

## Kevin Michael Dalton

Associate Scientist, SLAC National Accelerator Laboratory

### Publications

---

#### PUBLICATIONS

- **Sensitive detection of structural dynamics using a statistical framework for comparative crystallography** *SCIENCE ADVANCES*  
Hekstra, D. R., Wang, H. K., Klureza, M. A., Greisman, J. B., Dalton, K. M.  
2025; 11 (49): eadj2921
- **Scaling and merging time-resolved pink-beam diffraction with variational inference** *STRUCTURAL DYNAMICS-US*  
Zielinski, K. A., Dolamore, C., Wang, H. K., Henning, R. W., Wilson, M. A., Pollack, L., Srajer, V., Hekstra, D. R., Dalton, K. M.  
2024; 11 (6)
- **Laue-DIALS: Open-source software for polychromatic x-ray diffraction data** *STRUCTURAL DYNAMICS-US*  
Hewitt, R. A., Dalton, K. M., Mendez, D. A., Wang, H. K., Klureza, M. A., Brookner, D. E., Greisman, J. B., McDonagh, D., Srajer, V., Sauter, N. K., Brewster, A. S., Hekstra, D. R.  
2024; 11 (5): 054701
- **Scaling and Merging Time-Resolved Laue Data with Variational Inference.** *bioRxiv : the preprint server for biology*  
Zielinski, K. A., Dolamore, C., Wang, H. K., Henning, R. W., Wilson, M. A., Pollack, L., Srajer, V., Hekstra, D. R., Dalton, K. M.  
2024
- **Sensitive Detection of Structural Differences using a Statistical Framework for Comparative Crystallography.** *bioRxiv : the preprint server for biology*  
Hekstra, D. R., Wang, H. K., Klureza, M. A., Greisman, J. B., Dalton, K. M.  
2024
- **Resolving DJ-1 Glyoxalase Catalysis Using Mix-and-Inject Serial Crystallography at a Synchrotron.** *bioRxiv : the preprint server for biology*  
Zielinski, K. A., Dolamore, C., Dalton, K. M., Smith, N., Termini, J., Henning, R., Srajer, V., Hekstra, D. R., Pollack, L., Wilson, M. A.  
2024
- **Resolving conformational changes that mediate a two-step catalytic mechanism in a model enzyme.** *bioRxiv : the preprint server for biology*  
Greisman, J. B., Dalton, K. M., Brookner, D. E., Klureza, M. A., Sheehan, C. J., Kim, I., Henning, R. W., Russi, S., Hekstra, D. R.  
2023
- **A unifying Bayesian framework for merging X-ray diffraction data** *NATURE COMMUNICATIONS*  
Dalton, K. M., Greisman, J. B., Hekstra, D. R.  
2022; 13 (1): 7764
- **An information theoretic framework reveals a tunable allosteric network in group II chaperonins.** *Nature structural & molecular biology*  
Lopez, T., Dalton, K., Tomlinson, A., Pande, V., Frydman, J.  
2017; 24 (9): 726-733
- **The Mechanism and Function of Group II Chaperonins.** *Journal of molecular biology*  
Lopez, T., Dalton, K., Frydman, J.  
2015; 427 (18): 2919-2930
- **The Dynamic Conformational Cycle of the Group I Chaperonin C-Termini Revealed via Molecular Dynamics Simulation** *PLOS ONE*  
Dalton, K. M., Frydman, J., Pande, V. S.  
2015; 10 (3)

- **The dynamic conformational cycle of the group I chaperonin C-termini revealed via molecular dynamics simulation.** *PloS one*  
Dalton, K. M., Frydman, J., Pande, V. S.  
2015; 10 (3)