Additions and Corrections

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Shaomeng Wang, George W. A. Milne,* Marc C. Nicklaus, Victor E. Marquez, Jeewoo Lee, and Peter M. Blumberg: Protein Kinase C. Modeling of the Binding Site and Prediction of Binding Constants.

Page 1326. The second and third sentences should read as follows:

The structure–activity studies for PKC together with the modeling studies have focused attention on the ketone at C_3, the hydroxyl groups at C_4, C_9, and C_{20}, and a hydrophobic domain as probable elements of the phorbol pharmacophore, although contributions of the ester oxygens at C_{12} and C_{13} have also been proposed.[10–17] Of the various models, the three-point pharmacophore made up of the ketone oxygen at C_3, and the hydroxyl groups at C_9 and C_{20} together with a lipophilic domain was adopted as the starting point for the current report. This model used as a starting point is that proposed by Rando et al.[10,16]