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Corrigendum

Corrigendum to “A three-dimensional pharmacophore model for dipeptidyl peptidase IV inhibitors” [Eur. J. Med. Chem. 43 (2008) 1603–1611]

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The author regrets to note that the incorrect Fig. 4 was published. The correct Fig. 4 is reproduced below.

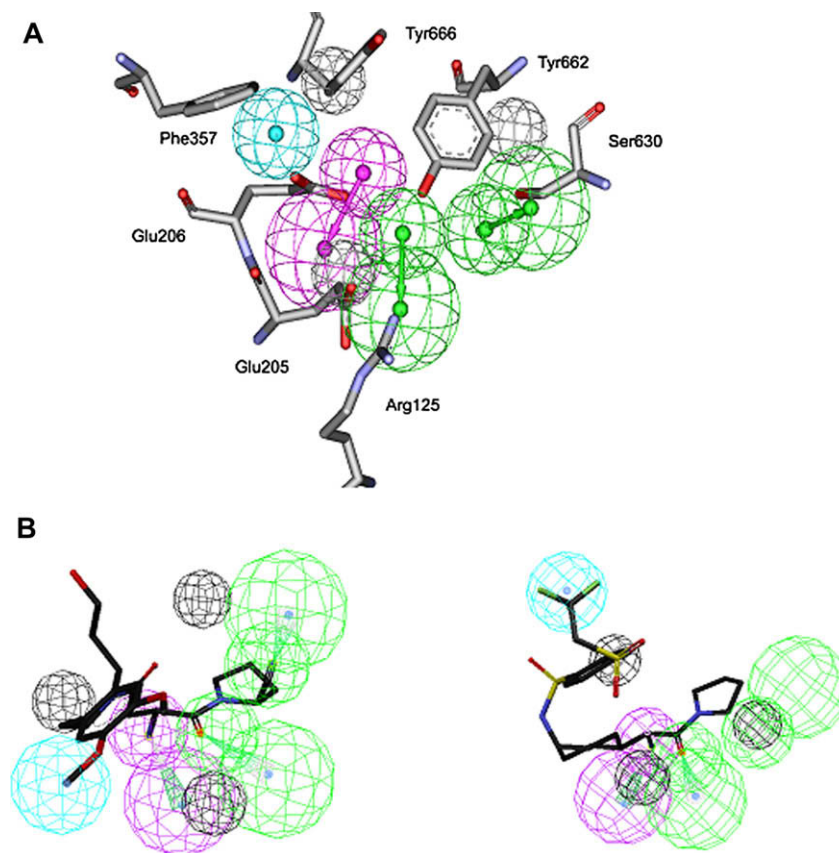


Fig. 4. Mapping of Hypo1 to protein structure and selected compounds. (A) Mapping of Hypo1 onto the DPP-IV active site. The chemical features of Hypo1 were complementary to DPP-IV active site. The two H-bond acceptor and one H-bond donor features made close contact to the opposite donor residues Arg125 and Ser630, and acceptor residues Glu205 and Glu206. The hydrophobic feature was close to Phe357. Two of the three excluded volumes were mapped to the residues Tyr662 and Tyr666 and the third one located between Arg125 and Glu205. Protein residues are shown in grey, and the H-bond acceptor, donor and hydrophobic features of Hypo1 are shown in green, magenta, cyan and black individually. (B) Mapping of Hypo1 to selected compounds. The compounds are shown in grey and the Hypo1 features colors are the same as shown in (A). (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

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