Poster Presentation

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Conservation of cofactor pockets in proteins

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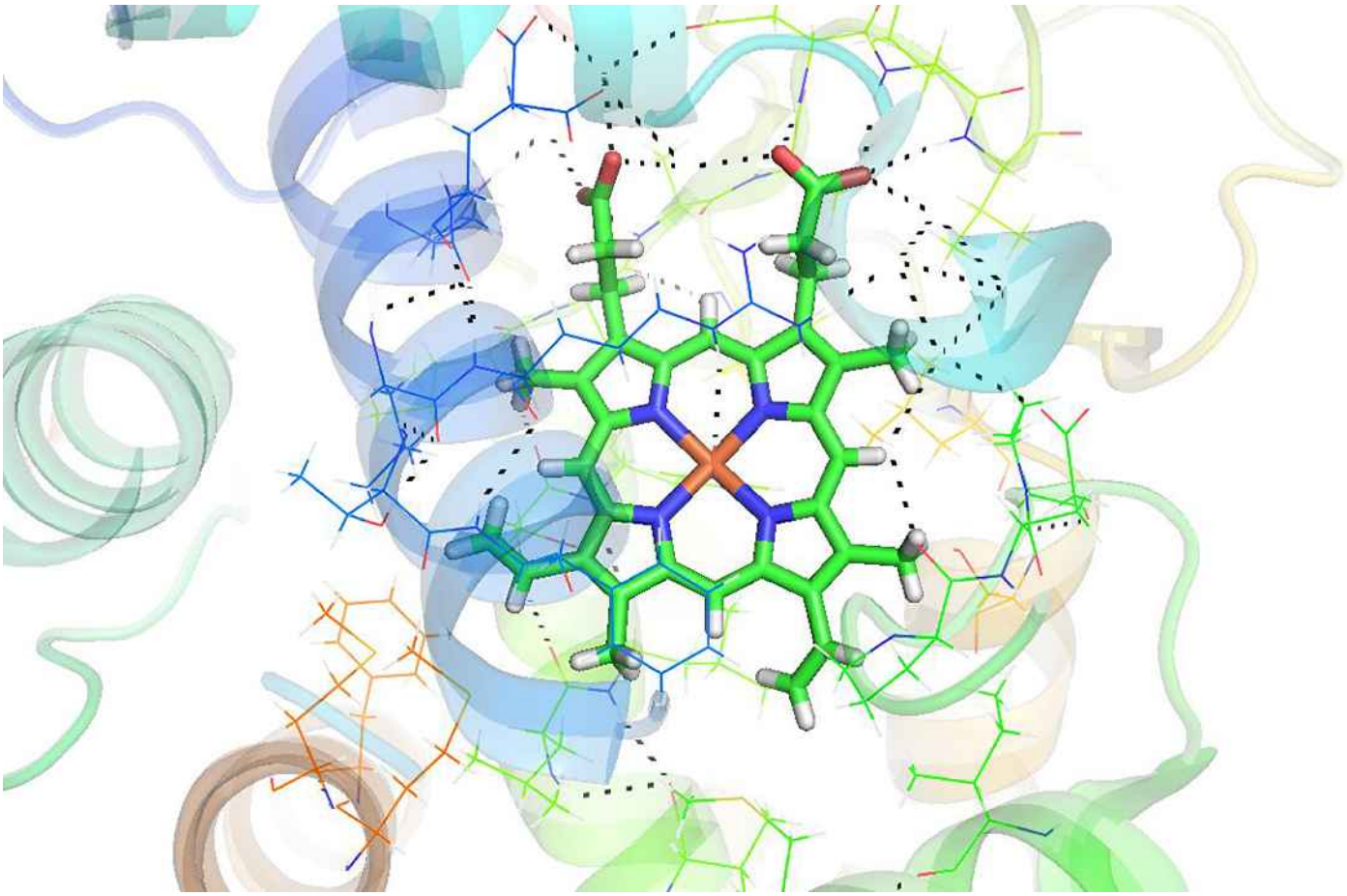
Enzymes, organic cofactors and metal ions are crucial for many biochemical reactions for catalysis. Nearly half of all enzyme reactions are catalyzed by cofactors. So far a systematic assessment of the enzyme residues interacting with organic enzyme cofactors in biocatalysts has not been performed. Here, we analyze the environment, physicochemical nature and pockets of thirty organic cofactors. The cofactor pocket and residues lining it share a remarkable degree of structural convergence despite the rest of the protein having different three-dimensional folds and different enzymatic functions. There is a common network of electrostatic and hydrophobic interactions stabilizing the cofactors. Functional groups of cofactors have complementary charge interactions with polar residues in the active site. Rings are positioned in snug nonpolar pockets either completely or partially. Distance matrices have been derived for each of the cofactor pockets based on the protein residues interacting with functional groups. These distance matrices and the representative pocket sizes of cofactor can be used as a fingerprint to identify a cofactor pocket. Examples of proteins from the PDB classified as with unknown function have been screened for the derived cofactor pocket criteria.



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