong-Wei Wang	Ph.D., <i>with distinction</i>
2010	Yale University Molecular Biophysics and Biochemistry	M.Phil.
2008	Syracuse University Biochemistry	B.S., <i>summa cum laude</i>

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

- 2024 Marvin L. Hackert Professorship in Structural Biology Fellow, UT Austin**
- 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**
- 2007 Barry M. Goldwater Scholar, Barry M. Goldwater Foundation**

Publications

Citations indices	All	Since 2020	(Google Scholar)
Citations	7825	4269	
h-index	31	30	
i10-index	49	46	

1. G.N. Hibshman, D.W. Taylor[†]. Structural basis for a dual-function type II-B CRISPR-Cas9. *Nucleic Acids Research*, in press.
2. K.A. Kiernan, and D.W. Taylor[†]. Visualization of a multi-turnover Cas9 after product release. *Nat Commun.*, in press.
3. G.N. Hibshman, D.W. Taylor. Visualizing the conformational landscape of CRISPR-Cas9 through kinetics-informed structural studies. *Methods Enzymol.* 2025; 712:41-53.
4. S. Musalgaonkar, J.N. Yelland, R. Chitale, S. Rao, H. Ozadam, D.W. Taylor, C. Cenik, Johnson AW. The assembly factor Reh1 is released from the ribosome during its initial round of translation. *Nat Commun.* 2025 Feb 3;16(1):1278.
5. R.F. Ocampo, J.P.K. Bravo, T.L. Dangerfiel, I. Necedal, S.A. Jirde, L.M. Alexander, N.C. Thomas, A. Das, S. Nielson, K.A. Johnson, C.T. Brown, C.N. Butterfield, D.S.A. Goltsman, D.W. Taylor[†]. DNA targeting by compact Cas9d and its resurrected ancestor. *Nat Commun.* 2025 Jan 7;16(1):457.
6. D. Degtev., J.P.K. Bravo., Emmanouilidi, A. et al. Engineered PsCas9 enables therapeutic genome editing in mouse liver with lipid nanoparticles. *Nat Commun* 15, 9173 (2024).
7. C.L. McCafferty CL, Papoulas O, Lee C, Bui KH, Taylor DW, Marcotte EM, Wallingford JB. An amino acid-resolution interactome for motile cilia identifies the structure and function of ciliopathy protein complexes. *Dev Cell.* 2024 Dec 12:S1534-5807(24)00719-6.
8. I. Strohkendl, A. Saha, C. C Moy, A.H. Nguyen, M. Ahsan, G. Palermo, R. Russell, D.W. Taylor[†]. Cas12a domain flexibility guides R-loop formation and forces RuvC resetting. *Mol Cell.* 2024 Jul 25;84(14):2717-2731.e6. doi: 10.1016/j.molcel.2024.06.007. Epub 2024 Jul 1.
9. G.N. Hibshman, J.P.K. Bravo, H. Zhang, T.L. Dangerfield, I.J. Finkelstein, K.A. Johnson, D.W. Taylor[†]. Unraveling the mechanisms of PAMless DNA interrogation by SpRY-Cas9. *Nat Commun.* 2024 Apr 30;15(1):3663. doi: 10.1038/s41467-024-47830-3.
10. E.A. Schwartz, J.P.K. Bravo, L.A. Macias, C.L. McCafferty, T.L. Dangerfield, J. N. Walker, J.S. Brodbelt, P.C. Fineran, R.D. Fagerlund, D.W. Taylor. RNA targeting and cleavage by the type III-Dv CRISPR effector complex. *Nat Commun.* 2024 Apr 18;15(1):3324. doi: 10.1038/s41467-024-47506-y.
11. J.P.K. Bravo, D.A. Ramos, R.F. Ocampo, C. Ingram, D.W. Taylor. (2024) Plasmid targeting and destruction by the DdmDE bacterial defence system. *Nature* 2024 Epub 2024 13 May.
12. J.A. Steens, J.P.K. Bravo, C.R.P. Salazar, C. Yildiz, A.M. Amieiro, S. Köstlbacher, S.H.P. Prinsen, A.S. Andres, C. Patinios A. Bardis, A. Barendregt, R.A. Scheltema, T.J.G. Ettema, J. van der Oost, D.W. Taylor, R.H.J. Staals. (2024) *Science* 2;383(6682):512-519.
13. D.W. Taylor. Structural biology of an organ. *Cell Reports* 42, 112622
14. C.L. McCafferty, E.L. Pennington, O. Papoulas, D.W. Taylor, E.M. Marcotte. Does AlphaFold2 model proteins' intracellular conformations? An experimental test using cross-linking mass spectrometry of endogenous ciliary proteins. *Commun Biol.* 2023 6, 421.
15. R.E. O'Brien, J.P.K. Bravo, D. Ramos, G.N. Hibshman, J.T. Wright, D.W. Taylor. Snapshots of R-loop formation by type I-C Cascade. *Mol. Cell* 83(5):746-758.e5.

