

X-ray Absorption Edge

An XAS edge discontinuity results when a core electron absorbs energy equal to or greater than its binding energy.

Edges are labeled according to the shell the core electron originates from.









Pre-edge Analysis The Pre-edge energy position and intensity can be used to determine Pre-edge 1. Covalency &/or Bond Strength peak area: 3 2. Ligand Field 3. Effective Charge on S Normalized Absorption 1.5 0.5 In this Example: Pre-edge peak 1.5 Red is 3 times more intense than Black: area: Red probably has a stronger Metal-S overlap. Red pre-edge is higher in energy: Red probably has a stronger ligand field. 2468 2472 2476 Energy (eV) Applications of pre-edge: a) Covalency determination in Electron Transfer Proteins. b) Ligand-Metal Overlap estimation in systems with non-innocent ligands. c) Determination of oxidation state of the metal site (Indirect) d) Determination of oxidation state of S



Excellent for fingerprinting & speciation analysis in a sample containing a mixture of S containing species





- Spectral differencea are due to 0.02 A difference in the single bond S-O distances: 1.70 in ECS vs 1.72 in DMS
- Small changes in bonding can lead to large shifts in valence MO energy levels and hence strikingly different spectral shapes.



- Need some chemical information to perform speciation analysis.
- Or have an extensive database of standards to choose from.









The Calibration Issue

- No I1 or I2 = No Internal Calibration
- Calibration is achieved by measuring the standard before and after the sample.
- For S, the typically used calibrant is Na₂S₂O₃ (lowest energy peak at 2472.02 eV)
- Higher error in estimating true energy position

If the goal is to know small energy shift between spectra very accurately- the following method should be used:



The Calibration Issue	
Other calibration methods commonly used and associated errors	
Calibrationfilename2472.050SCALIB_053.0012473.506LCYST_054.0012473.498LCYST_054.0022473.483LCYST_054.0032473.475LCYST_054.0042473.453LCYST_054.0052472.000SCALIB_053.001	
Method	Error
Interpolation of energy shift between the 2 calibrants and applying a linear shift per scan.	Artificial broadening of the average spectrum
Using only 1 before-calibration scan and applying the energy shift to the first scan of data.	Error in energy position.
Using an average of the before and after calibrant and applying it to each spectrum.	Error in energy position if large variations in mono energy.

Sample Considerations

- Amorphous solid samples ground to a very small particle size. Conc > 100 ppm.
- Homogeneous solution samples. Conc > 5mM in S, 200 uL
- Whole samples. e.g: Leaves, wood, soil. etc. Specific sections of the sample can be targeted to see differences in speciation.
- Solid samples with high S concentrations should be applied as a thin layer.
- Solution samples have to be placed within thin x-ray transparent windows-(4-5um polypropylene or other S-free film)
- For quantitative analysis : Homogenous S site structure
- For speciation analysis : The sample and the standards should be measured under the same experimental condition.







Data Analysis

- Linear Combination Analysis (DATFIT)
- Peak Deconvolution Analysis (EDG_FIT, PEAKFIT)
- EXAFS Analysis
- Structure Determination using Near-edge Analysis (MXAN)
- •DFT calculation of electronic structure and simulation of spectra (STOBE)
- •DFT and TD-DFT methods to simulate XAS spectra (ORCA, Gaussian)

Linear Combination Analysis

- Program: DATFIT (Part of EXAFSPAK) or other peak fitting software
- Data: 2 Column data file. (Energy and background subtracted normalized data)
- Standards: A complete set of standard data on species expected to be similar to those in the unknown mixture





- Perform several fits by sequentially increasing number of standards.
- A best fit:

a) has least number of standards b) fit over the entire energy range c) makes chemical sense

• E.S.D: 3 times the value printed in DATFIT (if fit is very good).



Considerations

- Data and standards should be free of self absorption.
- Data and standards should be normalized to 1.00.
- Data and standards should have very near flat pre-edges and post-edges.
- Always have your chemists hat on when using linear combination analysis.

Peak Deconvolution Analysis

- Program: Edg_Fit (Part of EXAFSPAK) or other peak fitting software
- Data: 2 Column data file. (Energy and background subtracted normalized data)
- Information: Some idea about the origin of the different spectral features





• A best fit:

a) has least number of unjustified peaks b) fit over a reasonable eV range c) a good fit to the second derivative.

• Error bar:

Is obtained by estimating standard deviation among chosen best fits.





