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Title (English)

Peroxidases: A computational study of ligand binding and enzyme kinetics

Title (Swedish)

Abstract

Heme-peroxidases can, from their intermediate states, compounds I and II (co I and II), oxidise several aromatic compounds. This work details computational docking results of the indoles melatonin and serotonin to structural models of ferric, co I and co II states of horseradish peroxidase (HRP) and myeloperoxidase (MPO). The results were interpreted to examine to what extent binding arrangement differences could explain differences in reduction reaction rates between HRP and MPO. The resulting docked ligands were found at the heme edge, proposed as the reactive site for co I and II reduction. Ligands docked to MPO had closer contacts with the heme edge than those of HRP. More space and favourable heme contacts are provided to indoles by MPO than by HRP. These observations could explain the higher reaction rates and lower substrate specificity of MPO co I relative to HRP co I, but not the remarkably small reaction rate differences between HRP and MPO co II. This inability could stem from conformation differences between MPO co I and co II not known today.

Keywords

Computer docking, horseradish peroxidase, myeloperoxidase, reaction rate, conformation

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