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ERRATUM

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Combined 3D-QSAR, Molecular Docking, and Molecular Dynamics Study on Piperazinyl-Glutamate-Pyridines/Pyrimidines as Potent $P2Y_{12}$ Antagonists for Inhibition of Platelet Aggregation

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This Erratum is to modify the list of authors and affiliations shown above, the Acknowledgment, and one other section of text.

Page 2563. After **Molecular Docking**, the first sentence should be the following: Docking simulations of piperazinyl-glutamate-pyridines/pyrimidines into the $P2Y_{12}$ binding pocket were performed using the Surflex-dock module (V 2.51) of another advanced version of SYBYL package (x 1.1) in this study.

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