Goldschmidt 2025 Abstract
https://doi.org/10.7185/gold2025.28482

A Computational Method for Comprehensive Analysis and Comparison of Metal Center Coordination Environments in Proteins

BENJAMIN I JELEN[1], SHAUNNA MORRISON[2] AND BETH CHRISTENSEN[1]

[1]Rowan University

[2]Carnegie Institution for Science

Protein metal binding sites enable a wide range of essential biological functions that are driven by the structure of the fold, interaction with other protein subunits, and the type of metal atom(s) bound. Investigating the evolution of proteins' structure and function, particularly metal binding folds, can reveal connections with changes in the geosphere through time. Here, we introduce the Coordination Sphere Analysis and Comparison (CSAC) workflow, a computational method designed to systematically analyze and compare metal-binding sites in 3D protein structures. CSAC enables high-throughput analysis of metal-binding coordination spheres across large datasets, identifying trends and significant differences between groups. Using Python-based scripts, the workflow integrates data from Protein Data Bank (PDB)[1] entries and computational predictions, allowing researchers to examine metal centers based on structural parameters, nearby residues, and calculated properties such as hydropathy and electronegativity. In a demonstration case, CSAC reveals a distinct shift in the hydropathy of iron-binding coordination environments between aerobic and anaerobic proteins. This trend, further explored through principal component analysis, shows a reduced use of cysteine in aerobic metal center binding, linking shifts in Earth's redox conditions to structural modifications in metalloproteins. The CSAC workflow, available under an open-access license, provides a tool for investigating metal coordination across proteins, supporting research in evolutionary biology, bioinorganic chemistry, and environmental science.

[1] Berman, Westbrook, Feng, Gilliland, Bhat, Weissig, Shindyalov & Bourne (2000), *Nucleic acids research* 28, no. 1: 235-242.

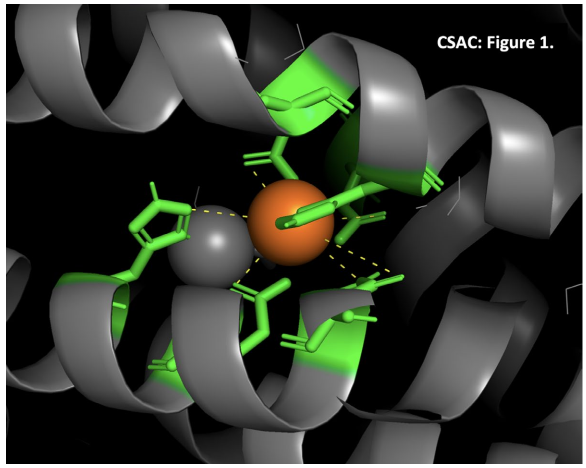

Figure 1: CSAC quickly analyzes and compares metal center environments across any custom set of protein structure files. Here, the Fe center (Orange) is coordinated by amino acid residues (green).