16. J.P. K. Bravo, T. Hallmark, B. Naegle, C.L. Beisel, R.N. Jackson, D.W. Taylor[†]. (2023) RNA targeting unleashes indiscriminate nuclease activity of CRISPR–Cas12a2. *Nature* 613, 582–587. [†]Corresponding author.
17. J.N. Yelland, J.P.K. Bravo, J.J. Black, D.W. Taylor, A.W. Johnson (2022) A single 2'-O-methylation of ribosomal RNA gates assembly of a functional ribosome. *Nat. Struct. and Mol. Biol.* 30, 91-98.
18. CL. McCafferty, G. Hoogerbrugge, C.Nichols, G. Pigino, D.W. Taylor, J.B. Wallingford, E.M. Marcotte. (2022) Integrative modeling reveals the molecular architecture of the Intraflagellar Transport A (IFT-A) complex. *Elife*, Nov 8;11:e81977.
19. W. Sae-Lee, C.L. McCafferty, E.J. Verbeke, P.C. Havugimana, O. Papoulas, C.D. McWhite, J.R. Houser, K. Vanuytsel, G.J. Murphy, K. Drew, A. Emili, D.W. Taylor, Marcotte EM. (2022) The protein organization of a red blood cell. *Cell Rep.* 40(3): 111103.
20. J.P.K. Bravo, C. Aparicio-Maldonado, F.L Nobrega, S.J.J. Brouns, D.W. Taylor. (2022) Structural basis for broad anti-phage immunity by DISARM. *Nat Commun.*13(1):2987.
21. E.A. Schwartz, T.M. McBride, J.P.K. Bravo, D. Wrapp, P.C. Fineran, R.D. Fagerlund, D.W. Taylor. (2022) Structural rearrangements allow nucleic acid discrimination by type I-D Cascade. *Nat Commun.* 13(1):2829.
22. M.J. Lucas, H.S. Pan, E.J. Verbeke, G. Partipilo, E.C. Helfman, L. Kann, B.K. Keitz, D.W. Taylor, Webb LJ. (2022) Cross-Seeding Controls A β Fibril Populations and Resulting Functions. *J Phys Chem B.* 126(11):2217-2229.
23. 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.
24. 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.
25. C.L. McCafferty, D.W. Taylor[†], E.M. Marcotte[†]. (2021) Improving integrative 3D modeling into low-to medium- resolution EM structures with evolutionary couplings. *Protein Science* 30(5), 1006-1021. [†]Corresponding authors.
26. M.J. Schepers, J.N. Yelland, N.A. Moran[†], D.W. Taylor[†]. (2021) Isolation of the Buchnera aphidicola flagellum basal body from the Buchnera membrane. *PLoS One*, 16(5) e0245710. [†]Corresponding authors.
27. Y. Zhou, J.P.K. Bravo, H.N. Taylor, J. Steens, R.N. Jackson[†], R.H.J. Staals[†], D.W. Taylor[†]. (2021). Structure of a type IV CRISPR-Cas effector. *iScience*, 24, 102201. [†]Corresponding authors.
28. J.P.K. Bravo, T.L. Dangerfield, David W. Taylor[†], K.A. Johnson[†]. (2021) Remdesivir is a delayed translocation inhibitor of SARS CoV-2 replication. *Mol. Cell* 81(7), 1548-1552.e4. [†]Corresponding authors.

