In crystallo reactivity of model proteins functionalized with a dirhodium

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Paddlewheel dirhodium tetracarboxylates are metal compounds with a widespread catalytic activity, useful for the development of artificial metalloenzymes.<sup>1</sup> The interaction of  $Rh_2(AcO)_4$ , *cis*-Rh<sub>2</sub>(AcO)<sub>2</sub>(TFA)<sub>2</sub> and Rh<sub>2</sub>(AcO)(TFA)<sub>3</sub> (AcO<sup>-</sup>= acetate ion; TFA<sup>-</sup>=trifluoroacetate ion) with the model proteins hen egg white lysozyme (HEWL) and bovine pancreatic ribonuclease (RNase A) has been studied by X-ray crystallography in order to evaluate the effect of metal ligands in directing the interaction between metal complexes and proteins.<sup>2,3</sup>

Depending on the interacting protein, Rh<sub>2</sub>(AcO)<sub>4</sub> demonstrated a different behavior. Indeed, upon reaction with HEWL, Rh<sub>2</sub>(AcO)<sub>4</sub> completely breaks down: monometallic Rh centers are found to be placed close to the side chains of Arg14, His15 and Lys33, dimetallic Rh-Rh units with Rh-Rh distances between 2.3 and 2.5 Å bind the side chains of Asp18, Asp101, Asn93, and Lys96, while a dirhodium unit with a Rh-Rh distance of 3.2-3.4 Å is coordinated by the C-terminal carboxylate and the side chain of Lys13 at the interface between two symmetry-related molecules. On the contrary, when the metal compound reacts with RNase A, it preserves its paddle-wheel structure, interacting with the protein via coordination of the dirhodium center to the side chains of His105 and His119.<sup>4</sup> Unexpectedly, *cis*-Rh<sub>2</sub>(AcO)<sub>2</sub>(TFA)<sub>2</sub> and Rh<sub>2</sub>(AcO)(TFA)<sub>3</sub> also bind the side chains of His105 and His119 via axial coordination, losing trifluoroacetate ligands by hydrolysis.

The reactivity of the RNase A-bound dirhodium center toward imidazole and glycine has been also studied at solid state. Dirhodium tetracetate/RNase A adduct reacts with these two molecules, providing unexpected results: both imidazole and the amino acid replace an acetate ligand of the dirhodium center in place of the solvent molecule at the axial site (Figure 1).

Overall, these data provide interesting insights into the reactivity of dirhodium tetracarboxylates with proteins, suggesting useful indications for the design of new Rh-containing biomaterials with potential applications in the field of catalysis. Results also corroborate the idea that the chiral nature of the protein environment may affect the reactivity of a metal complex bound to a protein.

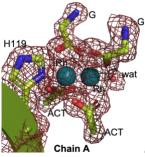


Figure 1. Product of the reaction of glycine (G) with the dirhodium tetracetate/RNase A adduct at crystal state.

## References

- [1] Popp B.V., Chen Z., Ball, Z.T. Sequence-specific inhibition of a designed metallopeptide catalyst. *Chem. Commun.* 2012; 48: 7492-7494.
- [2] Loreto D., Ferraro G., Merlino A. Unusual structural features in the adduct of dirhodium tetraacetate with lysozyme. *Int. J. Mol. Sci.* 2021; 22: 1496-1512.
- [3] Ferraro G., Pratesi A., Messori L., Merlino A., Protein interactions of dirhodium tetraacetate: a structural study. *Dalton Trans.* 2020; 49: 2412-2416.