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Biochemical and Biophysical Research Communications 357 (2007) 330

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Corrigendum

Corrigendum to “3D structure modeling of cytochrome P450 2C19 and its implication for personalized drug design” [Biochem. Biophys. Res. Commun. 355 (2007) 513–519]

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On p. 514, the second paragraph of the section titled “Modeling the 3D structure of CYP2C19” should read: “The sequence of CYP2C9 contains 492 amino acids and the sequence of CYP2C19 contains 490 amino acids. The sequence alignment between the CYP2C19 and CYP2C9 was performed with the in-house program SAMM (Shanghai Molecular Modeling). The identity score strongly depended on how the alignment was made. A score of 52% was obtained when the alignment was made under the constraint imposed by the secondary structure. When such a constraint was relaxed and the alignment was based purely on sequences, the score increased to 91%, which was very close to the score obtained with the NCBI BLAST (http://www.ncbi.nlm.nih.gov/blast/). As with the treatment in [16,20], we took the result obtained with the structural constraint. The result of alignment is shown in Fig. 1, where the segments (residues 1–10 and 480–490) for the CYP2C19 and the segment (residues 1–25) for the CYP2C9 are not shown because they are outside the protease domains. The identity of the two sequences is about 52%.”

On p. 515, the third line of the legend to Fig. 1 should read: “The identity of the two sequences is about 52%.”

Acknowledgment

We are grateful to Dr. Patrick Dansette for his valuable comments.

DOI of original article: 10.1016/j.bbrc.2007.01.185.

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doi:10.1016/j.bbrc.2007.03.111