

# EXAFS : Application to Biological Systems

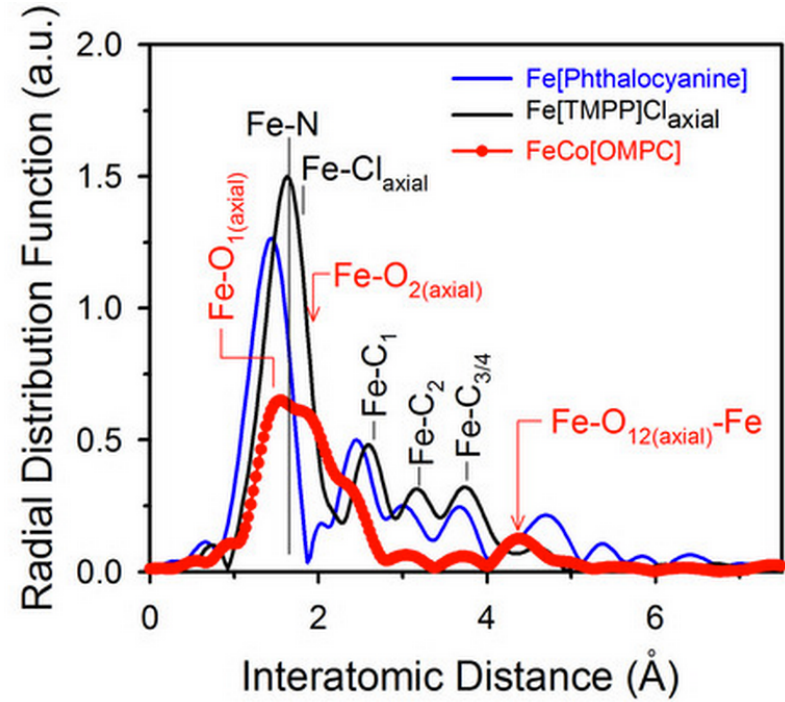
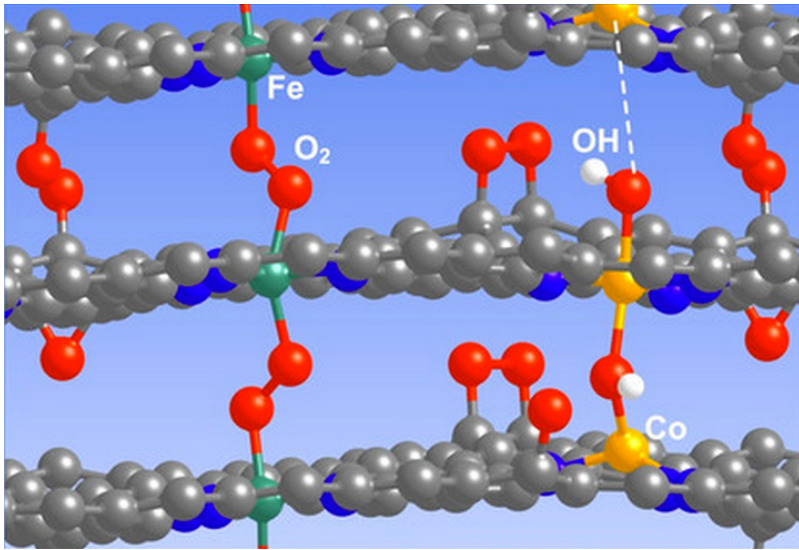
Ritimukta Sarangi  
Stanford Synchrotron Radiation Lightsource  
SLAC National Accelerator Laboratory

IUCr, Aug. 5. 2014

- Application of EXAFS to Metals in Biology
- Modern Approach to Biological XAS
- Single Crystal XAS
- Oxyhemoglobin
- DypB

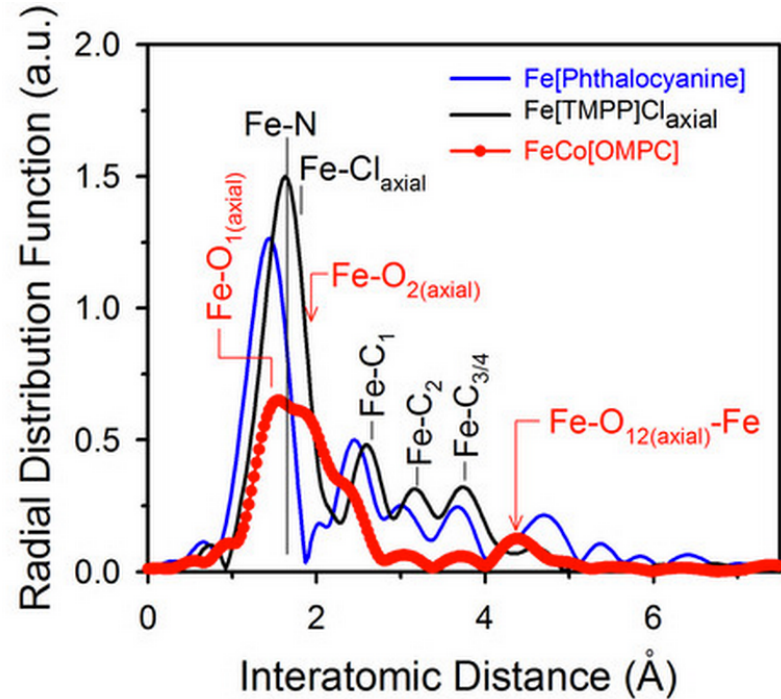
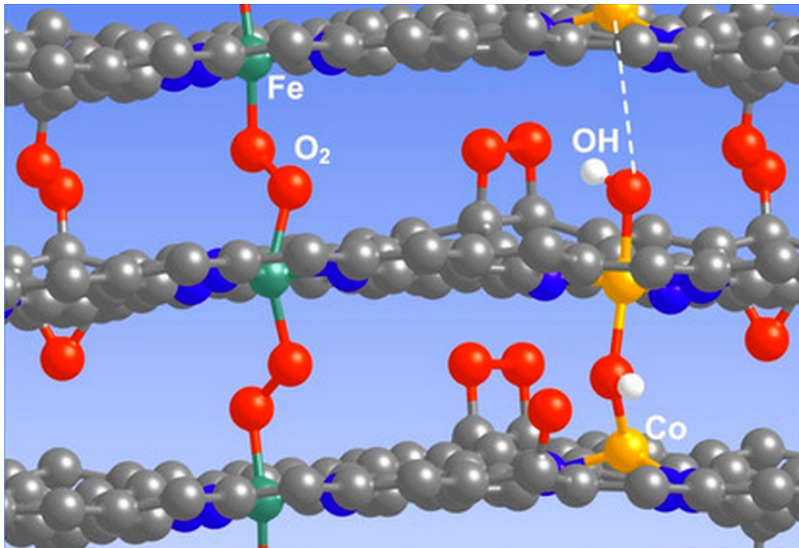
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# Ordered Systems

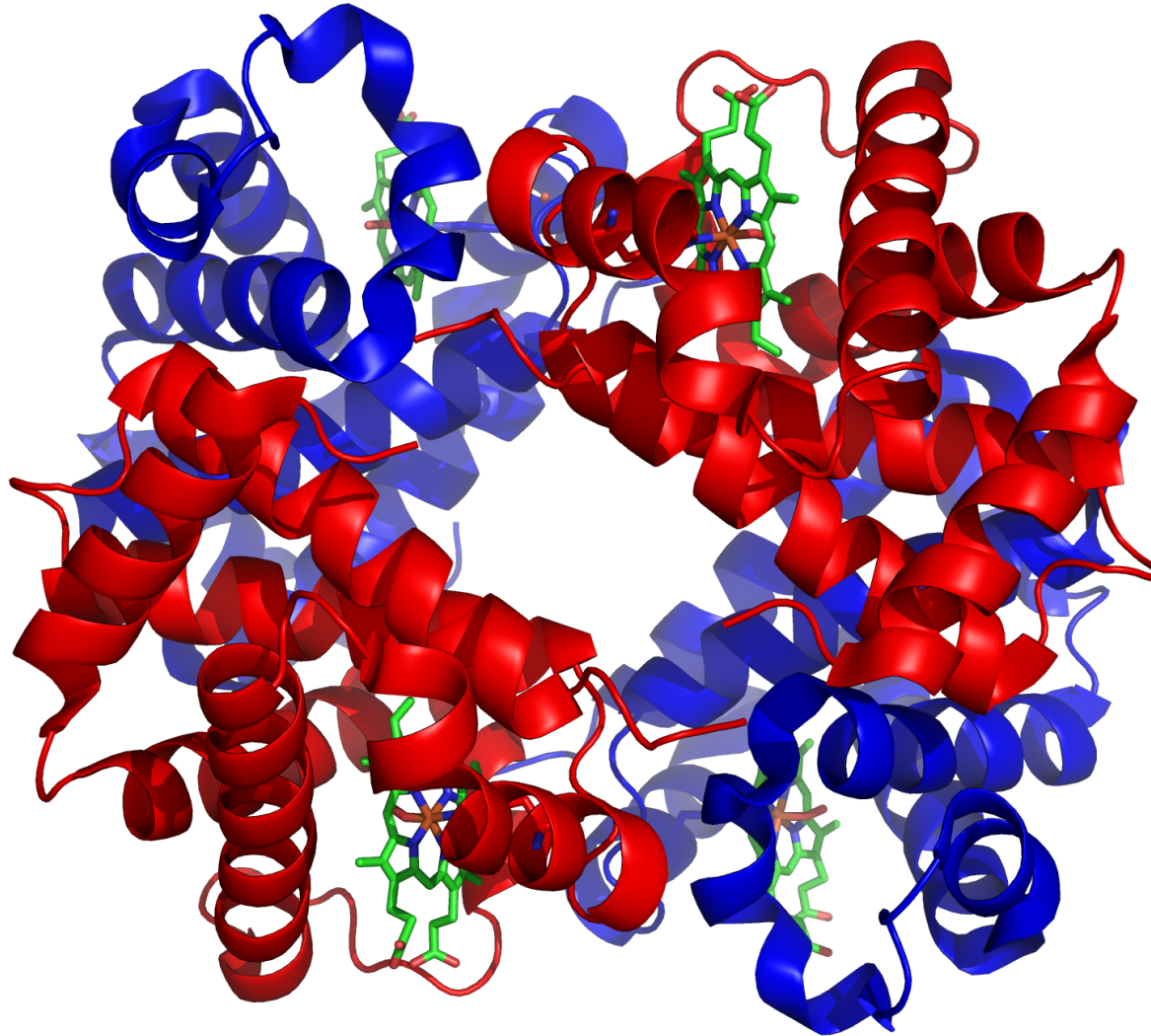


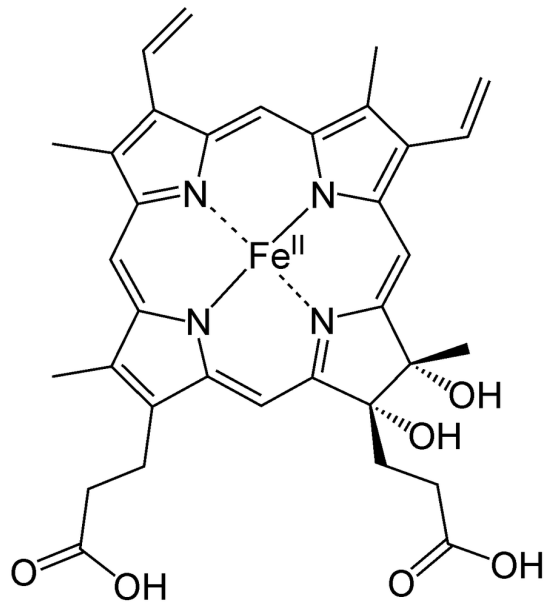


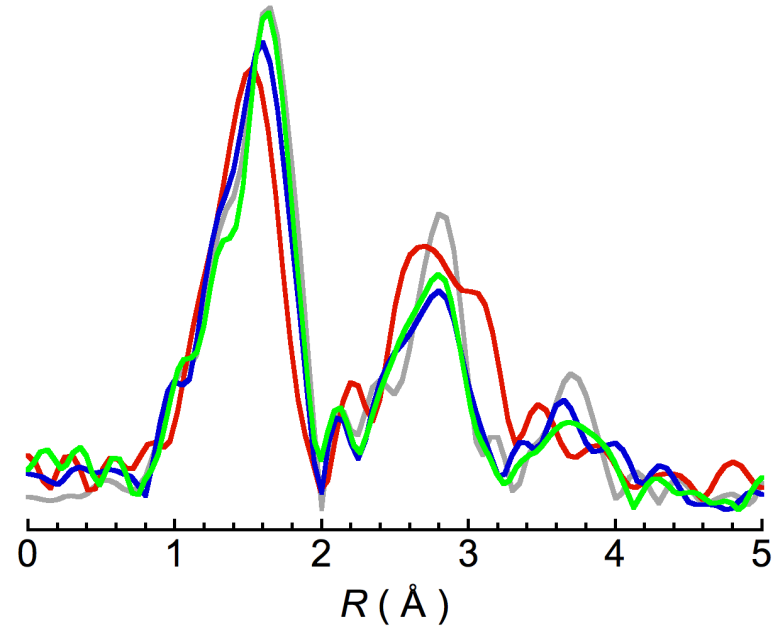
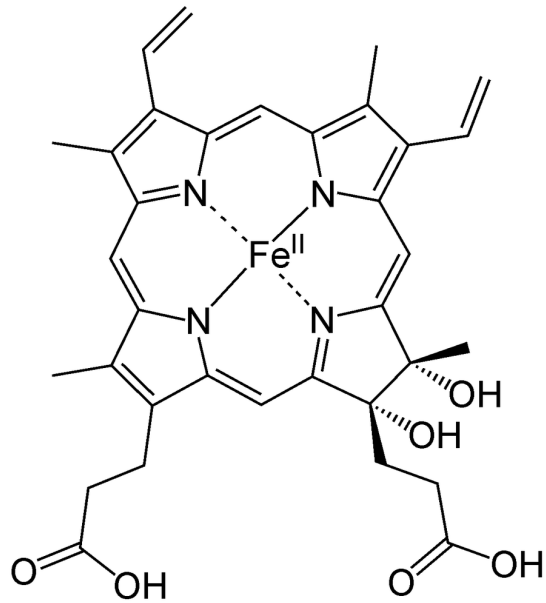
# Ordered Systems

