

Developing Electron Diffraction Methods to Probe Oxidation States in Metalloenzymes

Laura Pacoste¹, Rohit Kumar², Viljar Femoen¹, Vladislav Ignatev³, Dorothee Liebschner⁴, Pavel Afonine⁴, Billy Poon⁴, Michał Chodkiewicz³, Vivek Srinivas², Buster Blomberg¹, Hugo Lebrette^{2,5}, Hongyi Xu¹, Gerhard Hofer¹, Paulina Maria Dominiak³, Martin Högbom², Xiaodong Zou¹

¹Department of Chemistry, Stockholm University, Stockholm, Sweden, ²Department of Biochemistry and Biophysics, Stockholm University, Stockholm, Sweden, ³Biological and Chemical Research Center, Faculty of Chemistry, University of Warsaw, Warsaw, Poland, ⁴Molecular Biophysics and Integrated Bioimaging Division, Lawrence Berkeley National Laboratory, Berkeley, CA, USA ⁵Laboratoire de Microbiologie et Génétique Moléculaires, Centre de Biologie Intégrative, CNRS, Université Toulouse III, Toulouse, France.

E-mail of corresponding author: Laura.pacoste@su.se

Understanding oxidation state (OS) variations in enzyme metal-ion cofactors is essential for elucidating enzymatic mechanisms. While traditional spectroscopic techniques can be used to determine oxidation states in materials, they lack spatial resolution. Electron diffraction techniques, such as three-dimensional electron diffraction (3D ED/MicroED) and serial electron diffraction (SerialED), offer unique opportunities for OS determination with structural resolution by probing the electrostatic potential. However, accurately inferring OS from electrostatic potential maps remains challenging due to limitations in data collection and processing protocols, as well as constraints in available atomic scattering models used for refinement.

To study the impact of different atomic scattering models, both independent atom model (IAM) and transferable aspherical atom model (TAAM) based on the MATTS databank[1–3], were evaluated for refinement of an iron complex against 3D ED data. The results demonstrated that IAM significantly overestimates the impact of different OS on the atomic scattering amplitude. In contrast, TAAM significantly improved refinement accuracy and reduced map noise, highlighting the importance of accurate atomic scattering models for interpreting the electrostatic potential map.[4]

Furthermore, using a new serial electron diffraction (SerialED) protocol, we determined the structures of two redox states of the iron-containing protein ribonucleotide reductase R2 subunit (R2a). Isomorphous difference maps computed between the experimental data from the two redox states revealed a signal at the iron sites, which could be attributed to OS changes. Model-derived structure factors supported this interpretation, indicating that OS differences contributed ~12-14% to isomorphous difference peaks, while the remainder resulted from atomic displacement between redox states. These findings suggest that differences in scattering amplitude due to oxidation state changes are already detectable within the current accuracy and precision of the data.

Model-derived structure factors were computed based on TAAM, since this model accurately models partial charges. To compute structure factors using TAAM scattering factors, we developed the Python-based wrapper **pyDiSCaMB**, which served as an interface between the DiSCaMB library[5] and cctbx, the underlying library of Phenix[6]. This development is a crucial step toward implementing TAAM scattering factors in **phenix.refine**, which should enhance phase accuracy and reduce map noise. All in all, this study lays the foundation for oxidation state determination of metal-ion co-factors in metalloenzymes from electron diffraction data.

- [1] Kumar, P., Gruza, B., Bojarowski, S.A., and Dominiak, P.M. (2019) *Acta Cryst A*, **75** (2), 398–408.
- [2] Jha, K.K., Gruza, B., Sypko, A., Kumar, P., Chodkiewicz, M.L., and Dominiak, P.M. (2022) *J. Chem. Inf. Model.*, **62** (16), 3752–3765.
- [3] Rybicka, P.M., Kulik, M., Chodkiewicz, M.L., and Dominiak, P.M. (2022) *J. Chem. Inf. Model.*, **62** (16), 3766–3783.
- [4] Pacoste, L., Ignat'ev, V.M., Dominiak, P.M., and Zou, X. (2024) *IUCrJ*, **11** (5), 878–890.
- [5] Chodkiewicz, M.L. *et al.*, (2018) *J Appl Cryst*, **51** (1), 193–199.
- [6] Adams, P.D. *et al.*, (2010) *Acta Cryst D*, **66** (2), 213–221.

We acknowledge funding from the Swedish Research Council (2019-00815 and 2021-03992), the Knut and Alice Wallenberg Foundation (2018.0237 and 2023.0201). The National Science Center, Poland, provided the funding for PMD within the research grant no. 2024/53/B/ST4/02777. The Polish high-performance computing infrastructure PLGrid (HPC Centers: ACK Cyfronet AGH, WCSS) provided computer facilities and support within computational grant no. PLG/2023/016287. PVA acknowledges funding from the National Institutes of Health (grants R01GM071939, P01GM063210, and R24GM141254), as well as support from the Phenix Industrial Consortium and the US Department of Energy under Contract No. DE-AC02-05CH11231. SerialED data collection was carried out at the National Cryo-EM facility at Science for Life Laboratory in Solna (Sweden). XFEL data collection was carried out at the Linac Coherent Light Source (LCLS), SLAC National Accelerator Laboratory (proposal no. L10297), supported by the DOE Office of Science, OBES under Contract No. DE-AC02-76SF00515. XFEL data processing was performed in part at the National Energy Research Scientific Computing Center, supported by the DOE Office of Science, Contract No. DEAC02-05CH11231. The Rayonix detector used at LCLS was supported by the NIH grant S10 OD023453. Experiments at the LCLS were supported by the NIH grant P41GM139687