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Short communication

Comment on 'Comment on "Another look at the molecular mechanism of the resistance of H5N1 influenza A virus neuraminidase (NA) to oseltamivir (OTV)"'

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We have responded [1] to the comment of Rungrotmongkol et al. [2] on our previous publication [3] and we have elucidated what has been done from a modelling point of view in order to account for any incorrect, if any at all, choice of starting experimental N1 NA structure [1]. In our original study the 'open' conformation of the crystal structure of the complex of H5N1 NA with OTV (PDB ID: 2HU0) has been used as the starting point and the effects of mutations at the position His274 have been investigated [3]. Rungrotmongkol et al. [2] have questioned the relevance of our modelling [3] by emphasizing both that an improper initial structure (2HU0.PDB) has been used and that a 'closed' conformation of the N1:OTV co-crystal structure is more appropriate for such studies. We would like to point out that the most recent study by Wang et al. [4] has concluded that the 'open' form crystal structure of 2HU0 provides a novel and reliable structural basis for rational drug design against influenza virus.

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