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Středoevropský technologický institut, výzkumná skupina Chytré nanostroje Laboratoř metalomiky a nanotechnologií, Mendelova univerzita v Brně



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Hidden relationships between metalloproteins unveiled by structural comparison of their metal sites- review

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Abstrakt

Metalloproteins account for a substantial fraction of all proteins. They incorporate metal atoms, which are required for their structure and/or function. Here we describe a new computational protocol to systematically compare and classify metal-binding sites on the basis of their structural similarity. These sites are extracted from the MetalPDB database of minimal functional sites (MFSs) in metal-binding biological macromolecules. Structural similarity is measured by the scoring function of the available MetalS² program. Hierarchical clustering was used to organize MFSs into clusters, for each of which a representative MFS



identified. The comparison of was all representative MFSs provided a thorough structure-based classification of the sites analyzed. As examples, the application of the proposed computational protocol to all hemebinding proteins and zinc-binding proteins of known structure highlighted the existence of subtypes, validated structural known evolutionary links and shed new light on the occurrence of similar sites in systems at different evolutionary distances. The present

approach thus makes available an innovative viewpoint on metalloproteins, where the functionally crucial metal sites effectively lead the discovery of structural and functional relationships in a largely protein-independent manner. doi:10.1038/srep09486

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