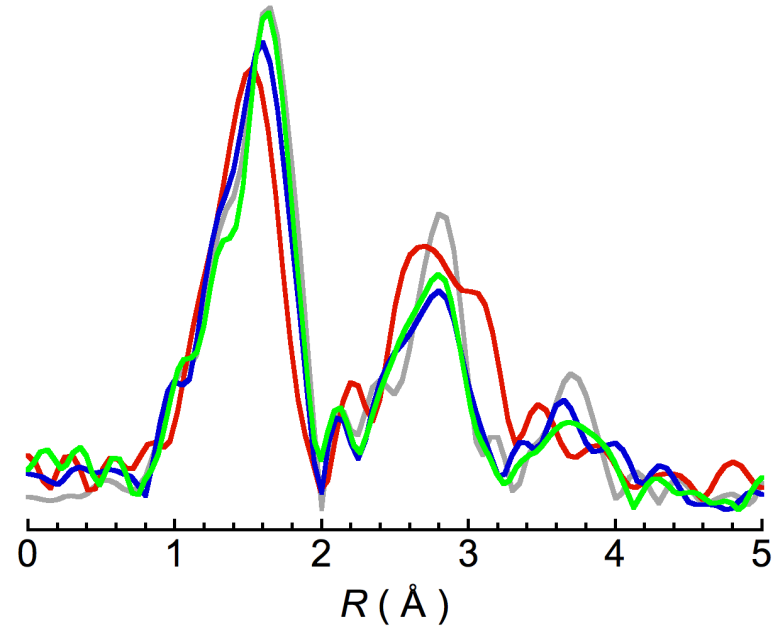
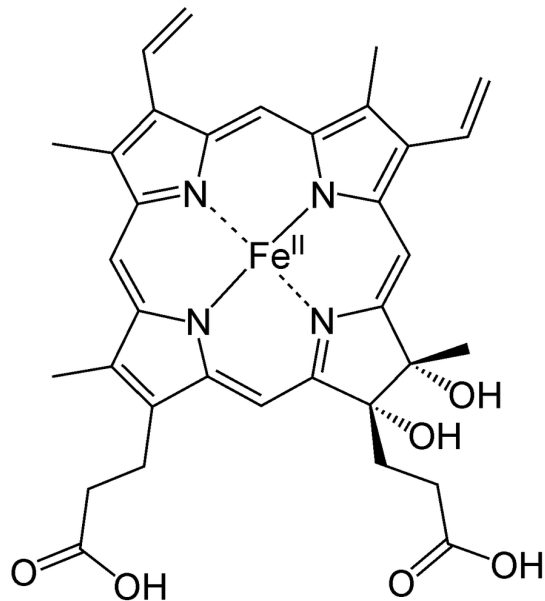


- EXAFS more ordered (data to high  $k$ )
- Shell by Shell analysis is popular and FT based fitting is helpful.
- Rigid structure - similarity between related systems.









- EXAFS are more disordered (data to  $k=11-15 \text{ \AA}$ ).
- Complete EXAFS analysis necessary for meaningful interpretation.
- Confidence mostly in first shell & second shell metal coordination.

- **Sample Requirement**

- ~1 mM in metal, 100 uL in volume, 20-30% glycerol/glassing agent.
- 0.1-1 mM for heavy metals  $Z > \text{Cu}$ , ~2mM for  $Z < \text{Fe}$ .
- Duplicates for photoreducing systems.



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- **Beamline Specification**

- Liq He cryostat (10-15K) : **must**
- 30+ element Ge Detector: **critical**
- BL equipped with fast shutters, beam filters, ease of detuning: **critical**
- Automated data measurement: required

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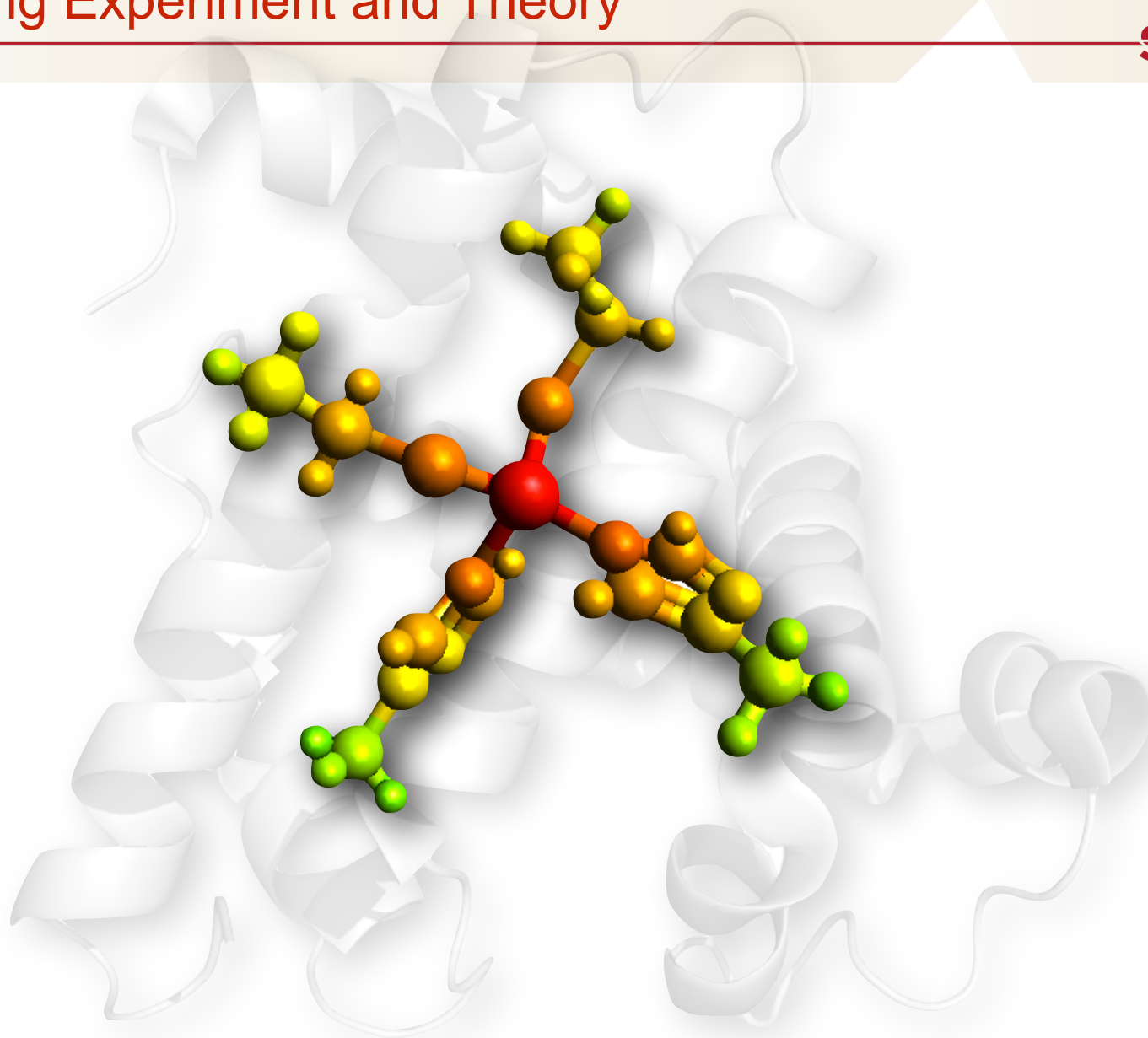
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- **Measurement Time**

- Time : 5-15 hours (per-sample, excluding duplicates)
- Reproducibility : At least once

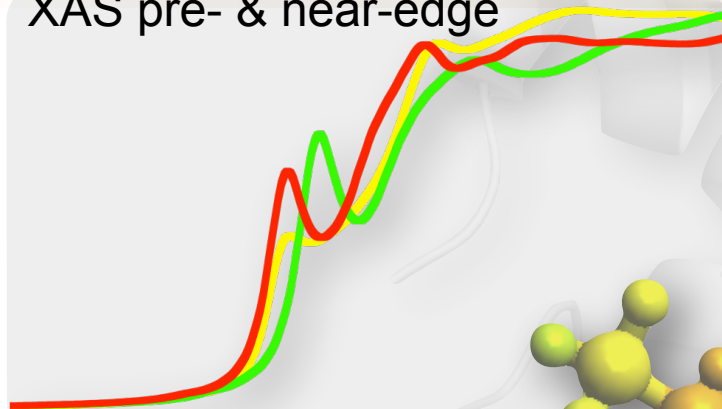
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# Combining Experiment and Theory