29. C.L. McCafferty, E.M. Marcotte[†], D.W. Taylor[†]. (2021) Simplified geometric representations of protein structures identify complementary interaction interfaces. *Proteins* 89, 348-360. [†]Corresponding authors.
30. R.E. O'Brien, I.C. Santos, D. Wrapp, J.P.K. Bravo, E.A. Schwartz, J.S. Brodbelt, D.W. Taylor[†]. (2020) Structural basis for assembly of non-canonical small subunits into type I-C Cascade. *Nature Communications* 11, 5931. [†]Corresponding author.
31. 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.
32. M. Liu, S. Gong, H. Yu, K. Jung, K.A. Johnson[†], D.W. Taylor[†]. (2020) Basis for discrimination by engineered CRISPR/Cas9 enzymes. *Nature Commun.* 11, 3576. [†]Corresponding authors.
33. M.J. Lucas, H.S. Pan, E.J. Verbeke, L.J. Webb[†], D.W. Taylor[†], B.K. Keitz[†]. (2020) Functionalized Mesoporous Silicas Direct Structural Polymorphism of Amyloid- β Fibrils. *Langmuir* 36, 7345-7355. [†]Corresponding authors.
34. 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.
35. E.J. Verbeke, Y. Zhou, A.P. Horton, A.L. Mallam, D.W. Taylor[†], E.M. Marcotte[†]. (2019) Separating distinct structures of multiple macromolecular assemblies from cryo-EM projections. *J. Struct. Biol.* 209, 107416. [†]Corresponding authors
36. D.W. Taylor[†]. (2019) The final cut: Cas9 editing. *Nat Struct Mol Biol* 26, 669-670.
37. Y. Zhou, S. Musalgaonkar, A.W. Johnson[†], D.W. Taylor[†]. (2019) Tightly-orchestrated rearrangements govern catalytic center assembly of the ribosome. *Nature Commun.* 10, 958. [†]Corresponding author.
38. 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[†], A.D. Ellington[†]. (2019) Supercharging enables organized assembly of synthetic biomolecules. *Nature Chem.* 11, 204-212. [†]Corresponding author.
39. M. Liu*, S. Gong*, H.H. Yu*, D.W. Taylor[†], K.A. Johnson[†]. (2019) Kinetic characterization of Cas9 enzymes. *Methods Enzymol.* 616, 289-311. [†]Corresponding author.
40. X. Yi*, E.J. Verbeke*, Y. Chang*, Daniel J. Dickinson[†], D.W. Taylor[†]. (2018) Snapshots of single particles from single cells using electron microscopy. *J. Biol. Chem.* 294, 1602-1608. [†]Corresponding author.
41. E.J. Verbeke, A.L. Mallam, K. Drew, E.M. Marcotte[†], D.W. Taylor[†]. (2018) Classification of single particles from human cell extract reveals distinct structures. *Cell Reports* 24, 259-268. [†]Corresponding author.

