

Homology modelling and ligand binding study of human cytochrome P4501A2

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Cytochrome P450 (CYP) is a family of enzymes responsible for organism detoxification[1][2]. However, some of the members of the CYP1A subfamily also catalyse the activation of heterocyclic amines (HAs), present in cooked meat, to carcinogenic compounds which have been shown to increase the risk of breast, colorectal and lung cancer[3][4].

In this work, we built models for the wild-type and some mutant enzymes of human cytochrome P450 1A2 using X-ray structures of mammalian CYPs as templates. We intend to relate the different catalytic properties the mutants and the wild-type concerning the metabolism of several experimentally tested substrates[5][6][7] with the relative binding free energy of the complexes they form, calculated using molecular mechanics and classical continuum electrostatics[8].

References

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