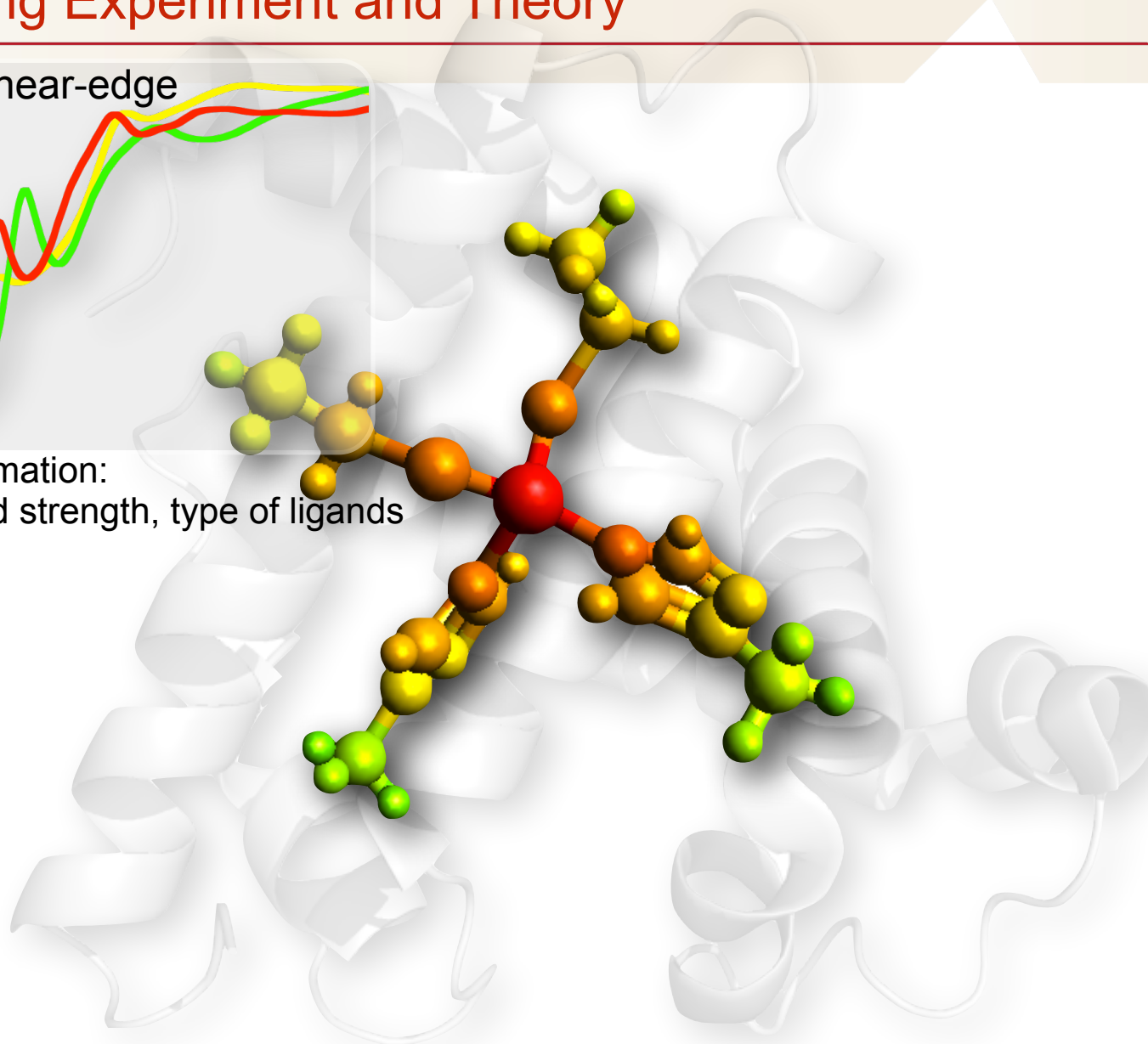


# Combining Experiment and Theory

XAS pre- & near-edge

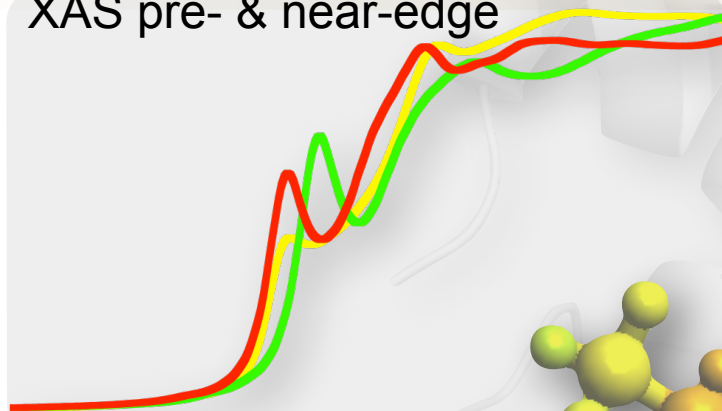


Electronic information:  
covalency, bond strength, type of ligands



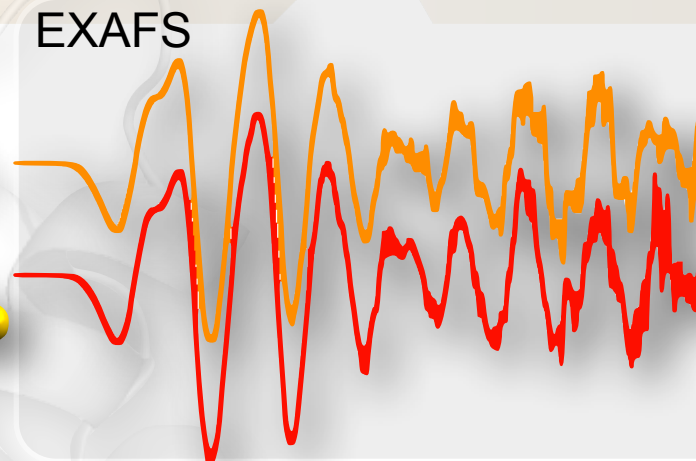
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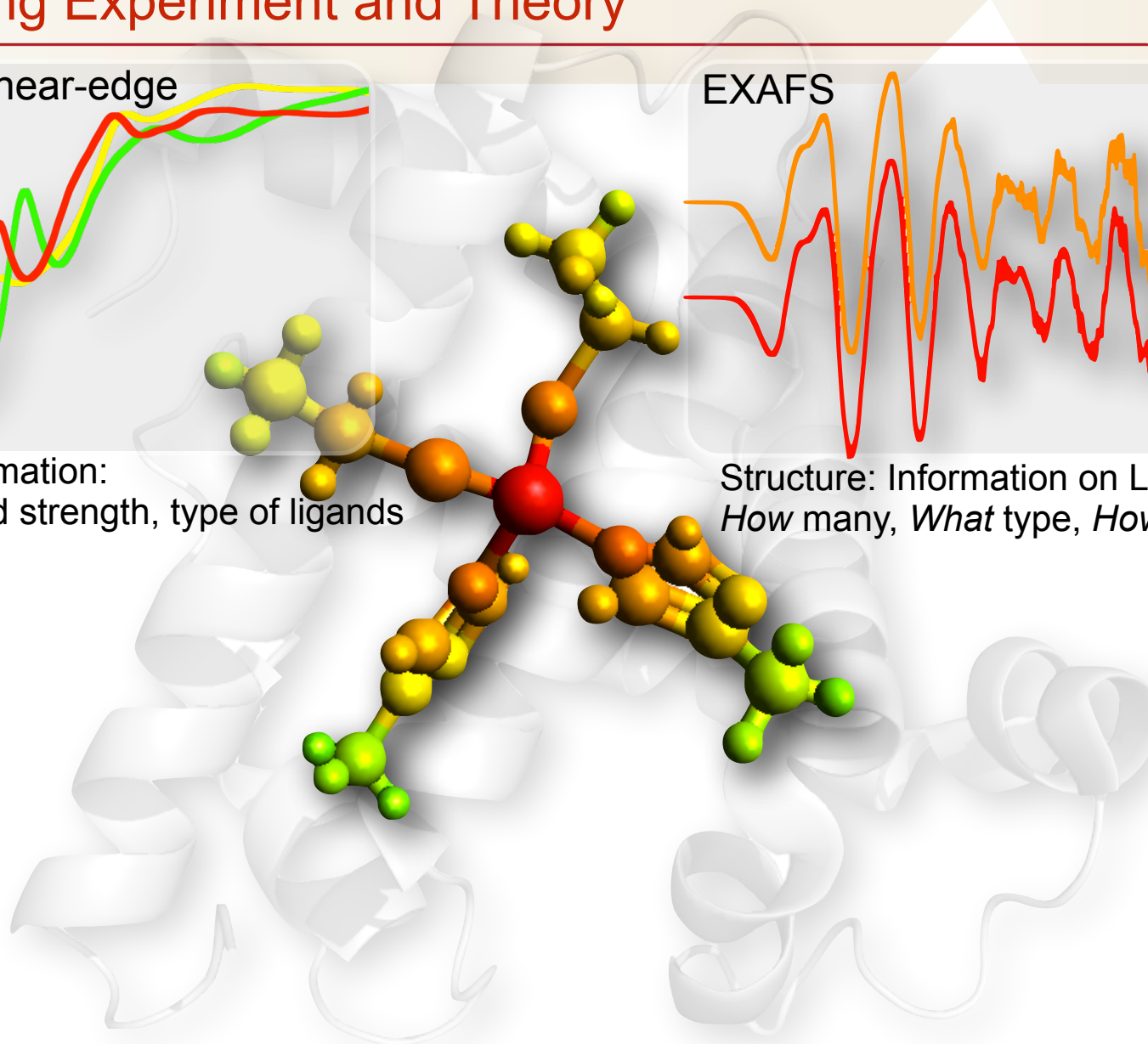


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EXAFS



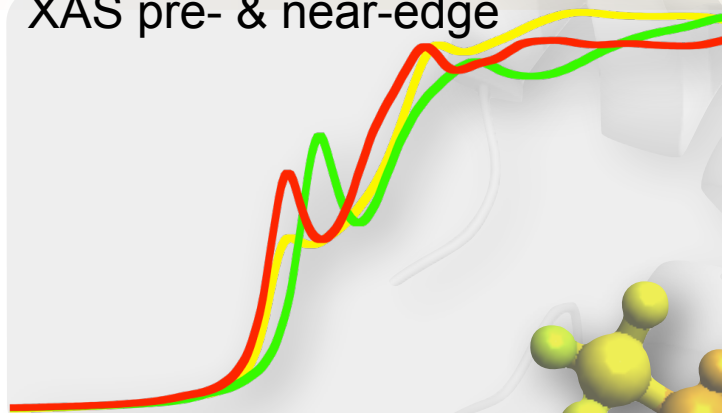
Structure: Information on Ligands  
*How many, What type, How far.*





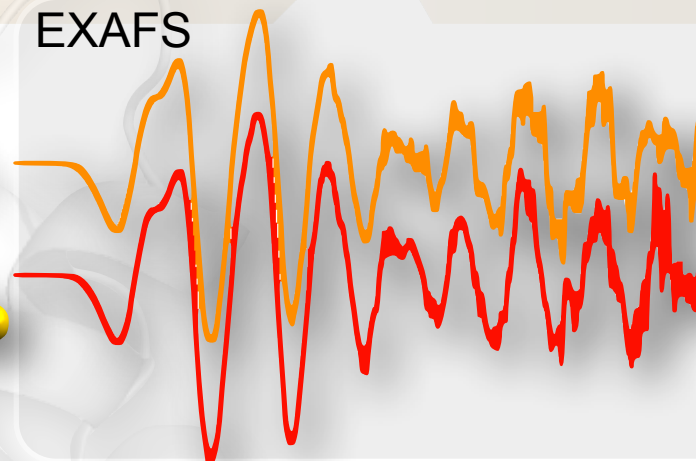
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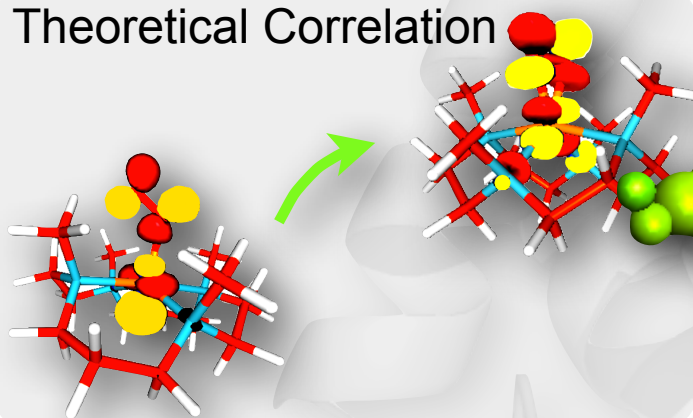
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EXAFS



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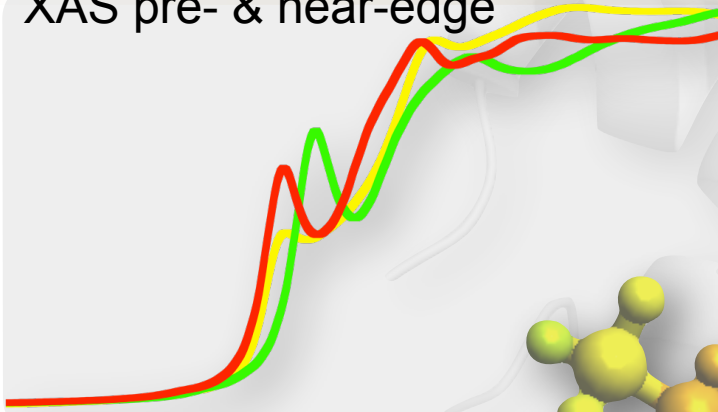
Theoretical Correlation



Detailed Electronic Information

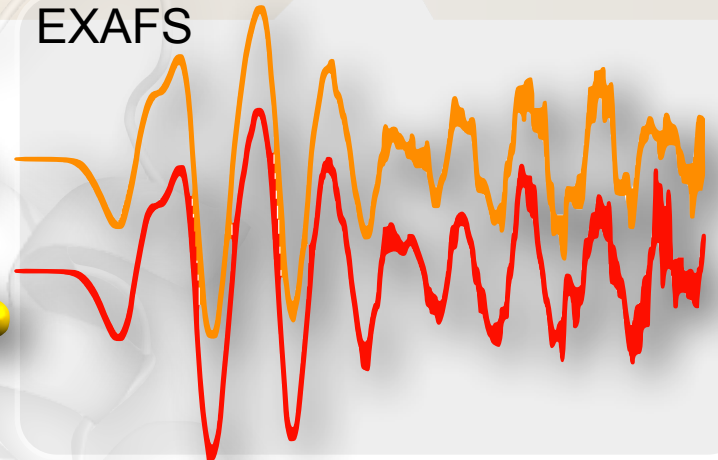
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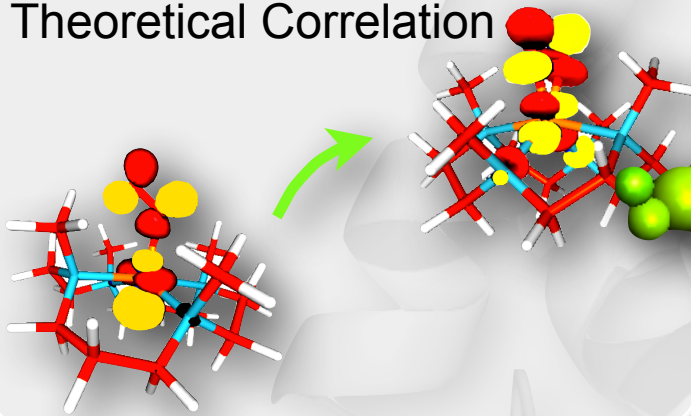
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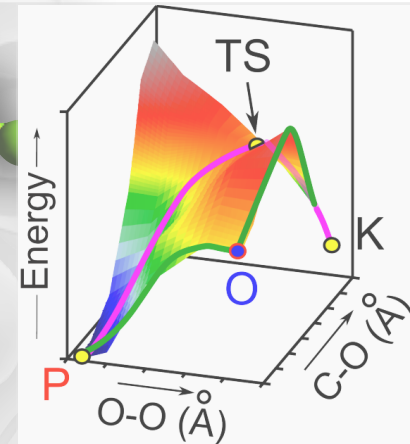


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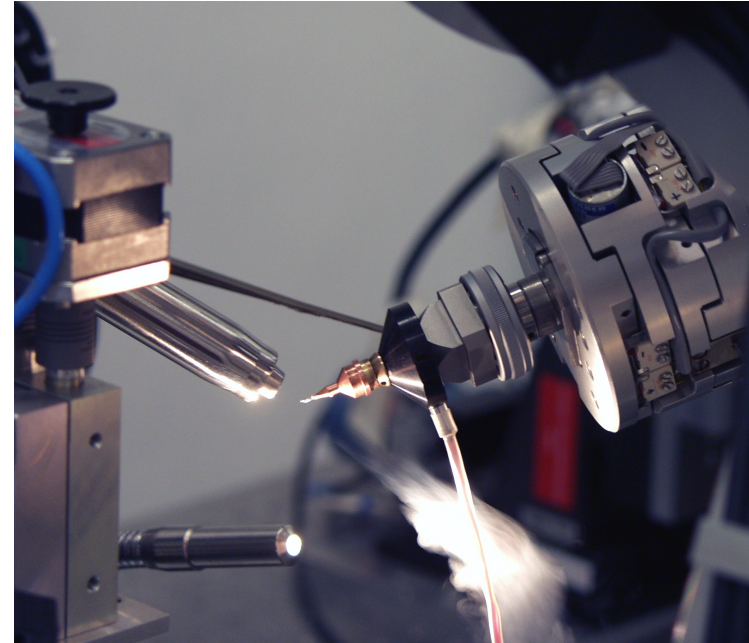
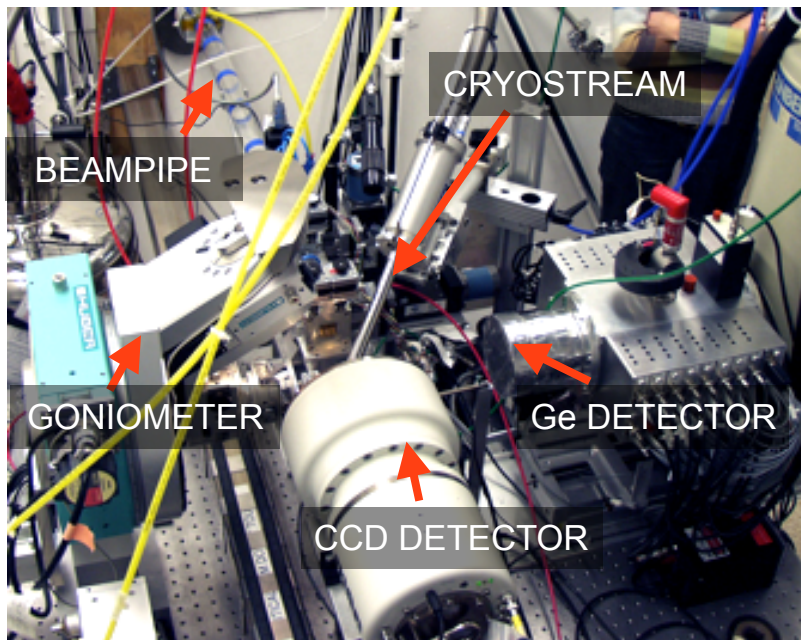


Detailed Electronic Information



Structure Function Correlation

- Application of EXAFS to Metals in Biology
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- Sequential measurement of X-ray diffraction and X-ray absorption is possible.
- Sample requirements: Single crystals for polarized measurements :  $\sim 100 \mu\text{m}$ .
- Smaller proteins with heavier transition metals (higher than Ni)  $\sim 50 \mu\text{m}$ .
- Multiple crystals for standard XAS measurements.

