Biochem. Cell. Arch. Vol. 11, No. 1, pp. 49-55, 2011 | *ISSN 0972-5075*

HOMOLOGY MODELING OF CYP1A1, CYP1B1 AND ITS SUBSEQUENT MOLECULAR DOCKING STUDIES WITH RESVERATROL AND ITS ANALOGUES USING AUTODOCK TOOLS 4.0

M. Kalim Ahmad Khan, Salman Akhtar[1] and Jamal M. Arif[*]

Department of Biotechnology, Microbiology and Bioinformatics, Integral University, Lucknow - 226 026, India.
[*]University of Hail, P.O. Box 2440, Hail, KSA.
e-mail: jmarif@gmail.com; arifjm@yahoo.com; j.arif@uoh.edu.sa

(Accepted 31 January 2011)

ABSTRACT – CYP1A1 and CYP1B1 are the inducible forms of cytochrome P450 expressed in extrahepatic tissues, which are responsible for the biotransformation of numerous exogenous compounds including carcinogens, xenobiotics and drugs. To test the interaction of exogenous compounds and CYP1A1 and CYP1B1, the unavailability of 3-D structures prompted us to construct them. Three-dimensional structures of CYP1A1 and CYP1B1 were constructed by using the software Modeller 9v9, taking the crystal structure of CYP1A2 (PDB_ID: 2HI4) as template and submitted the obtained model in the Protein Model Database (PMDB_ID of CYP1A1: PM0076866, PMDB_ID of CYP1B1: PM0076868). The validity of the CYP1A1 and CYP1B1 models was evaluated using PROCHECK, ERRAT, PROVE and WHATCHECK from Structural Analysis and Verification Server which indicated that the constructed models are respectively reliable with 95.1 % and 91.5% of the residues in the core regions of the Ramachandran's plot. The obtained models were tested and validated with Resveratrol and its analogues. The current models of CYP1A1 and CYP1B1 resulted in complete agreement with the wet lab data from these compounds. These structures will be extremely useful for in silico screening study of any compounds expected to be metabolized by these CYP isozymes.

Key words : CYP1A1, CYP1B1, Homology modeling, AutoDock Tools, Resveratrol.