42. 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.
43. S. Gong, H.H. Yu, K.A. Johnson[†], D.W. Taylor[†]. (2018) DNA unwinding is the primary determinant of CRISPR-Cas9 activity. *Cell Reports* 22, 359–371. [†]Corresponding author.
44. M.L. Hochstrasser*, D.W. Taylor*[†], J.E. Kornfeld*, E. Nogales, J.A. Doudna[†]. (2016) Structure and assembly of a minimal CRISPR-Cascade. *Mol. Cell* 63, 840-851. *These authors contributed equally to this work. [†]Corresponding author.
45. 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.
46. F. Jiang*, D.W. Taylor*, 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.
47. N. Miyazaki*, D.W. Taylor*, 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.
48. R.J. Tomko Jr., D.W. Taylor, Z.A. Chen, H.W. Wang, J. Rappsilber, M. Hochstrasser. (2015) A single α -helix drives extensive remodeling of the proteasomal lid and completion of regulatory particle assembly. *Cell* 163, 432-444.
49. D.W. Taylor*, 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.
50. 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.
51. 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.
52. 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.
53. 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.

54. 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.
55. 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.
56. 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.
57. 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.
58. 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.
59. 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.
60. 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.
61. 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.
62. 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

- 2024 Invited talk at University of Florida, October 2024
Invited talk at Biophysical Society Special Meeting, Trieste, Italy, October 2024
Invited talk at University of California, Berkeley, June 2024
- 2023 Invited Talk at Oklahoma State University, July 2023
Invited talk at University of Wisconsin Madison, April 2023
- 2023 Invited talk at Penn State University, April 2023
- 2023 Invited talk at Cornell University, March 2023
- 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.
- 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 2
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.

Teaching Experience and Career Development

- F2024 Structure and Function of Molecular Machines (BCH 339M) at UT Austin
CES score: 4.85 (out of 5)
- F2023 Structure and Function of Molecular Machines (BCH 339M) at UT Austin
CES score: 4.93 (out of 5)

F2022	Structure and Function of Molecular Machines (BCH 339M) at UT Austin CES score: 4.77 (out of 5) Science of Monsters (NSC 110H) at University of Texas at Austin CES score: 4.82 (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

National

2024	Electron microscopy session co-chair, American Crystallographic Society Annual Meeting
2024	Ad hoc member, NIH Study Section ZRG1 F04B-S
2023	Electron microscopy session co-chair, American Crystallographic Society Annual Meeting
2022-present	Review Committee, American Cancer Society Research Grants
2021-present	Scientific Advisory Board, Cell Reports Methods
2022	Ad hoc member, NIH Study Section MSFC
2017-present	Review committee, Brookhaven National Laboratory, Laboratory for Biomolecular Structure

University

2023	Member, Dean of the Graduate School and Senior Vice Provost for Graduate and Postdoctoral Studies Search Committee
2023-present	Chair, Biochemistry Graduate Studies Committee
2023-present	Chair, University General Faculty Standing Committee on Educational Policy
2022-2023	Vice Chair, University General Faculty Standing Committee on Educational Policy
2021-2022	Member, University General Faculty Standing Committee on Educational Policy
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
2020-present	Member, Interdisciplinary Life Sciences (ILS) Executive Committee, UT Austin
2019-2022	Advisor, Biochemistry Graduate Studies
2018-2019	Member, Biochemistry Undergraduate Curriculum Redesign Committee, College of Natural Sciences

College

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

2019-2023	Member, Diversity and Inclusion Committee, Department of Molecular Biosciences
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Current Research Support

American Cancer Society (2021-2024; \$795,000 Total direct costs listed for each). Structures of human DNA repair complexes.

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 (2022-2025; \$400,000). Structure and Function of CRISPR/Cas9 enzymes.

Welch Research Grant, Welch Foundation (2023-2026; \$300,000). F-1938-20170325.

Typewriter Therapeutics, Inc. (2022-2024; \$376,000) Structural and kinetic basis to understand the reactions catalyzed novel enzyme.

Metagenomi, Inc. (2023-2025; \$532,718). Structures of compact nucleases.

Tito's Handmake Vodka (2023-2026; \$1,000,000. RNA diagnostics and therapeut