## Small Sample Requirement

- Multiple crystals from small starting volume (~5 uL): solution XAS ~100 uL (~ 1mM).

## Applicable to Imperfect Crystals

- Twins, multiples, poorly diffracting, cracked etc. several crystals on loop to increase signal

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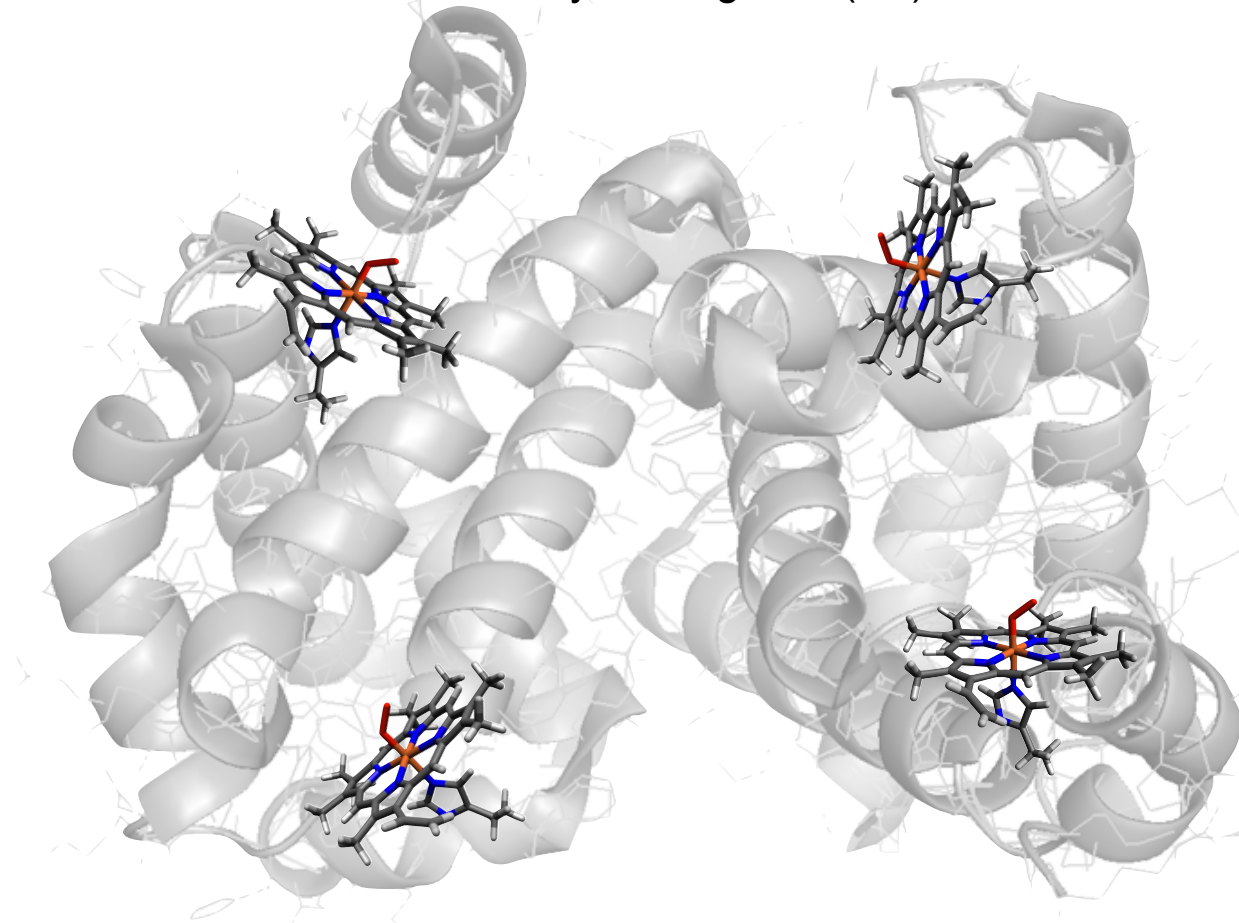
## Direct Comparison to Crystallography

- Solution EXAFS may vary from crystallography due to changes in H-bonding or due
- to crystal packing effects. Single crystal XAS is a direct in-state comparison.
  
- Monitor photoreduction in single crystals and correlate to photo-damage in crystallography.



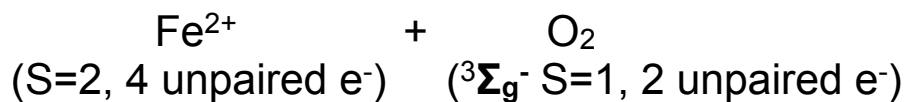
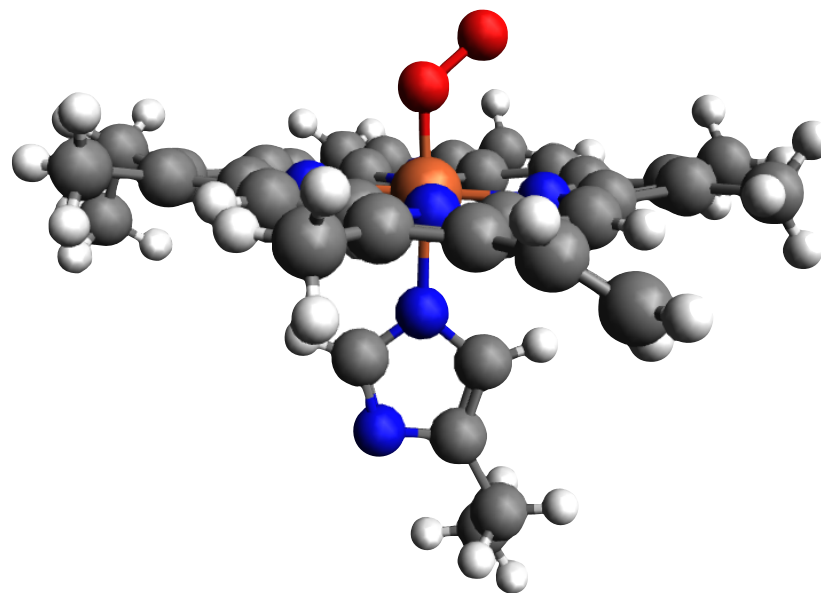
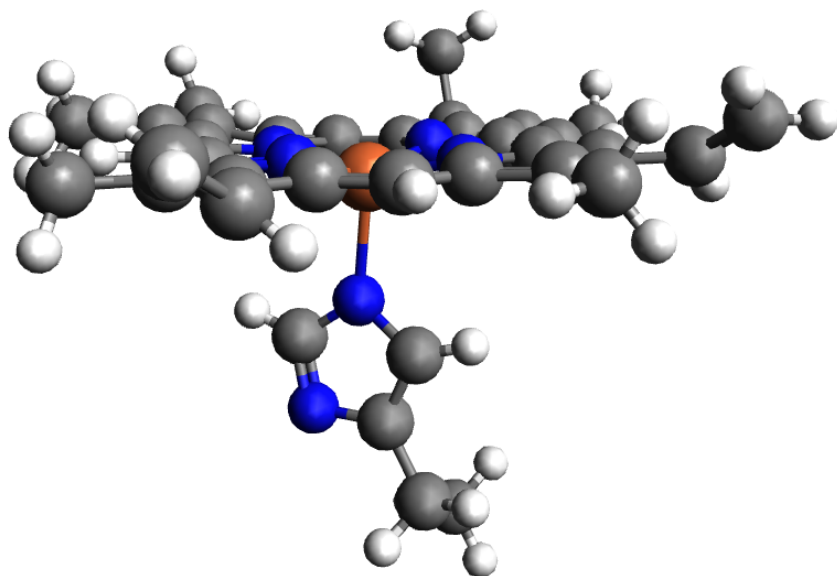
# Oxyhemoglobin

Human interaction with O<sub>2</sub> Mediated by Hemoglobin (Hb)



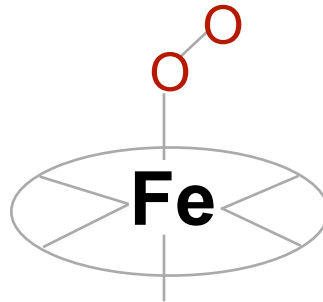
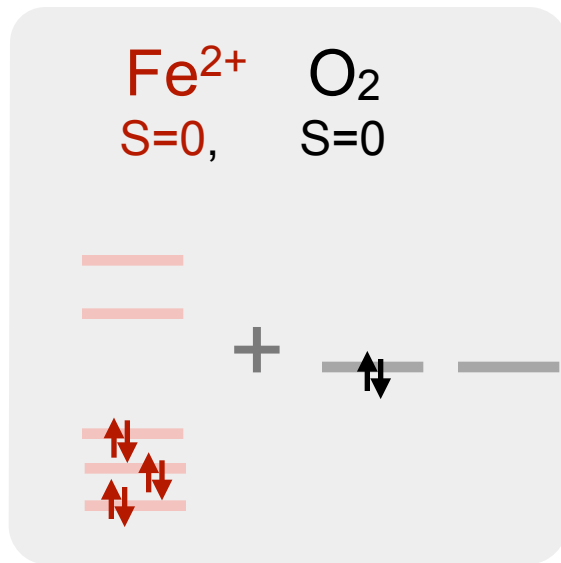
- Fe containing O<sub>2</sub> transport protein
- Contains an Fe-porphyrin (heme)
- Present in all vertebrates
- Binds upto 4 O<sub>2</sub> molecule per Hb

# Oxyhemoglobin

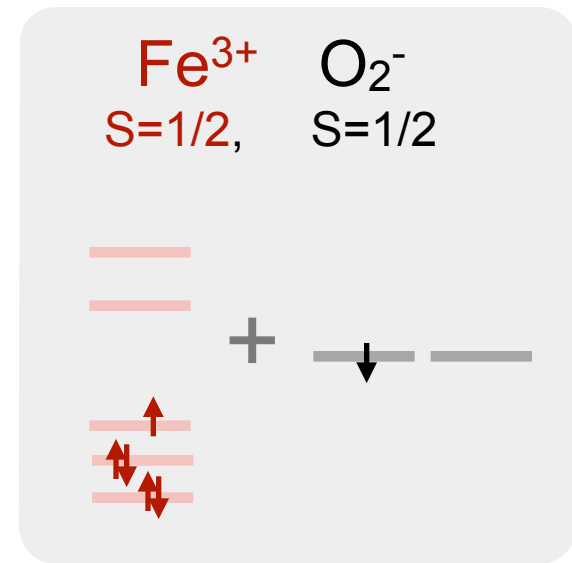


24 electrons undergo spin-pairing in the 4 subunits to form oxyhemoglobin!!

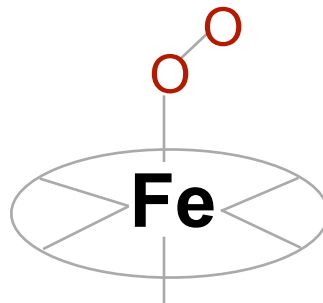
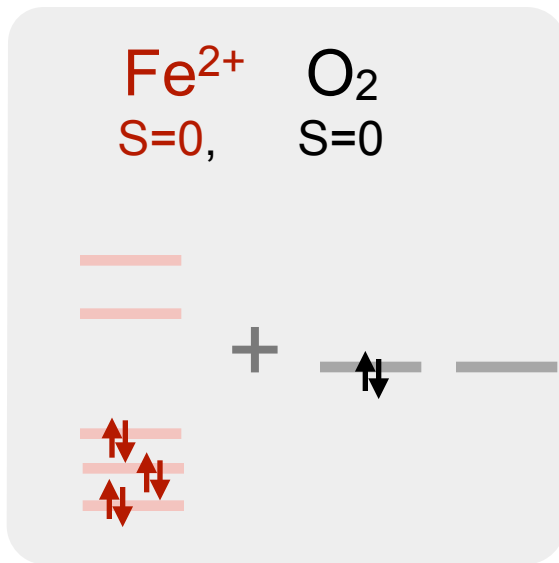
## Ferrous



