

Unraveling the mechanism of multicopper oxidases : from ensemble to single molecule ${\bf r}$

Gupta, A.

Citation

Gupta, A. (2014, April 29). *Unraveling the mechanism of multicopper oxidases : from ensemble to single molecule*. Retrieved from https://hdl.handle.net/1887/25397

Version: Not Applicable (or Unknown)

License: Leiden University Non-exclusive license

Downloaded from: https://hdl.handle.net/1887/25397

 $\textbf{Note:} \ \ \textbf{To cite this publication please use the final published version (if applicable)}.$

Cover Page



Universiteit Leiden



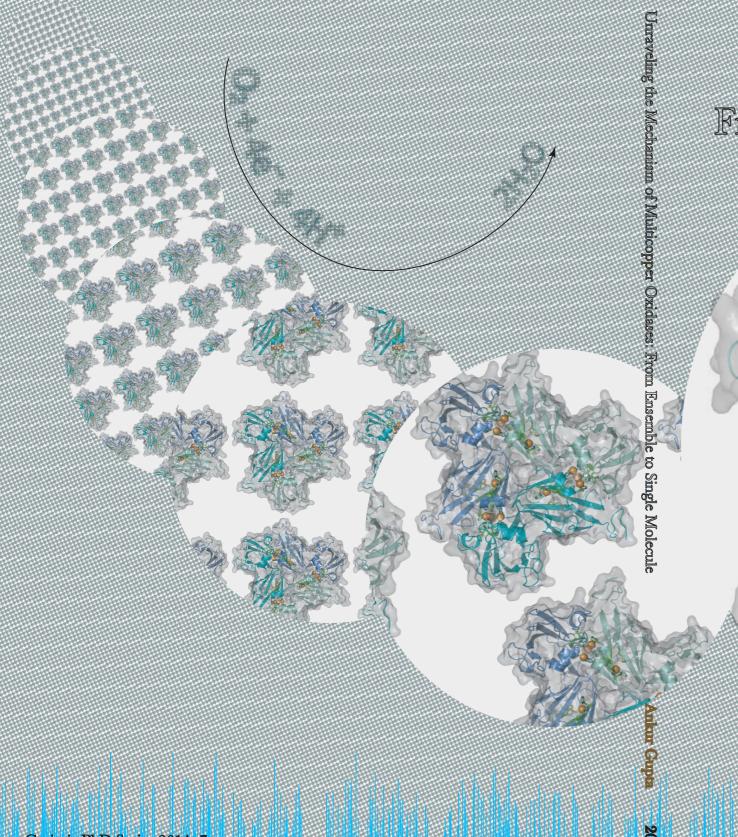
The handle http://hdl.handle.net/1887/25397 holds various files of this Leiden University dissertation

Author: Gupta, Ankur

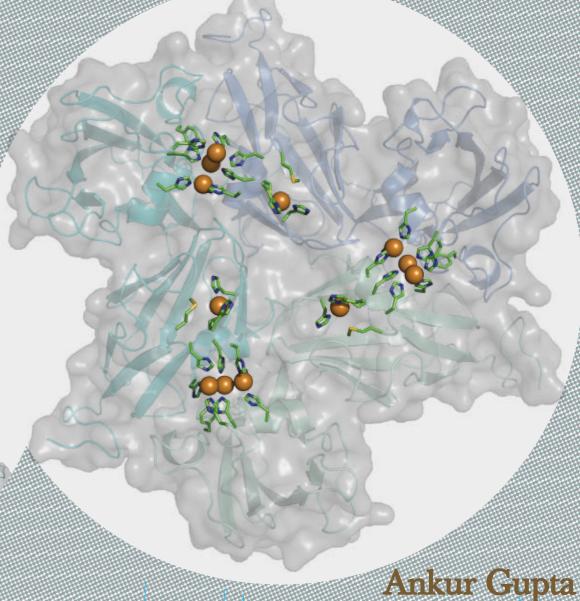
Title: Unraveling the mechanism of multicopper oxidases: from ensemble to single

molecule

Issue Date: 2014-04-29



Unraveling the Mechanism of Multicopper Oxidases:
From Ensemble to Single Molecule



Casimir PhD Series 2014-7 ISBN: 978-90-8593-182-9

Propositions

accompanying the thesis

"Unraveling the Mechanism of Multicopper Oxidases: From Ensemble to Single Molecule"

- It is likely that the protein small laccase utilizes a redox-active tyrosine residue (Y108) to transiently provide one electron towards O₂ reduction at the trinuclear Cu cluster (TNC) when there is a shortage of the reducing equivalents in the milieu. (*This thesis, Chapter 2*)
- 2. The small laccase protein containing only three Cu ions per monomer can catalyze four-electron reduction of O_2 to H_2O . (*This thesis, Chapter 3*)
- 3. From a functional viewpoint, it is questionable that the type 2 Cu site evolved before the binuclear type 3 Cu site in multicopper proteins. (*Nakamura, K. et al. Cell. Mol. Life Sci. 2005, 62, 2050; This thesis, Chapter 3*)
- 4. A small spread in the activation energy among a population of molecules is sufficient to explain more than one order of magnitude spread in the associated electron transfer rate constants. (*This thesis, Chapter 4*)
- 5. Internal dynamics of enzymes are best studied under steady-state conditions. (*This thesis, Chapter 4*)
- 6. Solomon and coworkers, through mutagenesis and spectroscopic studies, have postulated that the asymmetry at the active site is responsible for the nature of O₂ binding; however, they don't clearly evaluate how their mutations disturb the active site. (*Augustine, A.J. et al. J. Am. Chem. Soc. 2010, 132, 6057*)
- 7. The rates of intramolecular electron transfer evaluated from single-molecule measurements of Cu-containing nitrite reductases are too low to be compatible with ensemble steady-state measurements. (*Kuznetsova S. et al. PNAS, 2008, 105, 3250; Goldsmith R.H. et al. PNAS, 2011, 108, 17269*)

- 8. The measurements of intermolecular electron transfer kinetics on the variants of putidaredoxin and cytochrome P450 reveal the role of polar residues in partner recognition. (*Hiruma, Y. et al. ChemBioChem, 2014, 15, 80*)
- 9. Binning of single-molecule time trajectories shall be avoided as much as possible. (*Watkins, L.P. et al. J. Phys. Chem. B, 2005, 109, 617*)
- 10. Despite the widespread use of aminosilanes for surface functionalization, there exists no standard to assess the surface wettability of a silanized surface.
- 11. Self-plagiarism is not plagiarism.

Ankur Gupta Leiden, April 29, 2014