Stanford

Rahel Woldeyes

Basic Life Research Scientist

Bioengineering

Bio

BIO

The goal of my current research is to use high-resolution imaging techniques to interrogate outstanding questions in cardiac cell biology, with a focus on the signaling pathways that trigger heart muscle contraction. I currently use cryo-electron tomography-based imaging approaches to connect the molecular and cellular scales of biology and accelerate our understanding of human health and disease.

ACADEMIC APPOINTMENTS

- Basic Life Science Research Associate, Bioengineering

HONORS AND AWARDS

- K99/R00 MOSAIC Scholar, NIH/NHLBI (12/2021-current)
- Cardiovascular Imaging T-32 Fellowship, Stanford CVI-NIH/NIBIB (09/2019-11/2021)
- NSF GRFP Fellow, NSF/Graduate Research Fellowship Program (03/2013-12/2017)

Publications

PUBLICATIONS

- **Cryo-electron tomography reveals the structural diversity of cardiac proteins in their cellular context.** *bioRxiv : the preprint server for biology*
  Woldeyes, R. A., Nishiga, M., Vander Roest, A. S., Engel, L., Giri, P., Montenegro, G. C., Wu, A. C., Dunn, A. R., Spudich, J. A., Bernstein, D., Schmid, M. F., Wu, J. C., Chiu, et al
  2023

- **Altered Cardiac Energetics and Mitochondrial Dysfunction in Hypertrophic Cardiomyopathy.** *Circulation*
  Ranjbarvaziri, S., Kooiker, K. B., Ellenberger, M., Fajardo, G., Zhao, M., Vander Roest, A. S., Woldeyes, R. A., Koyano, T. T., Fong, R., Ma, N., Tian, L., Traber, G. M., Chan, et al
  2021

- **Comparing serial X-ray crystallography and microcrystal electron diffraction (MicroED) as methods for routine structure determination from small macromolecular crystals.** *IUCrJ*
  Wolff, A. M., Young, I. D., Sierra, R. G., Brewster, A. S., Martynowycz, M. W., Nango, E., Sugahara, M., Nakane, T., Ito, K., Aquila, A., Bhowmick, A., Biel, J. T., Carbajo, et al
  2020; 7 (Pt 2): 306–23

- **XFEL structures of the influenza M2 proton channel: Room temperature water networks and insights into proton conduction** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Thomaston, J. L., Woldeyes, R. A., Nakane, T., Yamashita, A., Tanaka, T., Koiwai, K., Brewster, A. S., Barad, B. A., Chen, Y., Lemmin, T., Uervirojnangkoorn, M., Arima, T., Kobayashi, et al
  2017; 114 (51): 13357–62

- **CryptoSite: Expanding the Druggable Proteome by Characterization and Prediction of Cryptic Binding Sites** *JOURNAL OF MOLECULAR BIOLOGY*
  Cimermancic, P., Weinkam, P., Rettenmaier, T., Bichmann, L., Keedy, D. A., Woldeyes, R. A., Schneidman-Duhovny, D., Demerdash, O. N., Mitchell, J. C., Wells, J. A., Fraser, J. S., Sali, A.
  2016; 428 (4): 709-719

- **High-density grids for efficient data collection from multiple crystals.** *Acta crystallographica. Section D, Structural biology*
  Baxter, E. L., Aguila, L., Alonso-Mori, R., Barnes, C. O., Bonagura, C. A., Brehmer, W., Brunger, A. T., Calero, G., Caradoc-Davies, T. T., Chatterjee, R., DeGrado, W. F., Fraser, J. S., Ibrahim, et al
  2016; 72: 2-11

- **High-resolution structures of the M2 channel from influenza A virus reveal dynamic pathways for proton stabilization and transduction** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Thomaston, J. L., Alfonso-Prieto, M., Woldeyes, R. A., Fraser, J. S., Klein, M. L., Fiorin, G., DeGrado, W. F.
  2015; 112 (46): 14260-14265

- **Mapping the conformational landscape of a dynamic enzyme by multitemperature and XFEL crystallography.** *eLife*
  Keedy, D. A., Kenner, L. R., Warkentin, M., Woldeyes, R. A., Hopkins, J. B., Thompson, M. C., Brewster, A. S., Van Benschoten, A. H., Baxter, E. L., Uervirojnangkoorn, M., McPhillips, S. E., Song, J., Alonso-Mori, et al
  2015; 4

- **E pluribus unum, no more: from one crystal, many conformations** *CURRENT OPINION IN STRUCTURAL BIOLOGY*
  Woldeyes, R. A., Sivak, D. A., Fraser, J. S.
  2014; 28: 56-62