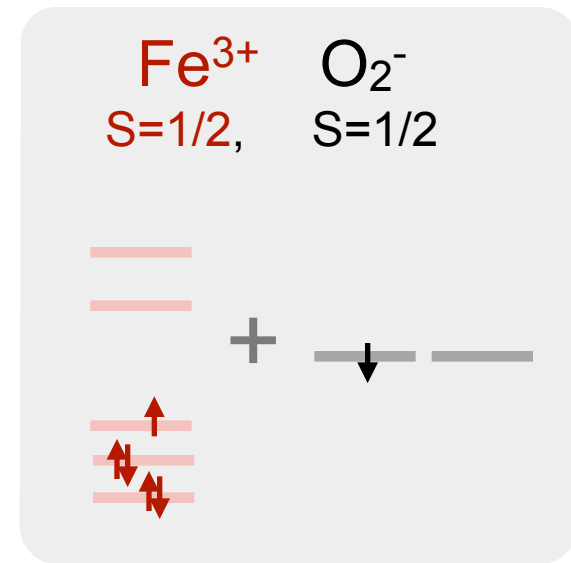
## Ferric



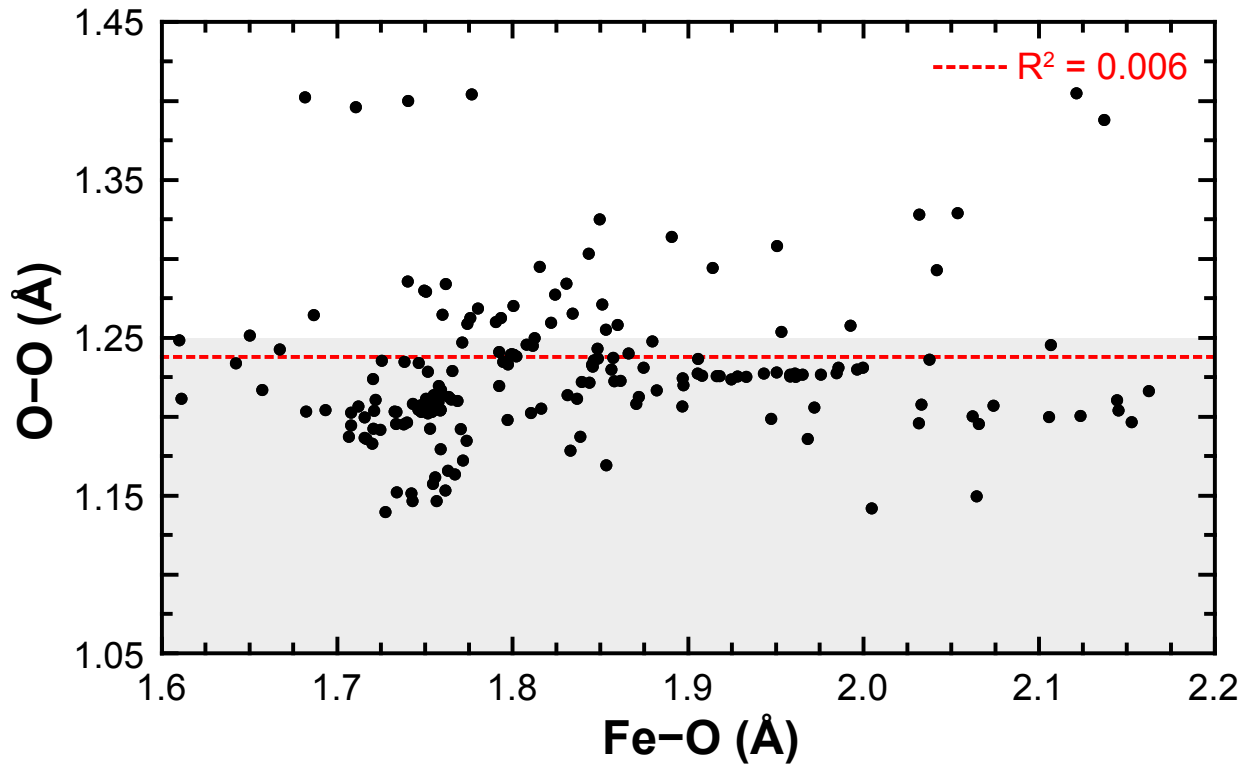
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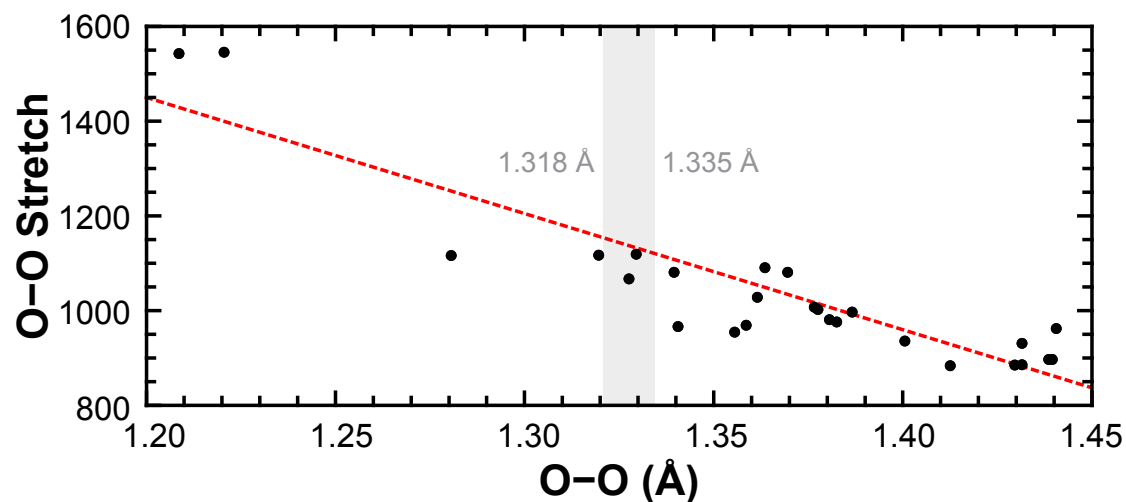
## Ferric



Is the metal center Reduced (**Ferrous**) or Oxidized (Ferric)?



- O-O Bond Distance indicates Reduced (Ferrous).
- Why is there a large spread in Fe-O ?

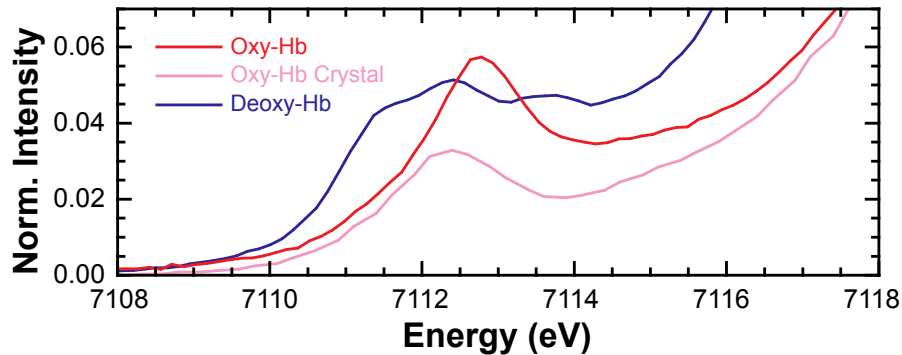
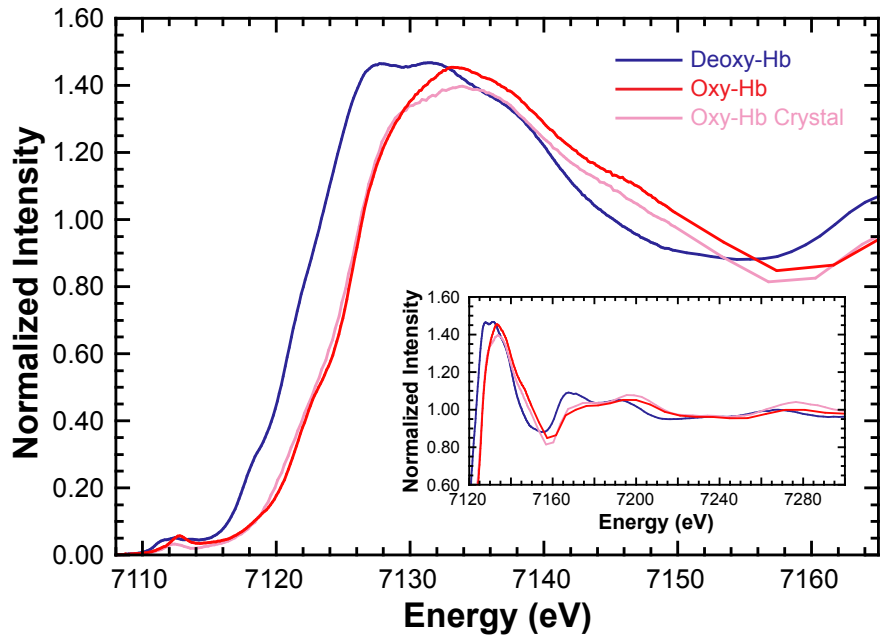


- O-O Bond Distance derived from spectroscopy (rRaman) indicates Oxidized (Ferric).

Discrepancy between solution spectroscopy and x-ray crystallography??



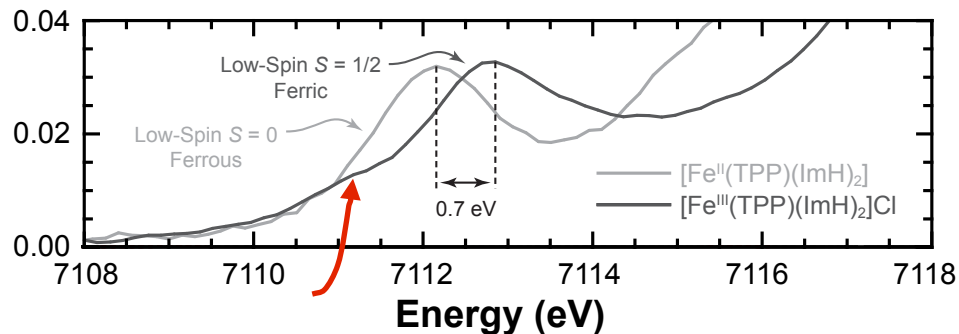
# Solution & Crystal XAS



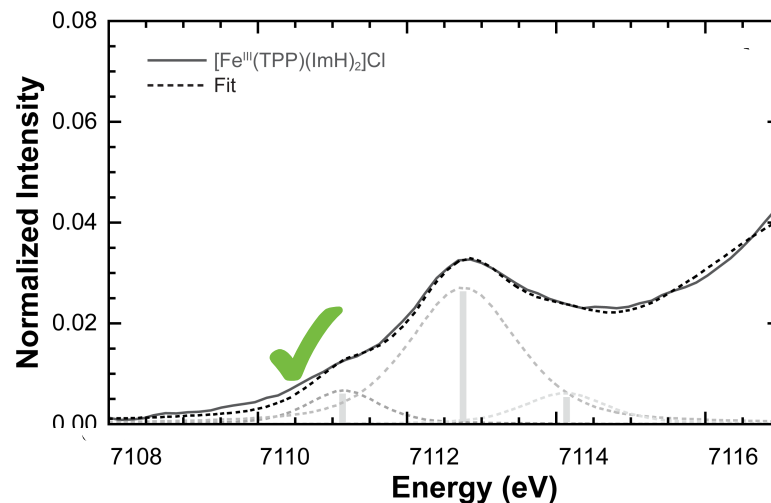
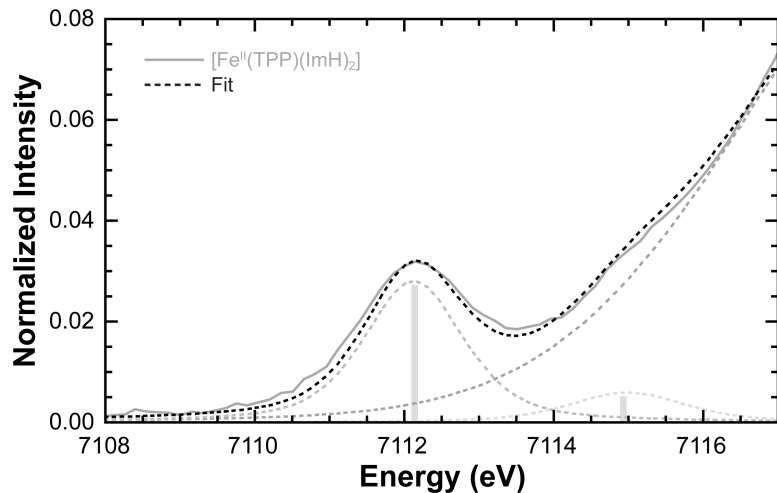
- Crystal near-edge similar to solution.
- Structure analysis shows very similar O<sub>2</sub> bound geometry.
- Fe K-edge and pre-edge distinctly different from starting material - deoxyHb
- *Curiously* - Fe K-pre-edge for oxyHb in solution and crystalline forms are different.
- Since geometric structure is similar, does this point to electronic changes?

# Model Comparison

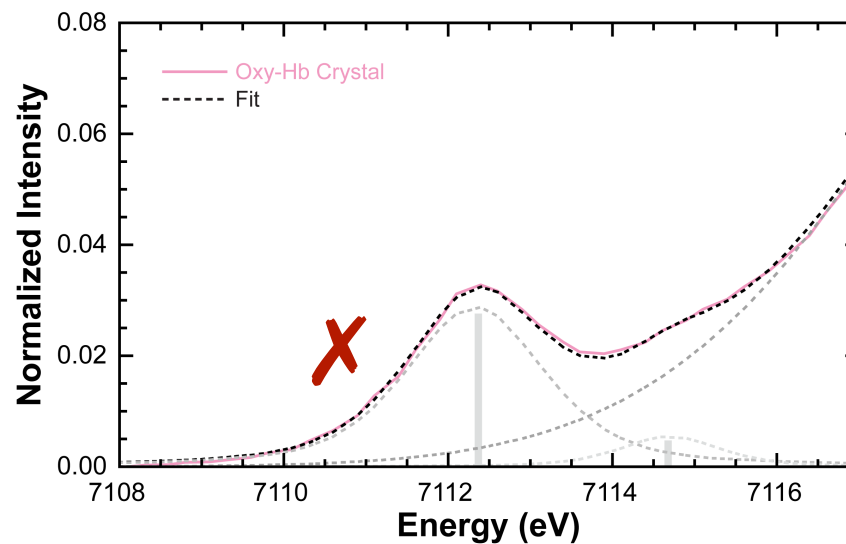
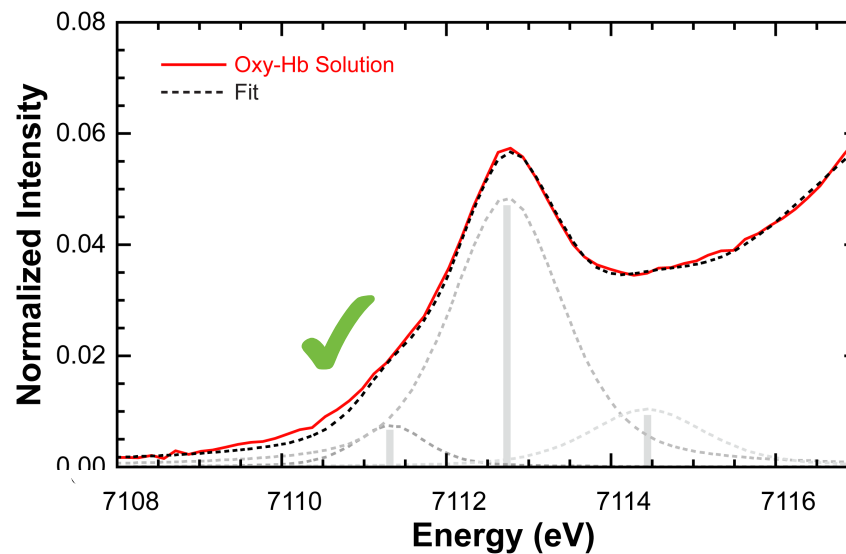
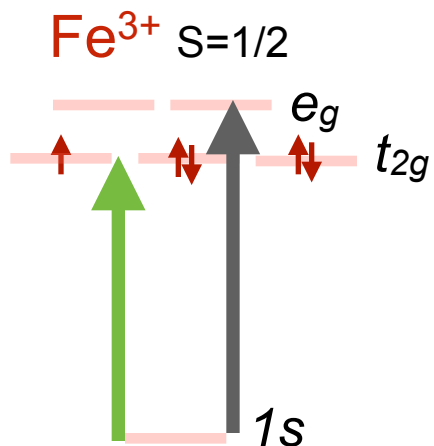
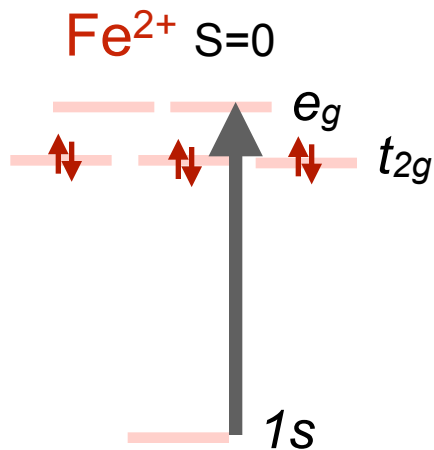
What do small molecule models with  $\text{Fe}^{3+}\text{O}_2^-$  and  $\text{Fe}^{2+}\text{O}_2$  look like?



