

MS25-P09 | STRUCTURE OF A NOVEL R2-LIKE LIGAND-BINDING OXIDASE REVEALED BY ELECTRON DIFFRACTION

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Electron diffraction (ED) has in recent years shown to be a promising method for protein structure determination when only micron-sized three-dimensional crystals are available that are beyond what can be resolved by conventional macromolecular X-ray crystallography (MX). However, up until now ED had only been applied to refine known protein structures that were already solved previously by MX. Here, we present the first unknown protein structure – a novel R2lox metalloenzyme – solved using ED. Despite encountering preferential orientation of the plate-like crystals, low signal-to-noise ratio, and a highly viscous sample environment, the structure could successfully be solved by molecular replacement using a search model of only 35% sequence identity. The resulting electrostatic scattering potential map at 3.0Å resolution was of sufficient quality to allow accurate model building and refinement. Our results illustrate that ED has the potential to become a widely applicable technique for structural biology, complementing MX when crystal volume is the limiting factor in structure elucidation.