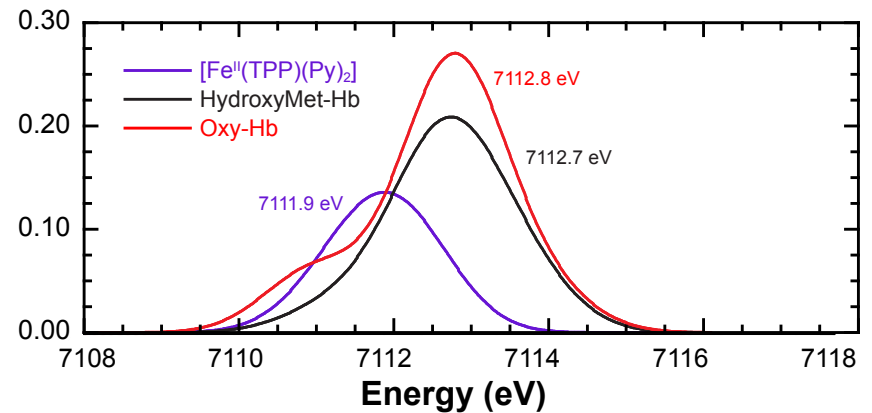
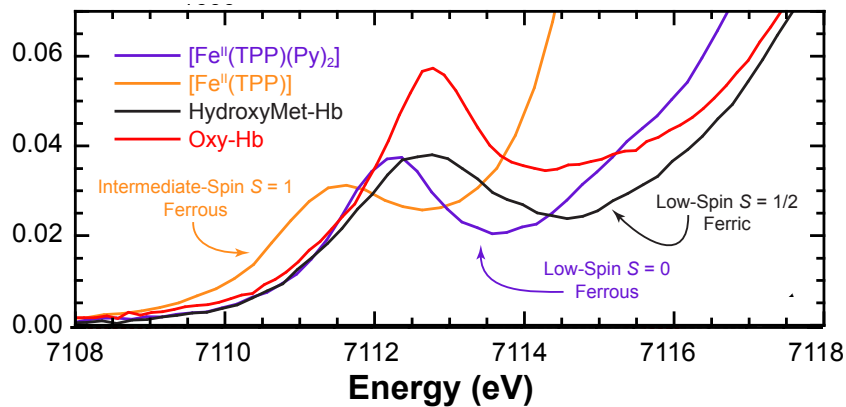
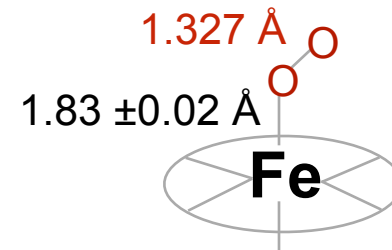
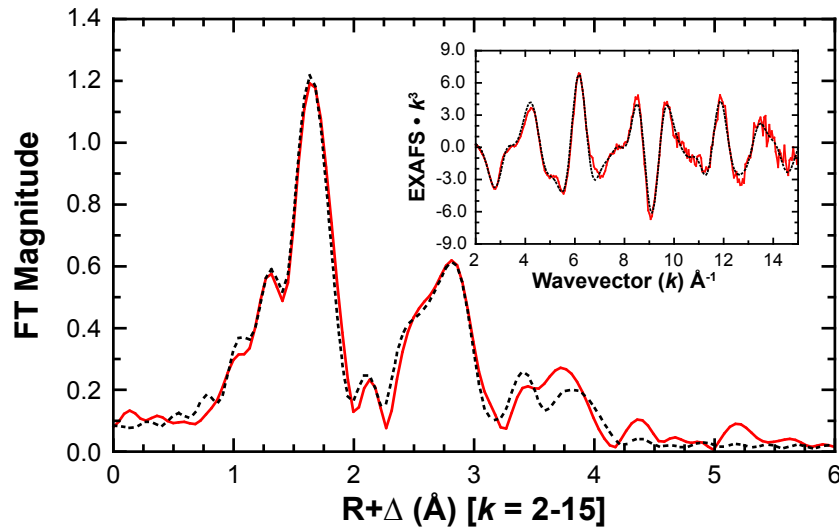
pre-pre-edge feature ??



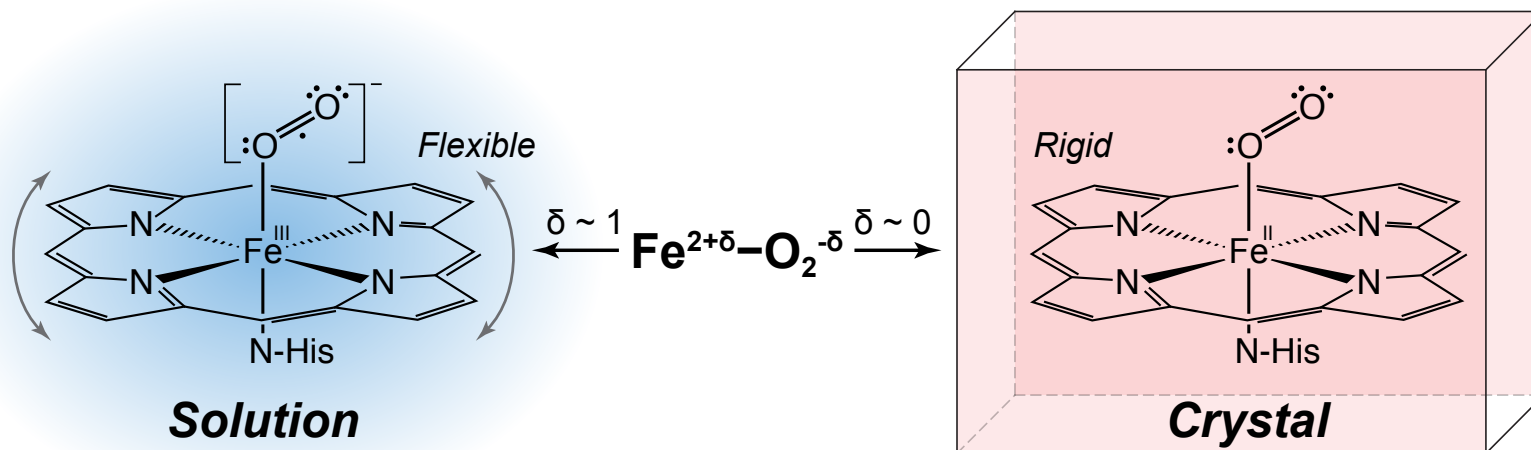
# Solution & Crystal Pre-edge



# Solution EXAFS and DFT



- DFT reproduces EXAFS distances and the differences in pre-edge.



- Differences in Crystallography and Solution Spectroscopy Real.
- Electronic structure of oxyhemoglobin consists of both the ferrous and ferric components.
- Ferric dominates in solution and Ferrous dominates in crystal form.

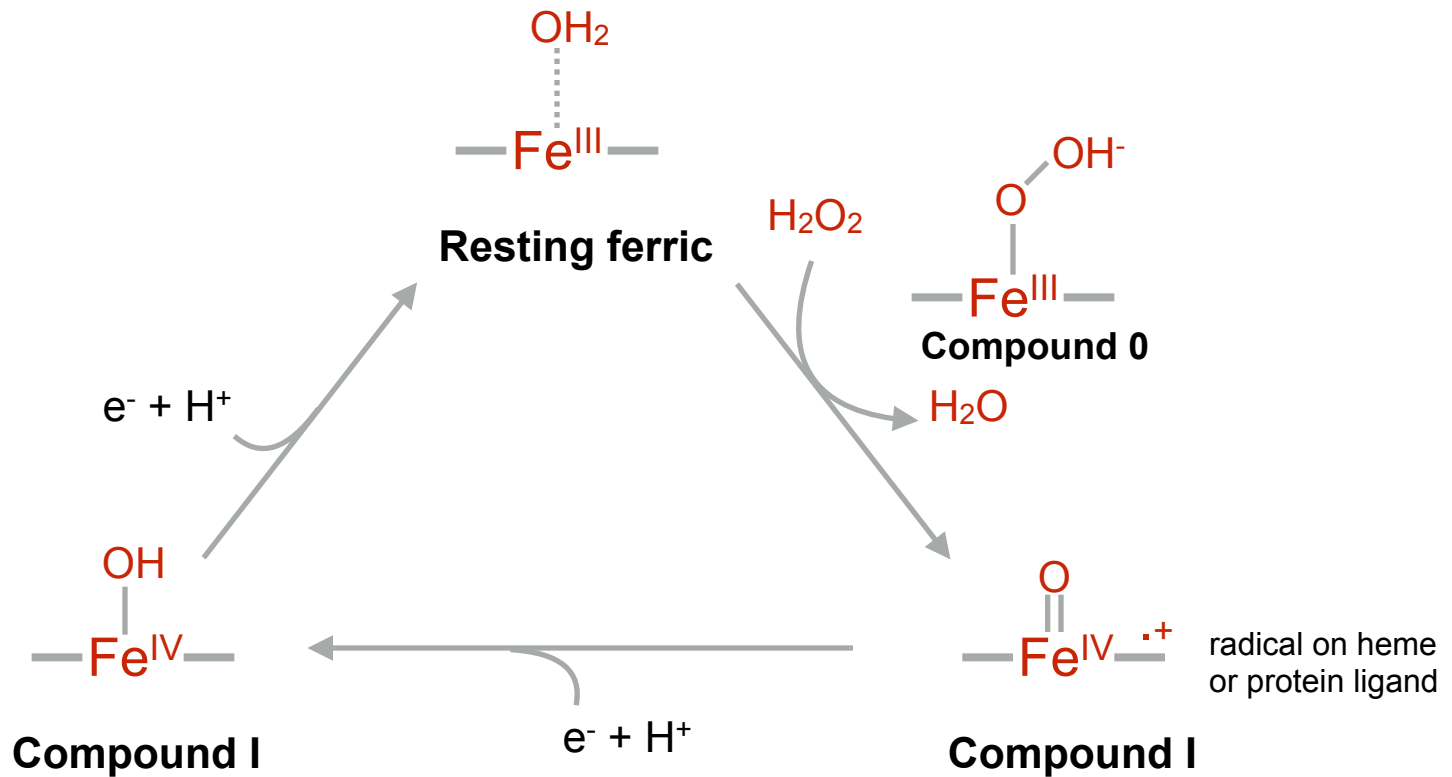
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# Dye-decolorizing Peroxidase B (DypB)



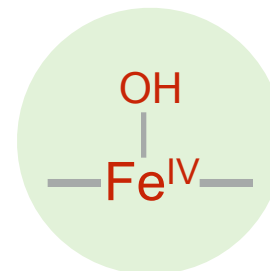
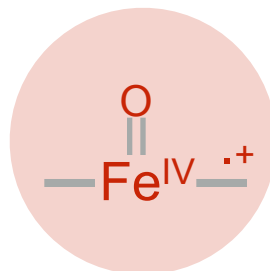
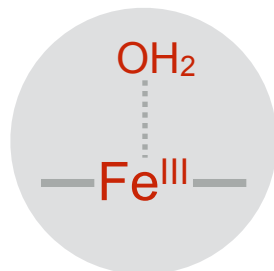
- Recently discovered heme protein with peroxidase-like activity.
- Capable of oxidizing anthraquinone dyes, lignin and even  $Mn^{2+}$ .
- Remarkable specificity for a wide range of reductive substrates.

# Peroxidase Catalytic Cycle

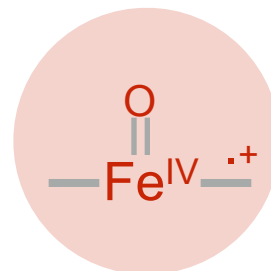
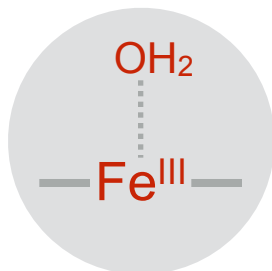




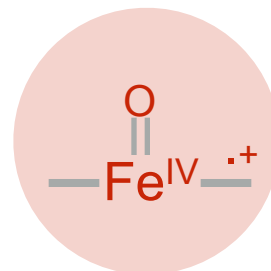
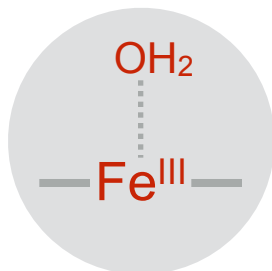
# Characterizing Compound I & II



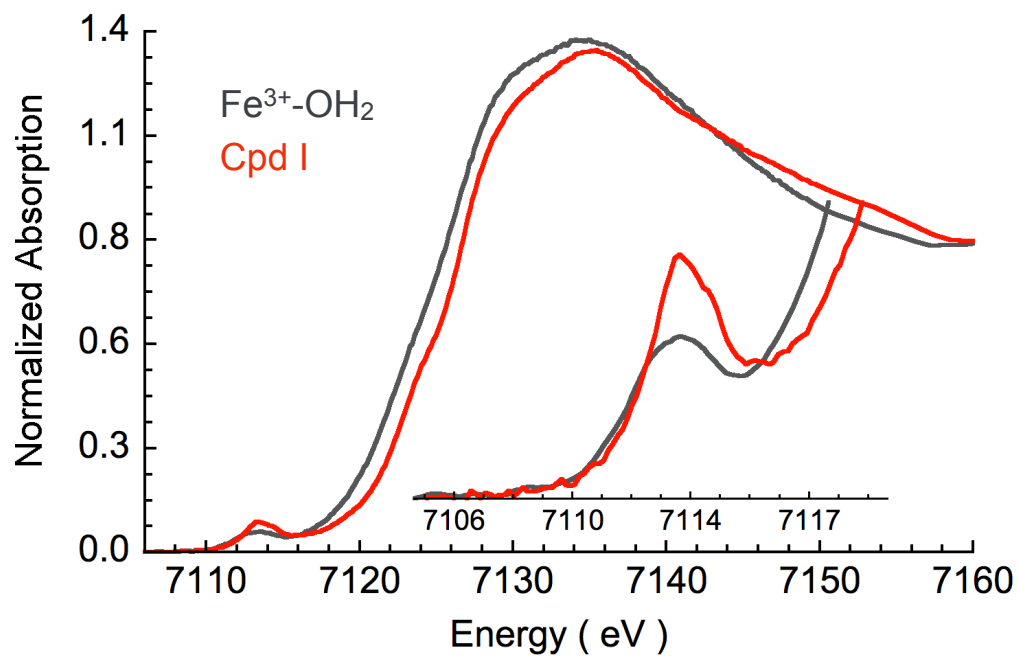
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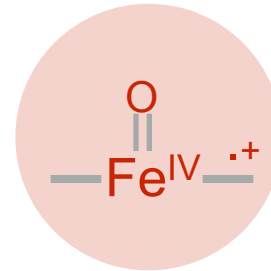
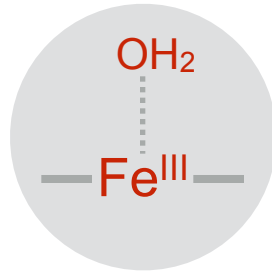
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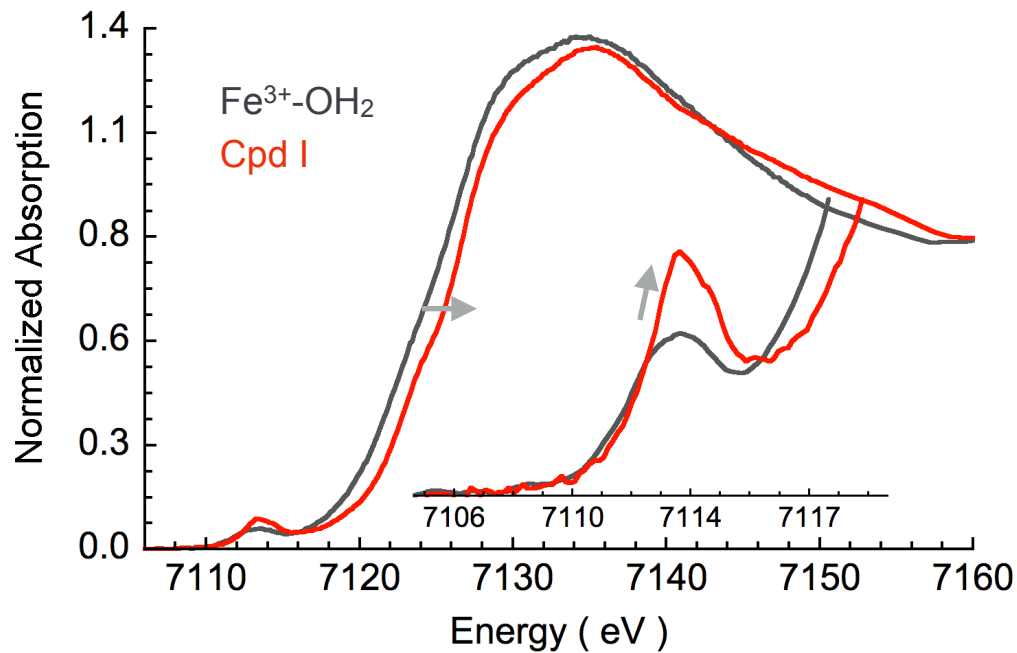
Cytochrome c Peroxidase



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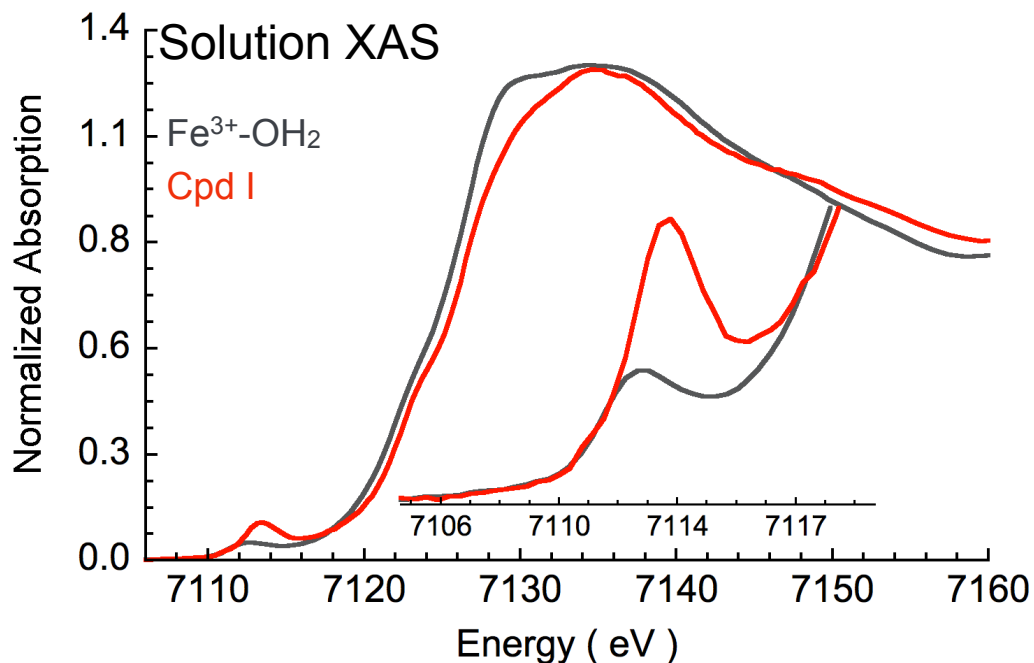
Cytochrome c Peroxidase



## Expected Spectral Change

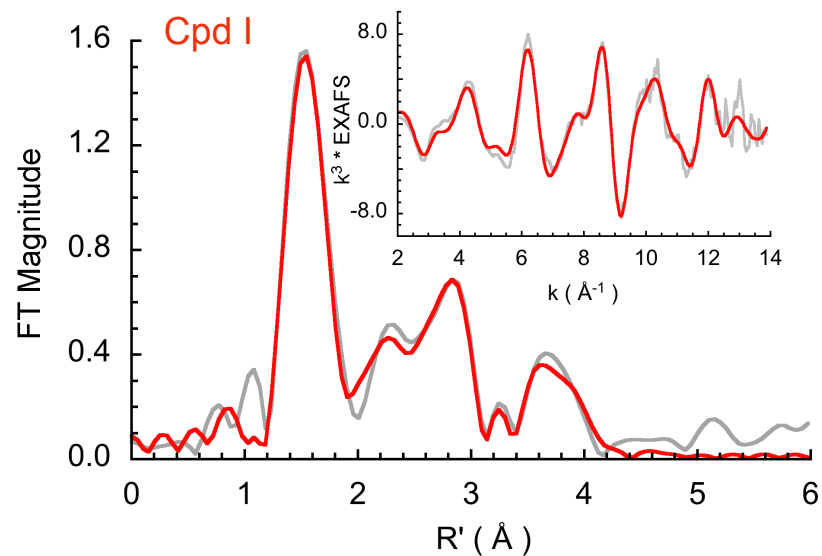
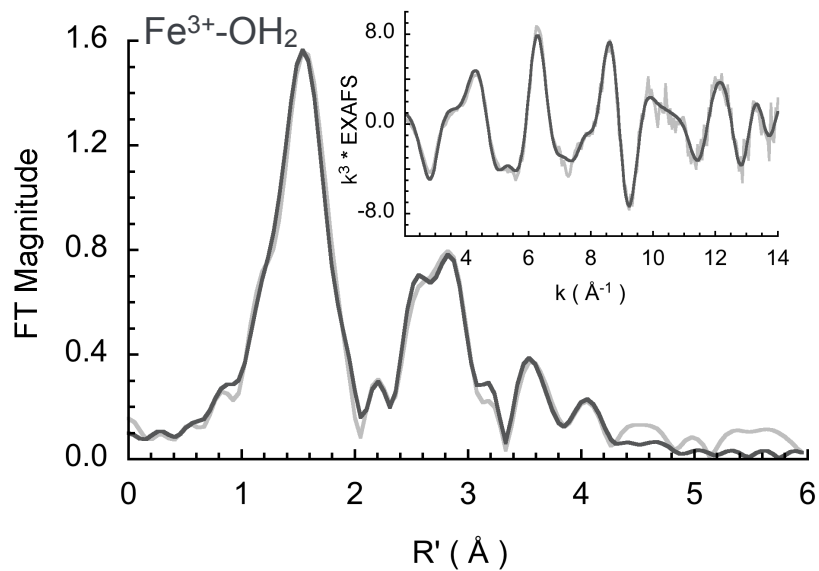
- > 1 eV shift in rising edge
- > intensity & energy of pre-edge

# Solution XAS & EXAFS on DypB

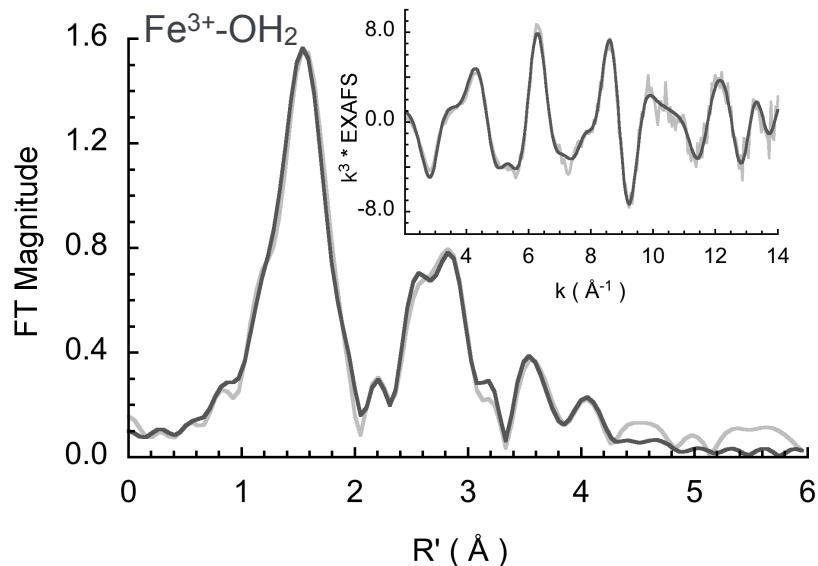


- ✓ > 1 eV shift in rising edge
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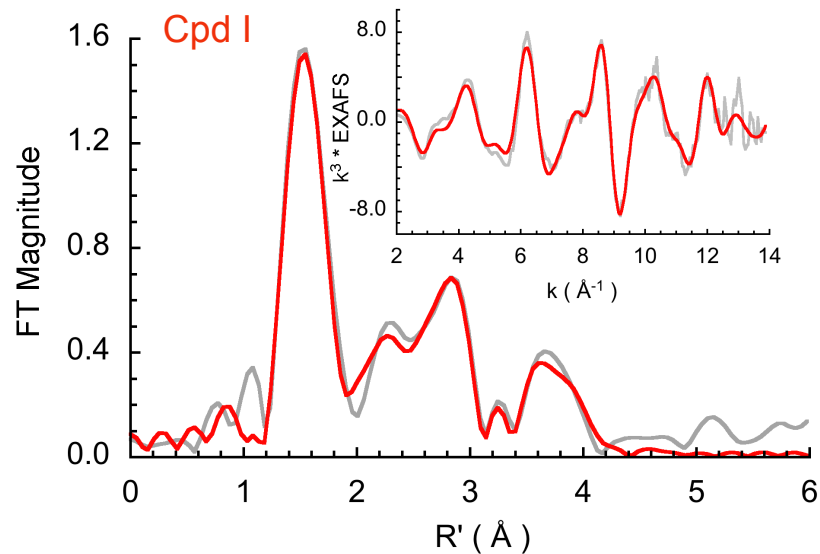
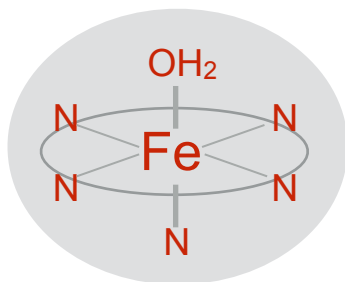
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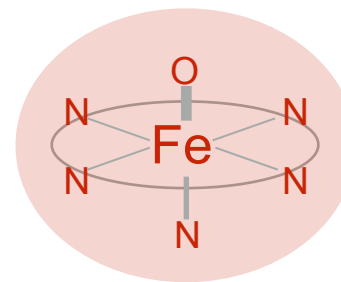
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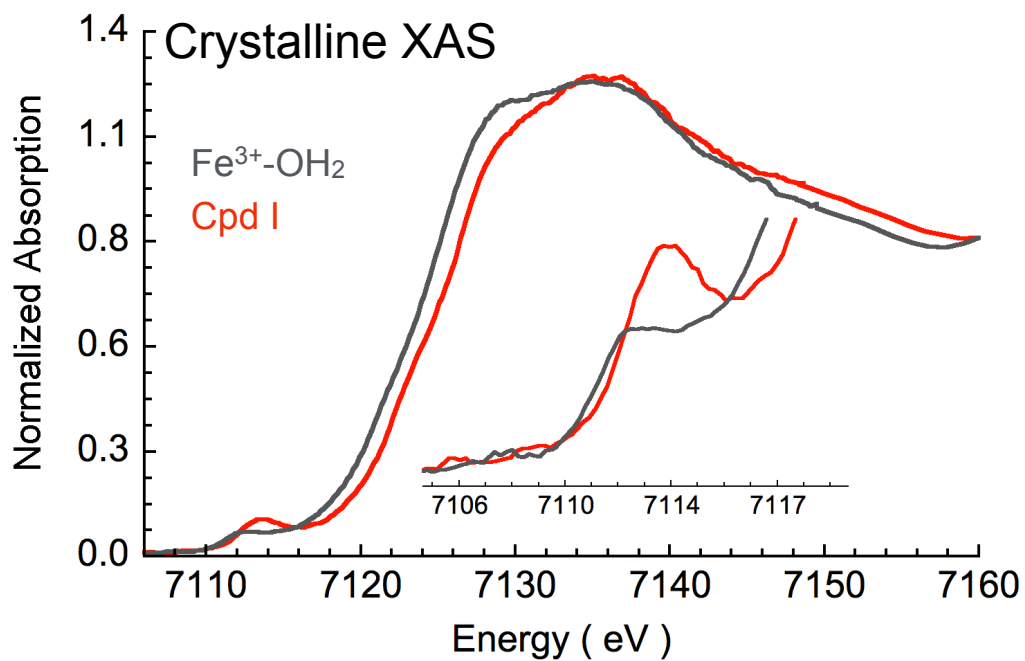
2 Fe-N 1.92  $\text{\AA}$ , 4 Fe-N 2.02  $\text{\AA}$



1 Fe-O 1.67  $\text{\AA}$ , 5 Fe-N 2.00  $\text{\AA}$

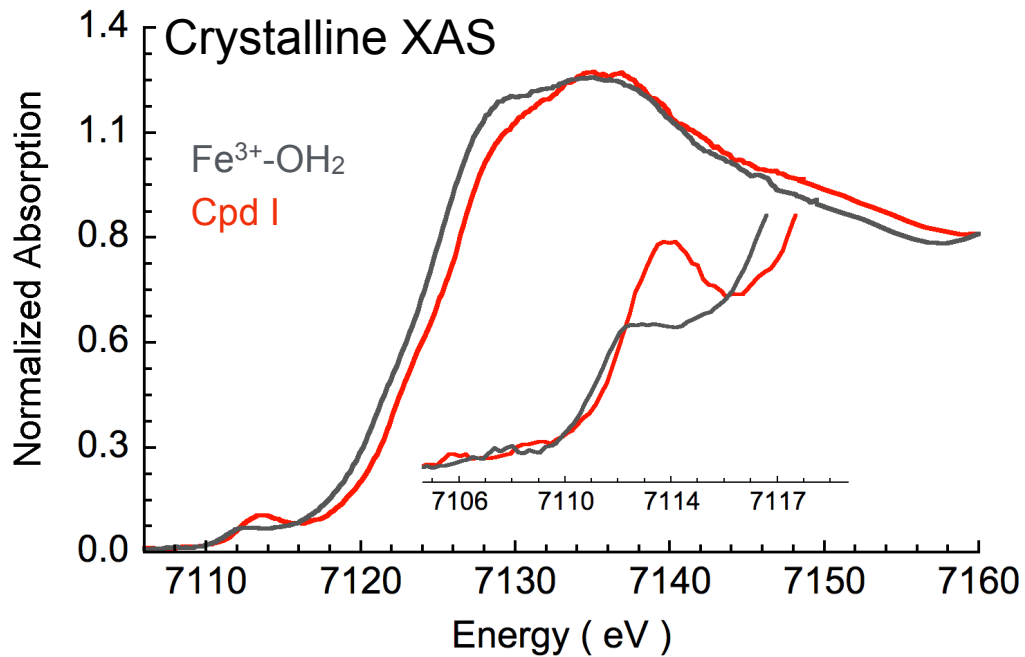


# Optimizing Crystallization Conditions



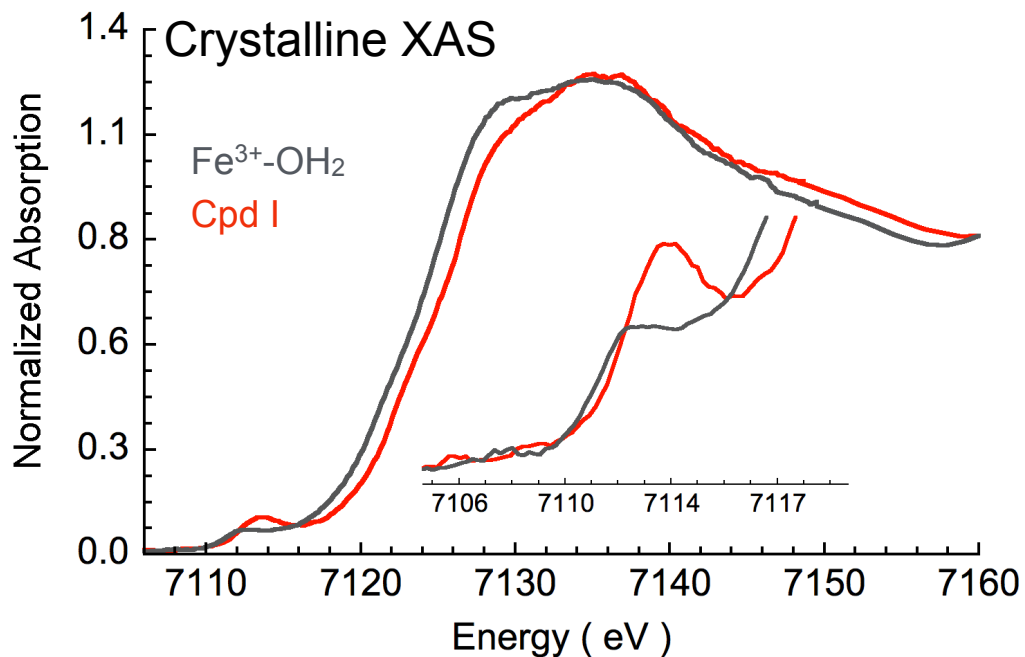


# Optimizing Crystallization Conditions



- ✓ > 1 eV shift in rising edge
- ✓ > intensity & energy of pre-edge
- ? *Some differences in solution & xtal*

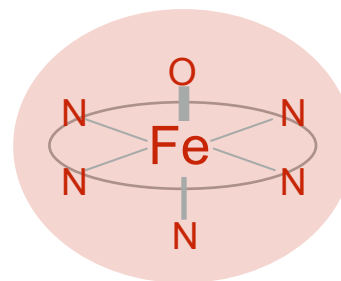
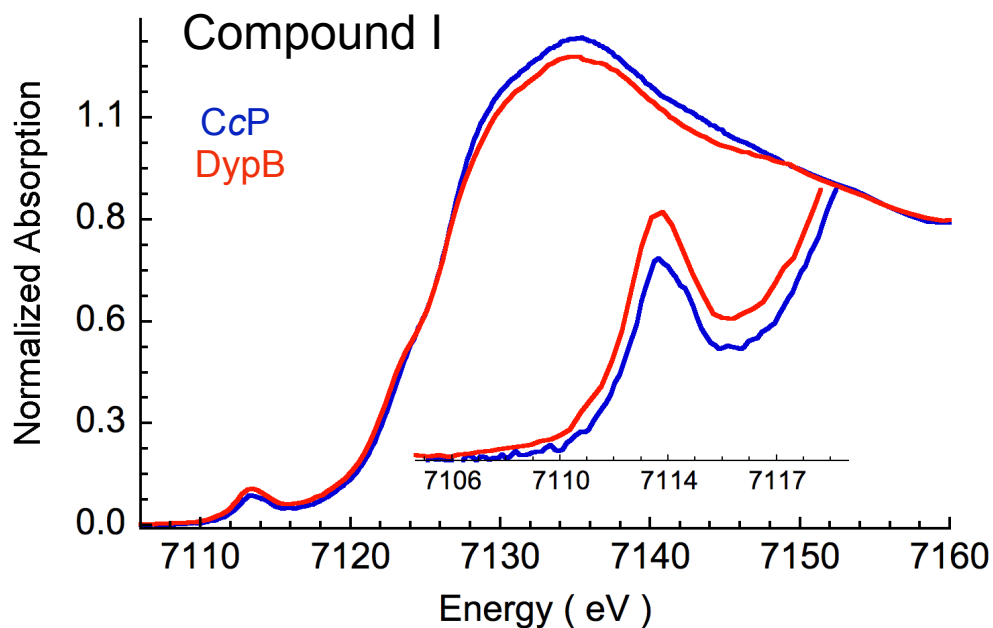
# Optimizing Crystallization Conditions



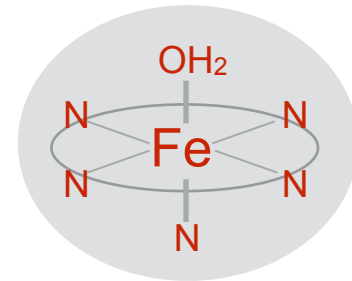
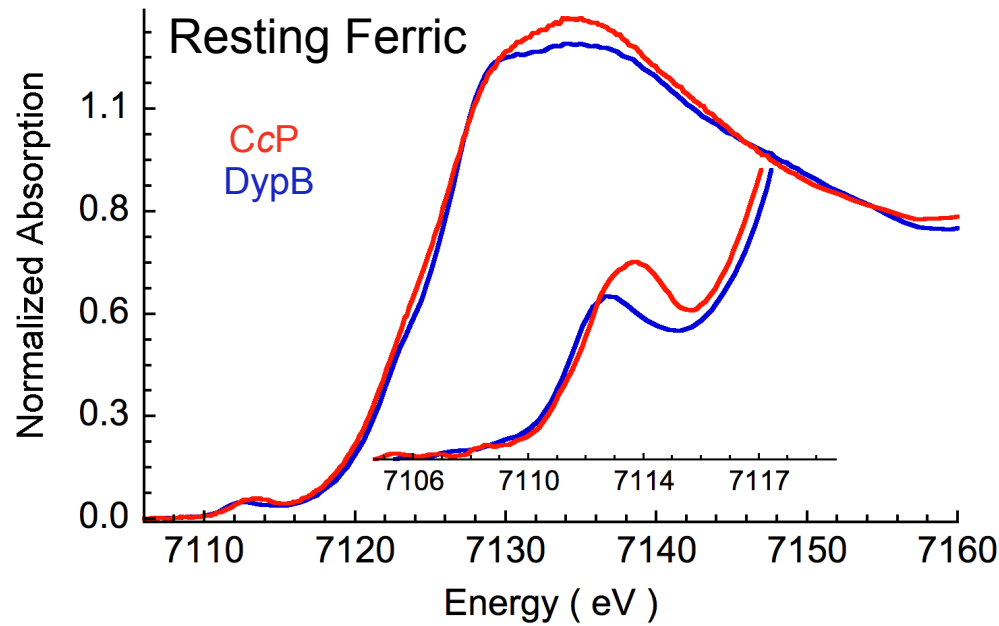
- ✓ > 1 eV shift in rising edge
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Electronic structure validation for crystallography.

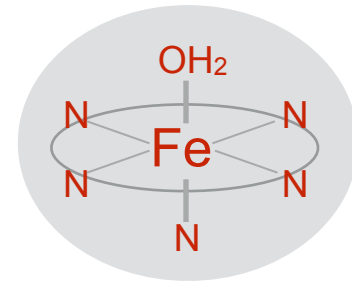
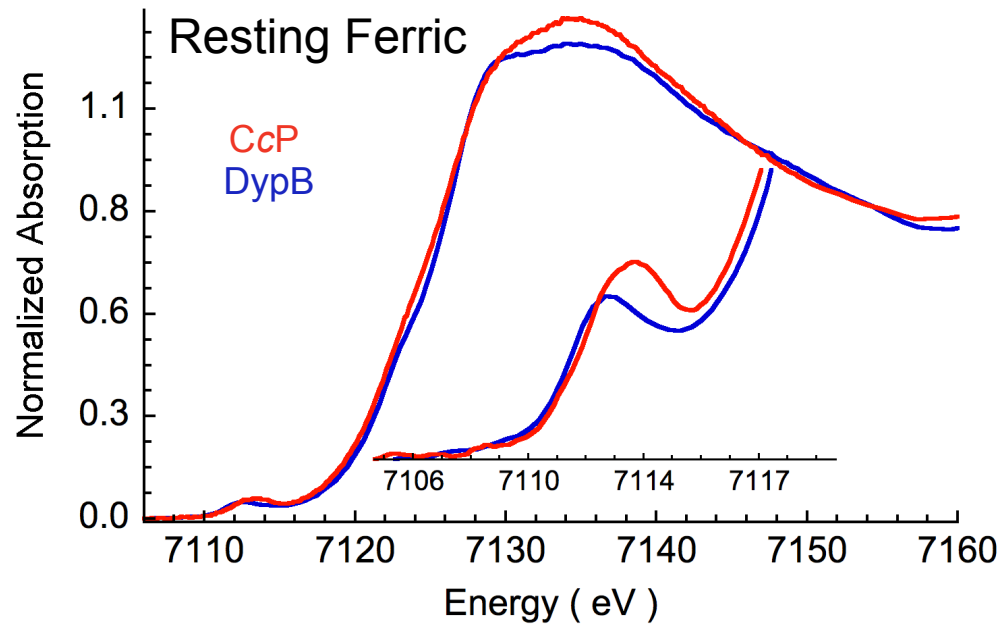
# Ongoing Work: Electronic Structure of DypB



# Ongoing Work: Electronic Structure of DypB



# Ongoing Work: Electronic Structure of DypB



- Why are the ferric forms of CcP and DypB different?
- What are the differences in ligand field that lead to differences in the pre-edges?
- Is it a first sphere or second sphere effect?

# Take Home Messages

- Biological EXAFS is a powerful technique that furnishes *atomic* resolution local structures of metalloprotein active site.
- XAS is a powerful technique to obtain valuable insights into the electronic structures of metalloproteins
- Solution and crystalline structures of metalloproteins may vary *intrinsically*.
- Researchers should feel encouraged to combine XAS and Crystallography, *routinely*.

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Thank You For Your Attention

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